

(TM)

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Sep 2 11:11:45 1999; Maspar time 8.17 Seconds
314.778 Million cell updates/sec
Tabular output not generated.

Title: >US-08-599-226-2
Description: (1-121) from US08599226.pep
Perfect Score: 872
Sequence: 1 EVGLVESGGGLVPGKSLRL.....LSTRASSLDVWGQCTIVTVSS 121

Scoring table:
PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq35
1:part1:2:part2:3:part3:4:part4:5:part5:6:part6:7:part7
8:part8:9:part9:10:part10:11:part11:12:part12:13:part13
14:part14:15:part15:16:part16:17:part17:18:part18
19:part19:20:part20:21:part21:22:part22:23:part23
24:part24:25:part25:26:part26:27:part27:28:part28
29:part29:30:part30:31:part31:32:part32:33:part33
34:part34:35:part35:36:part36:37:part37:38:part38
39:part39

Statistics: Mean 30.271; Variance 165.610; scale 0.183

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	872	100.0	121 27	W27569	Anti-TNF-alpha antibo	1.84e-56
2	718	82.3	241 26	W24063	Human WSX receptor ag	1.29e-44
3	706	81.0	121 18	R88848	Human antibody IM9 he	1.07e-43
4	698	80.0	248 3	R20059	Recombinant scd3d he	4.39e-43
5	698	80.0	475 3	R20057	Heavy chain of 3d6 an	4.39e-43
6	686	78.7	116 24	W19880	CEA-specific antibody	3.64e-42
7	686	78.7	121 11	R54058	Anti-cancer monoclonal	3.64e-42
8	686	78.7	140 11	R54063	Anti-cancer monoclonal	3.64e-42
9	686	78.7	140 11	R29578	Clin-1gg gamma.	3.64e-42
10	679	77.9	123 12	R66303	Human immunoglobulin	1.25e-41
11	678	77.8	119 19	R95216	Human foetal immunogl	1.49e-41
12	676	77.5	123 23	W08582	Human antibody C4.1 h	2.12e-41
13	675	77.4	122 10	R50311	Humanised heavy chain	2.53e-41
14	673	77.2	120 18	R52064	Heavy chain variable	3.60e-41
15	673	77.2	184 20	W03726	Humanised MAb 39-1.10	3.60e-41
16	672	77.1	115 4	R22571	Heavy chain VHS.5 fro	4.29e-41

17	670	76.8	506 2	R12134	ORF 3 of 4B9 human MA	6.10e-41
18	669	76.7	123 24	W15534	Anti-TGF beta-1 scfv	7.28e-41
19	667	76.5	120 29	W23952	Chimeric humanised Mu	1.03e-40
20	667	76.5	122 10	R50312	Humanised heavy chain	1.03e-40
21	667	76.5	240 29	W23954	Chimeric humanised Mu	1.03e-40
22	666	76.4	139 13	R70471	Humanised anti-KC-4 a	1.23e-40
23	666	76.4	139 10	R52823	Humanised murine KC-4	1.23e-40
24	665	76.3	122 10	R50315	Humanised heavy chain	1.47e-40
25	665	76.3	141 24	W24984	Monoclonal antibody P	1.47e-40
26	665	76.3	141 20	W01522	Monoclonal antibody P	1.47e-40
27	664	76.1	123 24	W15535	Anti-TGF beta-1 scfv	1.75e-40
28	662	75.9	120 25	W27553	Human Ab heavy chain	2.50e-40
29	662	75.9	281 25	W27560	Consensus single chain	2.50e-40
30	660	75.7	117 18	R52065	Heavy chain variable	3.55e-40
31	659	75.6	143 10	R54047	Sequence of the VIRE	4.23e-40
32	659	75.6	464 3	R15049	CD4-specific CDR-grat	4.23e-40
33	658	75.5	117 17	R52053	Heavy chain variable	5.04e-40
34	658	75.5	122 6	R30773	Consensus humanised m	5.04e-40
35	657	75.3	119 4	R23739	Recombinant heavy cha	6.01e-40
36	657	75.3	119 8	R41721	Aglycosylated antibod	6.01e-40
37	657	75.3	134 24	W16541	Abortion related foet	6.01e-40
38	654	75.0	118 20	W06208	Xenograft antibody ID	1.02e-39
39	653	74.9	119 30	W47586	Human hBR96-2A heavy	1.22e-39
40	653	74.9	121 29	W47417	Heavy chain variable	1.22e-39
41	653	74.9	130 29	W47581	Human monoclonal anti	1.22e-39
42	652	74.8	118 32	W57591	Chimeric antibody aga	1.45e-39
43	652	74.8	121 25	W16648	Anti-cancer specific	1.45e-39
44	652	74.8	137 32	W57603	Chimeric antibody fra	1.45e-39
45	652	74.8	309 39	W83322	Single chain Apo-2 an	1.45e-39

ALIGNMENTS

RESULT	1
ID	W27569 standard; Protein; 121 AA.
AC	W27569;
DT	19-MAR-1998 (first entry)
DE	Anti-TNF-alpha antibody heavy chain variable region.
KW	Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
KW	heavy chain; variable region; inhibition;
KW	treatment; sepsis; disease; autoimmune disease; infectious disease;
KW	malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW	cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW	bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW	keloid formation; scar tissue formation; pyrexia; HIVEC;
KW	periodontal disease; obesity; radiation toxicity;
KW	endothelial cell leukocyte adhesion molecule-1;
KW	human umbilical vein endothelial cell.
OS	Homo sapiens.
PN	W09729131-AL.
PD	14-AUG-1997.
PF	10-FEB-1997; U02219.
PR	25-NOV-1996; US-031476.
PR	09-FEB-1996; US-599226.
PA	(BADI) BASF AG.
PI	Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labrovsky B,
PI	Markovich JA, McGulness BT, Roberts AJ, Sakorafas P,
PI	Salfield JC, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR	WPI; 97-415302/38.
DR	N-PSDB; T88404.
PT	High affinity antibodies against human TNF alpha - useful to inhibit
PT	TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS	Claim 16; Page 76; 10pp; English.
CC	The present sequence is a novel anti-human tumour necrosis
CC	factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region.
CC	The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC	less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC	less (both determined by surface plasmon resonance), and
CC	neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC	L939 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC	inhibits TNF-alpha activity, can be used to treat sepsis,
CC	autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC	spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

instead

sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The CC also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).

Sequence 121 AA:

Query Match 100.0%; Score 872; DB 27; Length 121;
Best Local Similarity 100.0%; Pred. No. 1,846-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EVQLVESGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSATITWNSGHDY 60
1 EVQLVESGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSATITWNSGHDY 60
61 ADSVGRFTISRDNKNSLYLQMNSLRADDTAVYCAKVSYSTASSLDYWGQGLVTVS 120
121 s 121

Db 121 s 121
121 s 121

RESULT 2

ID W24063 standard; Protein: 241 AA.

AC W24063;

DT 17-MAR-1998 (first entry)

DE Human MSX receptor agonist antibody clone #17.

KW Human: MSX receptor; clone #17; identification: purification;

KW ligand: activator; antibody; agonist; proliferation; obesity;

KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;

KW Type II diabetes; polycystic ovarian disease;

KW cardiovascular disease; osteoarthritis; dermatological disorder;

KW hypertension; insulin resistance; hypercholesterolemia;

KW hypertriglyceridaemia; cancer; cholelithiasis.

OS Homo sapiens.

PN WO9725425-A1.

PD 17-JUL-1997.

PF 07-JAN-1997; U00325.

PR 20-JUN-1996; US-667197.

PR 08-JAN-1996; US-585005.

PA (GENE) GENENTECH INC.

PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

PI Rodrigues ML;

PI WPI: 97-372864/34.

PT MSX receptor and related antibodies and ligands - used to develop products for diagnosis and therapy, e.g. for improving haematopoiesis or for treating tumours

PS Example 14, Pages 122-123; 21pp; English.

CC The present sequence is an agonist antibody clone to the human MSX receptor, which can be used to identify and purify ligands and

CC activators. An anti-MSX receptor antibody can be used as an agonist

CC to activate the MSX receptor, leading to enhanced proliferation or

CC differentiation of a cell expressing the MSX receptor. It can also

CC be used to decrease body weight and/or fat-depot weight and/or food

CC intake in an obese mammal. MSX receptor ligands can be used to

CC enhance proliferation or differentiation of lymphoid, myeloid or

CC erythroid blood cell lineages. This is useful when a mammal,

CC especially a human, is suffering from decreased blood cell levels,

CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone

CC marrow transplantation therapy. It can also be used to repopulate

CC blood cells in a mammal. The products can also be used to treat,

CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,

CC polycystic ovarian disease, cardiovascular diseases,

CC osteoarthritis, dermatological disorders, hypertension, insulin

CC resistance, hypercholesterolemia, hypertriglyceridaemia, cancer

CC and cholelithiasis.

CC Sequence 241 AA:

Query Match 82.3%; Score 718; DB 26; Length 241;
Best Local Similarity 82.6%; Pred. No. 1,296-44;
Matches 100; Conservative 11; Mismatches 8; Indels 2; Gaps 2;

Db 1 GYRLVGGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSATITWNSGHDY 60
1 GYRLVGGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSATITWNSGHDY 60
61 ADSVGRFTISRDNKNSLYLQMNSLRADDTAVYCAKVSYSTASSLDYWGQGLVTVS 118
121 s 119

Db 61 ADSVGRFTISRDNKNSLYLQMNSLRADDTAVYCAKVSYSTASSLDYWGQGLVTVS 120
121 s 121

Db 121 s 121

RESULT 3

ID R88848 standard; Protein: 121 AA.

AC R88848;

DT 10-OCT-1996 (first entry)

DE Human antibody IM9 heavy chain variable region.

KW Heavy chain: variable region; human; plasmacytoma; antibody;

KW IM9; construction: CDR switched variable light chain region;

KW kappa-body fragment; in vitro; in vivo; diagnosis; therapy;

KW naked antibody; radioimmunotherapy; radioimmunodiagnosis;

KW radioimmunometric assays; ELISA; immunohistochemical;

KW cell line; complementarity determining region.

OS Homo sapiens.

PN WO9606625-A1.

PD 07-MAR-1996.

PF 25-AUG-1995; U10791.

PR 26-AUG-1994; US-296625.

PA (EHL) Lilly & CO ERI.

PI Ili CR, Ludwig JR, Ratchachalam R;

PI WPI: 96-160137/16.

PI N-PEDB: T12815.

PT Recombinant antibody comprising CDR-switched light chain variable

PT region - having VL domain framework and VH domain CDRs, useful in

PT radioimmunotherapy, ELISA assays, etc.

PS Example 2, Page 66; 162pp; English.

CC The present sequence is the heavy chain variable (VH) region

CC of the human plasmacytoma cell line IM9 antibody (Ab), IM9,

CC which was used in the construction of a CDR switched variable

CC light chain (VL) region (CSVL) Ab, or kappa-body fragment. A CSVL

CC comprises at least 1 VL region with 3 CDR, where 1 or more of the

CC CDR is derived from the corresponding CDR of a VH region of 1

CC (donor) Ab, and 4 framework (FW) regions where 1 or more of the

CC regions is derived from the corresponding FW region(s) from the VL

CC region of the same or different (acceptor) Ab.

CC The CSVL Ab, or kappa-body fragment can be used in vitro and

CC in vivo diagnostic and therapeutic applications, including naked Ab

CC therapy, radioimmunotherapy (i.e. when fused to a chelating peptide

CC incorporating yttrium-90 as the therapeutic radionuclide), in vivo

CC radioimmunodiagnosis, in vitro radioimmunometric assays, ELISA

CC and immunohistochemical applications.

CC Sequence 121 AA:

Query Match 81.0%; Score 706; DB 18; Length 121;
Best Local Similarity 77.7%; Pred. No. 1,076-43;
Matches 94; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Db 1 EVQLVESGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSATITWNSGHDY 60
1 EVQLVESGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSATITWNSGHDY 60
61 ADSVGRFTISRDNKNSLYLQMNSLRADDTAVYCAKVSYSTASSLDYWGQGLVTVS 120
121 s 121

Db 61 ADSVGRFTISRDNKNSLYLQMNSLRADDTAVYCAKVSYSTASSLDYWGQGLVTVS 120
121 s 121

Db 121 s 121

CA 2

QY 121 S 121

RESULT 4
ID R20059 standard: Protein: 248 AA.AC R20059;
DE 25-MAR-1992 (first entry)
KM Recombinant sc3d6 anti-HIV gp160 antibody.
KM Plasmid pUC3d6HC; human immunodeficiency virus; AIDS;
OS Complementarity determining region.
FH Homo sapiens.

FH Key Location/Qualifiers

FT region 2..31 /label= Framework_1_heavy_chain

FT region 32..36 /label= Framework_1_heavy_chain

FT region 37..50 /label= CDR_1_heavy_chain

FT region 51..67 /label= Framework_2_heavy_chain

FT region 68..99 /label= CDR_2_heavy_chain

FT region 100..116 /label= Framework_3_heavy_chain

FT region 117..127 /label= CDR_3_heavy_chain

FT region 128..142 /label= Framework_4_heavy_chain

FT region 143..165 /label= linker

FT region 166..176 /label= Framework_1_light_chain

FT region 177..191 /label= CDR_1_light_chain

FT region 192..203 /label= Framework_2_light_chain

FT region 204..235 /label= CDR_2_light_chain

FT region 236..242 /label= Framework_3_light_chain

FT region 243..253 /label= CDR_3_light_chain

FT region /label= Framework_4_light_chain

FT region /label= Framework_4_light_chain

FT region /label= Framework_4_light_chain

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FT region /label= Framework_4_light_chain

FT region /label= Framework_4_light_chain

CDR3

QY 61 ADSVEGRFTISRDNKNSLYLQNSLRPAEDTAVYCAKV-SYLSTAS--SLDY--WGOGT 115

Db 122 mvtvss 127
QY 116 LVTVSS 121RESULT 5
ID R20057 standard: Protein: 475 AA.AC R20057;
DE 25-MAR-1992 (first entry)
KM Heavy chain of 3d6 anti-HIV antibody.
KM Plasmid pUC3d6HC; human immunodeficiency virus; AIDS;
OS Complementarity determining region.
FH Homo sapiens.

FH Key Location/Qualifiers

FT peptide 1..19 /label= signal

FT region 20..49 /label= Framework_1

FT region 50..54 /label= CDR-1

FT region 55..68 /label= CDR-2

FT region 69..85 /label= Framework_2

FT region 86..117 /label= CDR_2

FT region 118..134 /label= Framework_3

FT region 135..145 /label= CDR_3

FT region 146..475 /label= Framework_4

FT region /label= Constant_region

FT region /label= Constant_region

FT region /label= Constant_region

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FT region /label= Constant_region

CDR3

Query Match 80.0%; Score 698; DB 3; Length 475;
Best Local Similarity 77.8%; Pred. No. 4,39e-43;
Matches 98; Conservative 13; Mismatches 10; Indels 5; Gaps 3;Db 20 evqlvesggglvpgprslrlscaasgftfndyamhvrqgpgkglewsgiswdsslsy 79
QY 1 EVOLVESGGGLVPGPRSLRLSCAASGFTFDYAMHWVRQAPGKLEWVSATITWNSGHIDY 60Db 80 adsvkgrftisrdnaknsllylqmslraedmalycvkgdydsqgyftvafdlwqgt 139
QY 61 ADSVEGRFTISRDNKNSLYLQNSLRPAEDTAVYCAKV-SYLSTAS--SLDY--WGOGT 115

CDR3

CDR3

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DE DT07-DEC-1997 (first entry) VH sequence.
DE CE7-specific antibody CEA5 VH sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT FTregion /label= CDRI
FT /note= "complementarity determining region 1"
FT region /label= CDR2
FT /note= "complementarity determining region 2"
FT FTregion /label= CDR3
FT /note= "complementarity determining region 3"
PD W09720933-A1.
PN 12-JUN-1997.
PE 09-DEC-1996; G03043.
PF 11-OCT-1995; GB-021295.
PR 07-DEC-1995; GB-025004.
PA 23-MAY-1996; GB-010824.
PA (CAMEB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ McCafferty JG, Osbourn JK;
PI WPI: 97-319779/29.
PT N-PSDS: T72130.
PT Specific binding members for human carcinoembryonic antigen - bind
PT to the A3-B3 extracellular domain of hCEA and are substantially
PT non-cross-reactive with human liver cells; used for diagnosing
PT cancer.
PS Claim 7; Fig 1a; 128bp; English.
CC This polypeptide sequence comprises the heavy chain variable
CC region (VH) of human carcinoembryonic antigen (hCEA)-specific
CC antibody CEA5. VH (T72126-32) and VL (T72133-35) gene sequences
CC were obtained for anti-hCEA antibodies CEA1-CEA7 (see M19876-85).
CC A claimed specific binding member (A) comprises an hCEA specific
CC antibody antigen binding domain that has a dissociation constant
CC for hCEA of less than 1 x 10-8 M, is non-cross-reactive with human
CC liver cells, and preferentially binds to the A3-B3 extracellular
CC domain of hCEA and/or to cell-associated hCEA over hCEA over
CC soluble hCEA. Preferred (A) include pairings of VH and VL
CC sequences from CEA1-7, or their CDR sequences, as well as CEA6
CC VH and VL variants. (A) is used to detect cells expressing hCEA,
CC in vivo or in vitro, especially tumor cells for diagnosing cancer,
CC e.g. adenocarcinoma of the colon, lung or breast.
SO Sequence 116 AA;
SQ
Query Match 78.7%; Score 686; DB 24; Length 116;
Best Local Similarity 83.3%; Pred. NO. 3,64e-42;
Matches 100; Conservative 6; Mismatches 9; Indels 5; Gaps 2
Db 1 evqlvesggyvyrvpggsirlscasagtfdddygmavrtqabqsklsvvgngimngstcy 60
QY 1 EVQLVESGGGVLPQRSURLSCASAGTFDDYVAHWNRQAQGKLEWVASATWNMGSHIDY 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 adsvkgftltardnaknslylgmslradeafavyccarry---a--ldyvggtlvts 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 ADSVGRTISRDNAKNSLYLGMSLRADRYAVTYCAKVSTLTSASSLDITWGSGTLTVTS 120
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 7
AC R54058 standard; Protein; 121 AA.
DT 01-MAR-1995 (first entry)
DE Anti-cancer monoclonal antibody heavy chain variable region.
KW Antibody; hypervariable region; complementarity determining region;
KW anti-cancer; CDR; CLN/SUZ H11 hydriome; immunoglobulin gamma; IgG;
KW heavy chain.
OS Homo sapiens.
FH Key
FT location/Qualifiers
FT FTregion 31..35
FT /label= hypervariable_region_1
FT region 49...59

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FT      region                               /label= hypervariable_region_2
FT      99..109                             /label= hypervariable_region_3
PD      24-MAY-1994.
PE      06-NOV-1992; 321418.
PR      06-NOV-1992; JP-321418.
PA      (HAGI/) HAGIMAWA Y.
DR      WPI: 94-205039/25.
DR      N-PSDB: 064059.
PT      Anti-cancer human monoclonal antibody - useful for the treatment,
PT      prevention and diagnosis of human diseases
PS      Claim 2; Page 2; 11pp; Japanese.
CC      An anti-cancer human monoclonal antibody produced by the human/human
CC      hybridoma CLN/SUZ H11 has the gamma heavy chain variable region
CC      sequence R54058.
SQ      Sequence 121 AA;

Query Match      78.7%; Score 686; DB 11; Length 121;
Best Local Similarity 79.3%; Pred. No. 3,64e-42;
Matches 96; Conservative 11; Mismatches 13; Indels 1; Gaps 1;

Db      1 evqllesgdlvqpgsrlrlscasagftfnayamswwrgqpgkglewvsaltpsgstny 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy      1 EVQLVESGGGLVQPGSRSLRLSCAASGFTFDYAMHWYROAPRGKGLEWVSALITNSCHIDY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 adsvkgrftlsrdhsqntllqpmnlvedtavyegrvpyrstwypl-ywggqltvtvs 119
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy      61 ADSEGRFTISRDNKNSLYLNMSLRSEDYAVYCAKWSYLSFASSLDYWGCGTLTWS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      120 s 120
        |
Oy      121 S 121

                                CID 3

RESULT      8
ID      R54063 standard; Protein; 140 AA.
AC      R54063:
DT      01-MAR-1995 (first entry)
RV      Anti-cancer monoclonal antibody H-chain V region precursor.
KW      Antibody; hypervariable region; complementarity determining region;
KW      anti-cancer; CDR; CLN/SUZ H11 hybridoma; Immunoglobulin gamma; Igc;
OS      heavy chain.
OS      Synthetic.
FH      Key
FT      Peptide
FT      1..19 Location/Qualifiers
FT      /label= signal_peptide
FT      20..140
FT      /label= H-chain_variable_region
PV      J06141884-A.
PD      24-MAR-1994.
PE      06-NOV-1992; 321418.
PR      06-NOV-1992; JP-321418.
PA      (HAGI/) HAGIMAWA Y.
DR      WPI: 94-205039/25.
DR      N-PSDB: 064055.
PT      Anti-cancer human monoclonal antibody - useful for the treatment,
PT      prevention and diagnosis of human diseases
PS      Example 6; Page 8; 11pp; Japanese.
CC      The heavy chain of an anti-cancer human monoclonal antibody
CC      produced by the human/human hybridoma CLN/SUZ H11 has the
CC      three hypervariable regions R54055-R54057. The antibody has a gamma
CC      heavy chain and a kappa light chain. The heavy chain V region was
CC      amplified using primers 064061 and 064062 in a PCR and the
CC      amplified cDNA was sequenced (064065).
SQ      Sequence 140 AA;

Query Match      78.7%; Score 686; DB 11; Length 140;
Best Local Similarity 79.3%; Pred. No. 3,64e-42;
Matches 96; Conservative 11; Mismatches 13; Indels 1; Gaps 1;

20 evqllesgdlvqpgsrlrlscasagftfnayamswwrgqpgkglewvsaltpsgstny 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

QY 1 EVOLVESGGGLVPGGRSLRLSCAASGFTFDYAMHWRAQAPGKLEWVSATITWNSGHIDY 60
DB 80 adsvkgrftisrdnaknsllylqmslraedtaayvycak 138
QY 61 ADVSGRFTISRDNKNSLYLQMSLRADTAAYVYCAVSTLSTASSDITWGGTIVTS 120
DB 139 s 139
QY 121 s 121

CDR3

RESULT 9
ID R29578 standard; Protein; 140 AA.
AC R29578;
DE 19-APR-1993 (first entry)
KW CLN-IgG gamma.
KW Polymerase chain reaction; amplify; PCR; high variability region;
KW heavy; VH; light; VL; chain; human; immunoglobulin; CLN-IgG; B-cell;
KW human/human; hybridoma; CLN/SUZ-H11; uterine; cancer; lymphoblast;
KW cancer cell antigen; biopolymer.
KW Synthetic.
FT Key Location/Qualifiers
FT region 50..54 /label=Hv-1
FT region 68..78 /note="See claim 1"
FT region 118..128 /label=Hv-2
FT region 118..128 /note="See claim 1"
FT region 118..128 /label=Hv-3
FT peptide 1..19 /note="See claim 1"
FT peptide 1..19 /note="Signal peptide"
FT protein 20..140 /note="Mature protein"
FT protein 20..140 /note="Mature protein"
PN MO9220799-A.
PD 26-NOV-1992.
PE 21-MAY-1992; J00650.
PR 22-MAY-1991; JP-145218.
PA (HAGT/) HAGIWARA Y.
PI Aotsuka Y;
DR WPI; 92-41577/50.
PT Antinociceptive sequence of human monoclonal antibody - useful in preventing, treating and diagnosing cancers and as reagents for purifying bio-polymers.
PS Disclosure; Page 13; 29pp; Japanese.
CC The sequence given represents the high variability regions of the gamma region of the human immunoglobulin, CLN-IgG. CLN-IgG is secreted by human/human hybridoma CLN/SUZ-H11. CLN/SUZ-H11 was obtained by fusion of B-cells of a uterine cancer patient with a human lymphoblast cell line. CLN/SUZ-H11 is specific to human cancer cell antigen. The claimed peptide sequences indicated in the features table may be used in the prevention, treatment and diagnosis of CC diseases, such as cancer, as biochemical reagents and for the CC purification of biopolymers.
SQ Sequence 140 AA;

Query Match 78.7%; Score 686; DB 6; Length 140;
Best Local Similarity 79.3%; Pred. No. 3,64e-42;
Matches 96; Conservative 11; Mismatches 13; Indels 1; Gaps 1;

DB 20 evqlleagsgdlvpggslrlscasgftfdyamaawvrgapqglewvsatitwsgstny 79
QY 1 EVOLVESGGGLVPGGRSLRLSCAASGFTFDYAMHWRAQAPGKLEWVSATITWNSGHIDY 60
DB 80 adsvkgrftisrdnaknsllylqmslraedtaayvycak 138
QY 61 ADVSGRFTISRDNKNSLYLQMSLRADTAAYVYCAVSTLSTASSDITWGGTIVTS 120
DB 139 s 139
QY 121 s 121

CDR3

RESULT 10
ID R66303 standard; Protein; 123 AA.
AC R66303;
DE 02-AUG-1995 (first entry)
KW Human immunoglobulin variable heavy chain #9.
KW Primer: PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pDB81; E.coli; mammalian.
OS Homo sapiens.
PN MO9426895-A.
PD 24-NOV-1994.
PE 10-MAY-1993; J00603.
PR 10-MAY-1993; MO-J00603.
PA (NISB) JAPAN TOBACCO INC.
PI Honjo I, Matsuda F;
DR WPI; 95-006791/01.
DR N-PSDB; Q78947.
PT DNA fragment comprising human immunoglobulin Vh genes - for the production of human immunoglobulin in mammalian hosts
PS Claim 18; Page 41-42; 130pp; Japanese.
CC Protein sequences (R66293-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M31, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with Taqi restriction enzyme. The fragments were separated by gel electrophoresis and 35-45 kb fractions were collected. The fragments CC were ligated with ClaI-digested cosmid vector pDB81. The ligation CC products were in vitro packed and infected into E.coli 490R. The CC fragments were then subcloned by colony hybridisation. The Vh genes and CC the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
SQ Sequence 123 AA;

Query Match 77.9%; Score 679; DB 12; Length 123;
Best Local Similarity 93.9%; Pred. No. 1.25e-41;
Matches 92; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 20 evqlleagsgdlvpggslrlscasgftfdyamaawvrgapqglewvsatitwsgstny 79
QY 1 EVOLVESGGGLVPGGRSLRLSCAASGFTFDYAMHWRAQAPGKLEWVSATITWNSGHIDY 60
DB 80 adsvkgrftisrdnaknsllylqmslraedtaayvycak 117
QY 61 ADVSGRFTISRDNKNSLYLQMSLRADTAAYVYCAK 98

RESULT 11
ID R95216 standard; Protein; 119 AA.
AC R95216;
DE 16-DEC-1996 (first entry)
KW Human foetal immunoglobulin 56p1/Cb variable heavy chain.
KW Antibody: fusion protein; single chain; inhibition; tumour;
KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
KW Immunodassay; Lewis(X) carbohydrate antigen.
OS Homo sapiens.
PI Key Location/Qualifiers
FT domain 31..35 /label=CDR 1.
FT domain 50..66 /label=CDR 2.
FT domain 99..108 /label=CDR 3.
PN MO9613594-A1.
PD 09-MAY-1996.
PE 26-OCT-1995; U13811.
PR 28-OCT-1994; US-331398.
PR 28-OCT-1994; US-331396.
PR 28-OCT-1994; US-331397.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Benharri I., Brinkmann U., Fitzgerald D., Jung S., Lee B:
PI Padlan EA., Pal L., Pastan I., Willingham W.,
DR WPI.: 96-251462/25.
PT Single chain fusion proteins and antibodies - useful to diagnose and
PT treat cancer, specifically bind Lewis(X) related carbohydrate
PT antigen
PS Example 13: Figure 11A: 116PP: English.
CC A novel recombinant DNA molecule which encodes a single chain fusion
CC protein or antibody comprising the FV region of both the light and
CC heavy chains of an antibody (Ab), fused together, and an effector
CC molecule, where the fusion protein or Ab has the binding specificity
CC of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production
CC of such fusion proteins or antibodies. The fusion proteins can be
CC used in compositions as an immunotoxin to inhibit tumour cell growth
CC The single chain antibody can be used to detect the presence or
CC absence of cells bearing a Lewis(X) carbohydrate antigen in a
CC patient. The antibodies are also useful as multiple targeting
CC moieties, providing at least 2 kinds of biological activity. They
CC can also be used in diagnostic assays and for the imaging of tumours
CC when attached to a radiolabel and for the pathological diagnosis of
CC tumours. Humanised antibodies are less immunogenic than the mouse
CC Mabs B1, B3 and B5, making them more suitable for long term
CC treatment.. 119 AA:
SQ Sequence

```

Db      1 qveIvesggvvpqprslrlscasagfftsayamhwrvqbpqkglwvavlsydgsnkyy 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::: 1
Oy      1 EQQLVESGGGLVQPGKSPRLSCASAGFFTFDDYAMHWVQAQPGKGLWVSAITMNSGRHDY 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::: 1
Db      61 adsvvgrfttlradsnknlllylqmslrlaedcaavycarrs--atlyfydyggqtlrvs 118
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::: 1
Oy      61 ADSVGRFTTISRDNKNSLRYLQMSLRLEADDAVYYCAKYSTLSSASSLDYGGQTLTVTS 120
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::: 1
Db      119 s 119
      |
Oy      121 S 121

```

CDE 3

RESULT	12
ID	W08582 standard; Protein; 123 AA.
AC	W08582;
DE	23-SEP-1997 (first entry)
EV	Human antibody C4.1 heavy chain region.
KW	Tumour; immune response; cytotoxin; carcinoma; breast cancer.
OS	Homo sapiens.
FT	Key
FT	region
FT	location/Qualifiers
FT	/label= Framework_1
FT	31..35
FT	/label= CDR1
FT	36..49
FT	/label= Framework_2
FT	50..66
FT	/label= CDR2
FT	67..98
FT	/label= Framework_3
FT	99..112
FT	/label= CDR3
FT	113..123
FT	/label= Framework_4
PN	W09700271-A1.
PD	03-JAN-1997.
PE	13-JUN-1996; UI0287.
PR	14-JUN-1995; US-000238.
PR	15-JUN-1995; US-000250.
PA	(REGC) UNIV CALIFORNIA.
PI	Marks JD Schlier R;
DR	WPI; 97-077468/07.
PT	New C6 human antibody binding specifically to c-erbB-2 - useful for

PT treatme and diagnosis of tumours, with reduced risk of generating
 PR immune response
 PS Example 1: Page 58, 117pp: English.
 CC The present sequence represents a human antibody C4.1 heavy chain
 CC region, that binds specifically to c-erbB-2. C4.1 and C6.5 were tested
 CC for their binding of c-erbB-2, and while they both bind c-erbB-2 C6.5
 CC was found to bind c-erbB-2 under different conditions and so is the
 CC preferred antibody. A chimeric molecule that binds specifically to
 CC tumour cells carrying c-erbB-2 consists of an effector compound attached
 CC to a C6 human antibody, e.g. C6.5. If the effector compound is a
 CC cytotoxin the chimeric molecule can be used to inhibit growth of
 CC c-erbB-2 positive tumours (especially breast and other carcinomas). If
 CC the effector compound is a label the chimeric molecule can be used to
 CC detect such cells, including *in vivo* localisation. The antibody can also
 CC be used for diagnosis/localisation, *in vivo* or *in vitro*, specifically by
 CC immunosay. The nucleic acid encoding the antibody, and a nucleic
 CC acid encoding a single chain polypeptide with the binding specificity
 CC of the antibody and comprising the binding portions of variable
 CC regions of light and heavy chains of the antibody, joined by a linker,
 CC can be used to produce recombinant proteins by standard methods. Unlike
 CC known anti-c-erbB-2 antibodies, C6 antibodies are fully human, so
 CC should elicit little, if any, immunogenic response.
 CQ Sequence 123 AA:

Query Match	77.5%	Score 676:	DB 23:	length 123:
Best Local Similarity	78.9%	Pred. No. 2,13e-41:		
Matches	97; Conservative	10; Mismatches	14; Indels	2; Gaps

Db	1	qvglvveesggglvdpqgsrlrlscaasgltfssyemawvrqapbkglwvyslsssgstlly	60
Qy	1	EVQLVESGGGLVQPGSRSLRLSCAASGFTEDDYAMHWRAQAPGKLEWVSALTITNSGHIDY	60
Db	61	adsvygrttisrdraknslylqmmsltraedtaayycardlgysygyvgjdywqgclvt	120
Qy	61	ADSVEGRTISRDNKNSLYLQMMSLTRAEDTAAYYCAK-VS-YLSTASLDLYWQGLVYT	118
Db	121	VSS	123
Qy	119	VSS	121

CIR 3

RESULT	13	standard: Protein: 122 AA.
ID	R50311	
AC	R50311:	
DT	05-OCT-1994	(first entry)
DE	Humanised heavy chain variable region Pfzhbc2-4.	
KW	Monoclonal antibody; Plasmodium falciparum; CDR;	
KW	complementarity determining region; fusion protein;	
KW	murine; variable; light; heavy; chain; malaria.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	region	31..35
FT		/label= CDR1
FT	region	50..66
FT		/label= CDR2
FT	region	99..111
FT		/label= CDR3
PV	WC9405690-A.	
PD	17-MAR-1994.	
PF	08-SEP-1993:	U08435.
PR	09-SEP-1992:	US-941654.
PA	(SMIK)	SMITHKLINE BEECHAM CORP.
PA	(USNA)	US SEC OF ARMY.
PI	Charoenvit Y,	Hoffman S,
PI	Sadoof JC,	Sylvester DR,
PI	WPI:	94-101115/12.
DR	N-PSDB:	044825.
PT	New engineered antibodies and fusion proteins for preventing	
PT	Plasmodium infection - conts. murine antibody CDR sequences, and	
PT	corresp. nucleic acid, vectors and transformed cells	
CC	Claim 5; Fig 5; 98pp; English.	
CS	Naturally-occurring (044841-42) and synthetic (044825-28)	

CC variable light chain and variable heavy chain sequences
 CC derived from murine mAb N52 are provided. Murine mAb N52,
 CC its variable chain peptides, CDRs, functional fragments,
 CC Fab fragments, and analogs are useful in prodn. of fusion
 CC proteins, esp. engineered antibodies. These prods. are
 CC used to protect humans against Plasmodium infections.
 SQ Sequence 122 AA;

Query Match 77.4%; Score 675; DB 10; Length 122;
 Best Local Similarity 76.2%; Pred. No. 2,53e-41;
 Matches 93; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFDYAMHWVRQAPGKGLVWVSISGDSNY 60
 Oy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFDYAMHWVRQAPGKGLVWVSISGDSNY 60
 Db 61 pldvtgrftlsrdnsknltlylqmslraedtaavycardr-kdygwalfdywgggtltv 120
 Oy 61 ADVSGRFTISRDNKNSLYLQMSLRADDAVYCAKVSYSTASL-DYWGQGTLLTVY 119
 Db 121 ss 122
 Oy 120 SS 121

CDR 3

RESULT 14
 ID R52064 standard; Protein: 120 AA.

DE Heavy chain variable region of human G36005 antibody.
 KW antibody; humanised; murine; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 OS Homo sapiens.
 FH Key
 FT misc_difference 13
 FT /note= "corresponding codon TGA"

FT Location/Qualifiers
 FT 1..30
 FT /label= framework_region_1
 FT /note= "FR 1"
 FT 31..35
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT 36..49
 FT /note= "FR 2"
 FT 50..59
 FT /note= "CDR 2"
 FT 60..98
 FT /note= "FR 3"
 FT 99..110
 FT /note= "CDR 3"

EP-592106-A1.
 PD 13-APR-1994.
 PR 07-SEP-1993; 307051.
 PR 09-SEP-1992; US-942245.
 PA (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
 DR WPI: 94-120230/15.
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 PS Example 1: Fig 4B: 230pp; English.
 CC Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation experiments
 CC were set up: (1) traditional loop grafting; (2) resurfacing approach
 CC using most similar chain; and (3) resurfacing approach using human
 CC sequences with most similar surface residues. The Ab used was the murine
 CC anti-N901 Ab (see R52064). Experiment 2 was carried out using the present
 CC sequence which represents the human G36005 Ab heavy chain variable region
 CC with 89 percent homology with anti-N901 Ab. N901/G36005 (R52065) was
 CC prep'd. by CDR grafting. Sequence numbering starts at 118 in the
 CC specification.

SQ Sequence 120 AA;

Query Match 77.2%; Score 673; DB 18; Length 120;
 Best Local Similarity 76.9%; Pred. No. 3.60e-41;
 Matches 93; Conservative 13; Mismatches 13; Indels 2; Gaps 2;

Db 1 qvqlvesggglvqpggsrlslscasgftfssyamsvrgapqkglewvavlsydsnkyy 60
 Oy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFDYAMHWVRQAPGKGLVWVSISGDSNY 60
 Db 61 adsvkgrftlsrdnsknltlylqmslraedtaavycardr-kdygwalfdywgggtltv 119
 Oy 61 ADVSGRFTISRDNKNSLYLQMSLRADDAVYCAKVSYSTASL-DYWGQGTLLTVY 119
 Db 120 s 120
 Oy 120 S 120

CDR 3

RESULT 15
 ID W03726 standard; Protein: 184 AA.

DE Humanised MAb 39-1.106 heavy chain variable region.
 KW Heavy chain; variable region; murine; mouse; anti-human; disease;
 KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;
 KW diagnosis; inhibition; B-cell; activation; treatment; disorder;
 KW immune; autoimmunity; allergic response; organ rejection; drug;
 KW graft versus host; cell imaging; tumour; targeted; delivery;
 OS Mus musculus.
 FH Key
 FT misc_difference 13
 FT /note= "corresponding codon TGA"

FT misc_difference 23
 FT /note= "corresponding codon TGA"
 FT W03726
 FT 02-APR-1997 (first entry)
 DE Humanised MAb 39-1.106 heavy chain variable region.
 KW Heavy chain; variable region; murine; mouse; anti-human; disease;
 KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;
 KW diagnosis; inhibition; B-cell; activation; treatment; disorder;
 KW immune; autoimmunity; allergic response; organ rejection; drug;
 KW graft versus host; cell imaging; tumour; targeted; delivery;
 OS Mus musculus.
 FH Key
 FT misc_difference 13
 FT /note= "corresponding codon TGA"

FT Location/Qualifiers
 FT 1..30
 FT /label= framework_region_1
 FT /note= "FR 1"
 FT 31..35
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT 36..49
 FT /note= "FR 2"
 FT 50..59
 FT /note= "CDR 2"
 FT 60..98
 FT /note= "FR 3"
 FT 99..110
 FT /note= "CDR 3"

EP-592106-A1.
 PD 13-APR-1994.
 PR 07-SEP-1993; 307051.
 PR 09-SEP-1992; US-942245.
 PA (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
 DR WPI: 94-120230/15.
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 PS Example 1: Fig 4B: 230pp; English.
 CC Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation experiments
 CC were set up: (1) traditional loop grafting; (2) resurfacing approach
 CC using most similar chain; and (3) resurfacing approach using human
 CC sequences with most similar surface residues. The Ab used was the murine
 CC anti-N901 Ab (see R52064). Experiment 2 was carried out using the present
 CC sequence which represents the human G36005 Ab heavy chain variable region
 CC with 89 percent homology with anti-N901 Ab. N901/G36005 (R52065) was
 CC prep'd. by CDR grafting. Sequence numbering starts at 118 in the
 CC specification.

Fri Sep 3 09:52:58 1999







US-08-599-226-2.rag

Page 8

Qy	61	ADSVBGRRTISRDNKNSLYIQNMSLRAPEDIAVYCCAKVSTLSTASSLDITWGQGLTVYS	120
Db	175 s 175		
Oy	121 s 121		

C.M.

Search completed: Thu Sep 2 11:12:23 1999
Job time : 38 secs.

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9610824.6
CC FILING DATE: 23-MAY-1996
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/GB92/02240
CC FILING DATE: 02-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/244,597
CC FILING DATE: 01-JUN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: David W. Clough
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 28111/33308
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-474-6300
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 116 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 116 AA; 12686 MW; 69766 CN;

Query Match 78.7%; Score 686; DB 2; Length 116;
Best Local Similarity 83.3%; Pred. No. 9,13e-38;
Matches 100; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

Db 1 EVQLVESGGGVVPGPGRSRLSCAASGFTPDYGMASVVRQAPGKGLVWVSQISNRRY 60
Qy 1 EVQLVESGGGVVPGPGRSRLSCAASGFTPDYAMHVRQAPGKGLVWVSQISNRRY 60
Db 61 ADSVGRFTISDNKNSLYLQMSLRADTAIVYCAKRRY--A--LDYWGQGLTVYS 115
Qy 61 ADSVGRFTISDNKNSLYLQMSLRADTAIVYCAKRRY--A--LDYWGQGLTVYS 120

RESULT 2
ID US-08-331-398A-46 STANDARD; PRT: 119 AA. *CDR3*
AC xxxxxx
DT
XX
DE Sequence 46, Application US/08331398A
CC Patent No. 5608039
CC Sequence 46, Application US/08331398A
CC GENERAL INFORMATION:
CC APPLICANT: Pastan, Ira
CC APPLICANT: Willingham, Mark
CC APPLICANT: Fitzgerald, David
CC APPLICANT: Brinkmann, Ulrich
CC APPLICANT: Pal, Lee
CC TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
CC TITLE OF INVENTION: and their uses (as amended)
CC NUMBER OF SEQUENCES: 68
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC STREET: One Market Plaza, Stewart Street Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105-1492
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/331,398A
CC FILING DATE: 28-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/767,331

CC FILING DATE: 30-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/596,289
CC FILING DATE: 12-OCT-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hunter, Tom
CC REGISTRATION NUMBER: 38,498
CC REFERENCE/DOCKET NUMBER: 015280-126110US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 46:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..119
CC OTHER INFORMATION: /note="Human fetal immunoglobulin
CC OTHER INFORMATION: 56pI/CL Variable Heavy chain (V-H)"
CC SEQUENCE 119 AA; 13279 MW; 79818 CN;

Query Match 77.8%; Score 678; DB 1; Length 119;
Best Local Similarity 76.9%; Pred. No. 3,21e-37;
Matches 93; Conservative 15; Mismatches 11; Indels 2; Gaps 1;

Db 1 OEVLVESGGGVVPGPGRSRLSCAASGFTSSVAMHVRQAPGKGLVWVSQISNRRY 60
Qy 1 EVQLVESGGGVVPGPGRSRLSCAASGFTPDYAMHVRQAPGKGLVWVSQISNRRY 60
Db 61 ADSVGRFTISDNKNSLYLQMSLRADTAIVYCAKRRY--A--LDYWGQGLTVYS 118
Qy 61 ADSVGRFTISDNKNSLYLQMSLRADTAIVYCAKRRY--A--LDYWGQGLTVYS 120

Db 119 S 119
Qy 121 S 121 *6025*

RESULT 3
ID PCT-US93-08435-12 STANDARD; PRT: 122 AA.
AC xxxxxx
DT
XX
DE Sequence 12, Application PC/TUS9308435
CC Patent No. 5608039
CC Sequence 12, Application PC/TUS9308435
CC GENERAL INFORMATION:
CC APPLICANT: SmithKline Beecham, Corporation
CC APPLICANT: U. S. Government, Secretary of
CC APPLICANT: the Navy
CC APPLICANT: U. S. Government, Secretary of
CC TITLE OF INVENTION: Novel Antibodies for Confering Passive
CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
CC NUMBER OF SEQUENCES: 61
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Howson and Howson
CC STREET: Box 457, 321 Norristown Road
CC CITY: Spring House
CC STATE: PA
CC COUNTRY: USA
CC ZIP: 19477
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25

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CC CURRENT APPLICATION DATA: PCT/US93/08435
CC APPLICATION NUMBER: 76.2%; Pred. NO. 5.14e-37;
CC FILING DATE: 09-SEP-1992
CC CLASSIFICATION: 13; Mismatches 15; Indels 1; Gaps 1;
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/941,654
CC FILING DATE: 09-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bak, Mary E.
CC REGISTRATION NUMBER: 31,215
CC REFERENCE/DOCKET NUMBER: SBC P50107
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 540-9200
CC TELEFAX: (215) 540-5818
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 122 AA; 13370 MW; 87746 CN;
D QUERY MATCH
D Best Local Similarity 77.4%; Score 675; DB 3; Length 122;
D Matches 93; Conservative 13; Mismatches 15; Indels 1; Gaps 1;
Db 1 EVOLLESGGGLVDPGGSLRLSCAASGFTFSYAMSWMRQAPKGLEWVSISDGSTYY 60
Dy 1 EVOLLESGGGLVDPGSRSLSCAASGFTFDYAMHWVRQAPKGLEWSALTWNNGHIDY 60
Dy 61 PDVTAGRTISRDNKNLTLYLQMSLRADPAVVYCAKLIIYGVDYGYAMDWGCGTLTY 120
Dy 61 ADSEGRFTISRDNKNSLYLQMSLRADPAVVYCAKVSTLAS-SLDWGGGLTVY 119
Dy 121 SS 122
Dy ||
Dy 120 SS 121
Oy 120 SS 121
RESULT 4 STANDARD; PRT; 122 AA.
XX US-07-'934-373C-21 xxxxxx
XX AC xxxxxx
XX DT
XX DE
XX Sequence 21, Application US/07934373C
XX Patent No. 5821337
XX GENERAL INFORMATION:
XX APPLICANT: Paul J. Carter
XX APPLICANT: Leonard G. Prestea
XX TITLE OF INVENTION: Immunoglobulin Variants
XX NUMBER OF SEQUENCES: 48
XX CORRESPONDENCE ADDRESSES:
XX ADDRESSEE: Genentech, Inc.
XX STREET: 1 DNA Way
XX CITY: South San Francisco
XX STATE: California
XX COUNTRY: USA
XX ZIP: 94080
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: WinPatIn (Genentech)
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/07/934,373C
XX FILING DATE: 21-Aug-1992
XX CLASSIFICATION: 530
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: PCT/US92/05126
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CC      FILING DATE: 15-JUN-1992
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/715272
CC      FILING DATE: 14-JUN-1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Lee, Wendy M.
CC      REGISTRATION NUMBER: 40,378
CC      REFERENCE/DOCKET NUMBER: P0709P2
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 650/225-1994
CC      TELEFAX: 650/952-9881
CC      INFORMATION FOR SEQ ID NO: 21:
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 122 amino acids
CC          TYPE: Amino Acid
CC          TOPOLOGY: Linear
CC      SEQUENCE 122 AA; 13077 MW; 86439 CN;

Query Match              77.3%; Score 674; DB 2; Length 122;
Best Local Similarity 79.5%; Pred. No. 6.02e-37;
Matches    97; Conservative   8; Mismatches 16; Indels 1; Gaps

Db      1 EVQLVESGGGLYVQSGSLRLSCAASGFTFSYAMSWRQAQPKGLEWVSIVISGDGSGTYY 60
Oy      1 EVQLVESGGGLYVQGRSRISRKLSCAASGTFEDDYAHHWWRQAQPKGLEWVSATITNSGHIDY 60
Db      61 ADYVAGRTISRDNRSKNLTLYLQNMSLRAPEDTAAYVYCARGRYGYSLSGLYDYGQGLTVTV 120
Oy      61 ADVSEGRFTISRDNAKNSLYLQNMSLRAPEDTAAYVCARVSYLSTASSSL-DYWGQGLTVTV 119
Db      121 SS 122
Oy      120 SS 121

                CDE3

RESULT_ 5
ID      PCT-US93-07832-21        STANDARD;           PRT;       122 AA.
XX      AC                      xxxxxx
XX      DE                      Sequence 21, Application PC/TUS9307832
XX      CC                      Sequence 21, Application PC/TUS9307832
XX      CC                      GENERAL INFORMATION:
XX      CC                      APPLICANT: Genentech, Inc.
XX      CC                      TITLE OF INVENTION: Immunoglobulin Variants
XX      CC                      NUMBER OF SEQUENCES: 40
XX      CC                      CORRESPONDENCE ADDRESS:
XX      CC                      ADDRESSEE: Genentech, Inc.
XX      CC                      STREET: 460 Point San Bruno Blvd
XX      CC                      CITY: South San Francisco
XX      CC                      STATE: California
XX      CC                      COUNTRY: USA
XX      CC                      ZIP: 94080
XX      CC                      COMPUTER READABLE FORM:
XX      CC                      MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
XX      CC                      COMPUTER: IBM PC compatible
XX      CC                      OPERATING SYSTEM: PC-DOS/MS-DOS
XX      CC                      SOFTWARE: patin (Genentech)
XX      CC                      CURRENT APPLICATION DATA:
XX      CC                      APPLICATION NUMBER: PCT/US93/07832
XX      CC                      FILING DATE: 19930820
XX      CC                      CLASSIFICATION:
XX      CC                      PRIOR APPLICATION DATA:
XX      CC                      APPLICATION NUMBER: 07/715272
XX      CC                      FILING DATE: 14-JUN-1991
XX      CC                      PRIOR APPLICATION DATA:
XX      CC                      APPLICATION NUMBER: PCT/US92/05126
XX      CC                      FILING DATE: 15-JUN-1992
XX      CC                      PRIOR APPLICATION DATA:
XX      CC                      APPLICATION NUMBER: 07/934373
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CC FILING DATE: 21-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME:
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 70925PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE:
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
SQ SEQUENCE 122 AA; 13077 MW; 86439 CN;

Query Match	77.3%;	Score 674;	DB 3;	Length 122;
Best Local Similarity	79.5%;	Pred. No. 6.02e-37;		
Matches	97;	Conservative	8;	Mismatches 16; Indels 1; Gaps 1

[illegible]

Db	121	SS	122
QY	120	SS	121

22

RESULT	6	
ID	US-07-942-245-35	STANDARD; PRT; 120 AA

Sequence 35, Application US/07942245

CC Sequence 35, Application US/07942245
CC Patent No. 5639641

CC GENERAL INFORMATION:
CC APPLICANT: PEDERSEN, Jan T.
CC APPLICANT: SEARLE, Stephen M. J.
CC APPLICANT: REES, Anthony R.
CC APPLICANT: ROGUSKA, Michael A.
CC APPLICANT: GUILD, Braydon C.
CC TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
CC TITLE OF INVENTION: ANTI-BODIES
CC NUMBER OF SEQUENCES: 522
CC
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sughine, Mion, Zlman, Macpeak & Seas
CC STREET: 2100 Pennsylvania Avenue, N.W.

CC INFORMATION FOR SEQ ID NO: 35:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 120 AA; 13421 MW; 76517 CN;

Query Match	77.2%;	Score 673;	DB 1;	Length 120;
Best Local Similarity	76.9%;	Pred. No. 7.04e-37;		
Matches	93;	Conservative	13;	Mismatches 13; Indels 2; Gaps 2;

Dd	1	QVQLVESGGGVVQGRSRITSCAASGTFSSYIAHWYRQAPGKLENAVAVSYGSKRY	60
Qy	1	EVQLVESGGGVLPGRSRILSCAASGTFPDYIAHWYRQAPGKLENAVSAITNMGHIDY	60
Dd	61	ADSKGRRTIRDSKNTLYIQNNSLAEEDTAVYYCARDR-KDGMGALFEDYWGGLTVY	119
Qy	61	ADVEGRRTIRDSKAKNSLYIQNNSLAEEDTAVYYCAKSYLSTASSL-DYWGGLTVY	119

Db	120 S	120
QY	120 S	120

5

RESULT	7	
ID	PCT-US93-08435-14	STANDARD; PRT; 122 AA

DE Sequence 14, Application PC/TUS9308435

CC Sequence 14, Application PC/TUS9308435

CC APPLICANT: Smithline Beecham, Corporation
CC APPLICANT: U. S. Government, Secretary of
CC APPLICANT: the Navy
CC APPLICANT: U. S. Government, Secretary of
CC APPLICANT: the Army
CC TITLE OF INVENTION: Novel Antibodies for Conferring Passive
CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
CC NUMBER OF SEQUENCES: 61
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Howson and Howson
CC STREET: Box 457, 321 Norristown Road
CC CITY: Spring House
CC STATE: PA
CC COUNTRY: USA

CC CONVECTION DATA:
CC APPLICATION NUMBER: US/07/942,245
CC FILING DATE: 09-SEP-1992
CC CLASSIFICATION: 530
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 293-7060
CC TELEFAX: (202) 293-7860
CC TELEX: 6491103

CC REGISTRATION NUMBER: 31.215
CC REFERENCE/DOCKET NUMBER: SBC P501070
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 540-9200
CC TELEFAX: (215) 540-5818
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids

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CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 122 AA; 13329 MW; 88138 CN;
SO

Query Match          76.5%; Score 667; DB 3; Length 122;
Best Local Similarity 75.4%; Pred. No. 1,81e-36;
Matches 92; Conservative 13; Mismatches 16; Indels 1; Gaps 11;

Db      1 EVOLLSEGGGLVQPGGSLRLSCAASGFTSSYAMSWRQAQAGKLEWYSEISDGGSTYY 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      1 EQLVLESGGVLQPGSLRLSCAASGFTFDYAMHWYQAQAGKLEWYSAITNMSGHID 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 PDITYGRTISRNSKNPTLYIQNLSLRADRYAVYCASLITYGIDGIAADIWGGTLYTV 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 ADSEVGRFTISRDNKNSLYIQNLSLRADRYAVYCAVSYLSTAS-SLDYWGGLTLYTV 119
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 SS 122
      ||
QY      120 SS 121
      ||

RESULT      8      STANDARD;      PRT;      139 AA.
XX      US -08-129-930B-96
XX      xxxxxx
XX
XX
XX      Sequence 96, Application US/08129930B
DE
CC      Sequence 96, Application US/08129930B
CC      Patent No. 5804187
CC      GENERAL INFORMATION:
CC      APPLICANT: do Couto Dr., Fernando J.R.
CC      APPLICANT: Ceriani Dr., Roberto L.
CC      APPLICANT: Peterson Dr., Jerry A.
CC      APPLICANT: Padlan Dr., Eduardo A.
CC      TITLE OF INVENTION: Analogue Peptides With Broad
CC      TITLE OF INVENTION: Carcinoma Specificity, and Kit and
CC      TITLE OF INVENTION: Diagnostic Vaccination and
CC      TITLE OF INVENTION: Therapeutic Methods
CC      NUMBER OF SEQUENCES: 96
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSSEE: V. AMZEL & ASSOC.
CC      STREET: 2055 No. 5804187th Broadway, Suite 201
CC      CITY: Walnut Creek
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94596
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/129,930B
CC      FILING DATE: September 30, 1993
CC      CLASSIFICATION: 424
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Amzel Ph.D., Viviana
CC      REGISTRATION NUMBER: 30,930
CC      REFERENCE/DOCKET NUMBER: CRFCC-008A
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (510) 521-1333
CC      TELEFAX: (510) 521-3541
CC      TELEX: n.a.
CC      INFORMATION FOR SEQ ID NO: 96:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 139 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: peptide
CC

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SQ	SEQUENCE	139 AA; 15158 MM; 106646 CN;
Query Match	76.4%:	Score 666; DB 2; Length 139;
Best Local Similarity	73.6%:	Pred. No. 2,1le-36;
Matches	89; Conservative	13; Mismatches 18; Indels 1; Gaps 1.
Dd	20 EYOWMESGGGLVVGSGSLRLSCASGAFSSYSAMSWRROAPKGLEWVAEISGNGTAAAY 79 1 EVQLVESGGGLVQGERSLRISCASSGTFTFDYDANHWTRORPAGKLEWVSALTNNHSHIDY 60 +	
Oy	61 ADVSAGRRTISRDNANKNSLYIQNMSLRAEDPTAAYVCARVSYLSSTASSLDYGQCTLTAVTS 120 + :	
Dd	139 S 139 +	
Oy	121 S 121 <div style="text-align: center;">() () { }</div>	
RESULT	9	
ID	US -08 -652-558-39	STANDARD; PRT; 120 AA.
AC	xxxxxx	
DT		
XX		
DE	Sequence 39, Application US/08652558	
CC	Sequence 39, Application US/08652558	
CC	Patent No. 5861155	
CC	GENERAL INFORMATION:	
CC	APPLICANT: LIN, AUGUSTINE YEE-'THARN	
CC	TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES	
CC	TITLE OR INVENTION: THEREOF	
CC	NUMBER OF SEQUENCES: 32	
CC	CORRESPONDENCE ADDRESSES:	
CC	ADDRESSEE: BANNER & WITCOFF	
CC	STREET: 75 STATE STREET, 23RD FLOOR	
CC	CITY: BOSTON	
CC	STATE: MASSACHUSETTS	
CC	COUNTRY: USA	
CC	ZIP: 02109	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: Wordperfect 6.1	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/08/652,558	
CC	FILING DATE: JUNE 6, 1996	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: PCT/TB94/00387	
CC	FILING DATE: NOVEMBER 21, 1994	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: YARKWICH, LEON R.	
CC	REGISTRATION NUMBER: 30,237	
CC	REFERENCE/DOCKET NUMBER: 95,497-L	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: 617-345-9100	
CC	TELEFAX: 617-345-9111	
CC	INFORMATION FOR SEQ ID NO: 39:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 120 amino acids	
CC	TYPE: amino acid	
CC	STRANDNESS: single	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: Protein	
CC	SEQUENCE 120 AA; 13479 MM; 83766 CN;	
SQ		
Query Match	76.3%:	Score 665; DB 2; Length 120;
Best Local Similarity	71.1%:	Pred. No. 2,47e-36;
Matches	86; Conservative	20; Mismatches 13; Indels 2; Gaps 2;

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 117 AA; 12946 MW; 76467 CN;
Query Match 75.7%; Score 660; DB 1; Length 117;
Best Local Similarity 76.7%; Pred. No. 5,42e-36;
Matches 92; Conservative 13; Mismatches 12; Indels 3; Gaps 1;
DB 1 QVQLVSGGCVOPGRSLRLSCAASGFTSSSGMHWVRQAPGKLEWAVYSSGFTIY 60
OY 1 EVQLVESGGGLVOPGSRSLSCAASGFTFDYAMHWVRQAPGKLEWVSATITWNSGHIDY 60
DB 61 ADVSGRFTISRDNKNSLYLQMSLRADTAHYICAR--MRKGYANDYMGQGLIYTVS 117
OY 61 ADVSGRFTISRDNKNSLYLQMSLRADTAHYICAKYSLTASSLDYMGQGLIYTVS 120
RESULT 14
US-07-942-245-24 STANDARD; PRT; 117 AA.
AC xxxxxx
DT
DT
DT
DE Sequence 24, Application US/07942245
XX
XX Patent No. 5639641
CC GENERAL INFORMATION:
CC APPLICANT: PEDERSEN, Jan T.
CC APPLICANT: SEARLE, Stephen M.J.
CC APPLICANT: REES, Anthony R.
CC APPLICANT: ROGUSKA, Michael A.
CC APPLICANT: GUIDI, Braydon C.
CC TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
CC TITLE OF INVENTION: ANTIBODIES
CC NUMBER OF SEQUENCES: 522
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
CC STREET: 2100 Pennsylvania Avenue, N.W.
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: United States
CC ZIP: 20037-3202
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: HP 9000/700 Workstation
CC OPERATING SYSTEM: UNIX
CC SOFTWARE: In house
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/942,245
CC FILING DATE: 09-SEP-1992
CC CLASSIFICATION: 530
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 293-7060
CC TELEFAX: (202) 293-7860
CC TELEFAX: 6491103
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 117 AA; 12972 MW; 73183 CN;
Query Match 75.5%; Score 658; DB 1; Length 117;
Best Local Similarity 88.8%; Pred. No. 7,42e-36;
Matches 87; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
DB 1 EVQLVESGGGLVOPGSRSLRLSCAASGFTFDYAMHWVRQAPGKLEWVSATITWNSGHIDY 60
OY 1 EVQLVESGGGLVOPGSRSLRLSCAASGFTFDYAMHWVRQAPGKLEWVSATITWNSGHIDY 60

DB 61 ADVSGRFTISRDNKNSLYLQMSLRADTAHYICAR 98
OY 61 ADVSGRFTISRDNKNSLYLQMSLRADTAHYICAR 98
RESULT 15
US-08-476-349A-99 STANDARD; PRT; 125 AA.
AC xxxxxx
DT
DT
DE Sequence 99, Application US/08476349A
XX
XX Patent No. 5750105
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A.
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Raab, Ronald W.
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/476,349A
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/379,072
CC FILING DATE: 25-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/912,292
CC FILING DATE: 10-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/856,281
CC FILING DATE: 23-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/735,064
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Teskin Esq., Robin L.
CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-161
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC POSITION IN GENOME:
CC CHROMOSOME/SEGMENT: 18/2
CC SEQUENCE 125 AA; 13543 MW; 93321 CN;
Query Match 75.5%; Score 658; DB 2; Length 125;
Best Local Similarity 78.4%; Pred. No. 7,42e-36;
Matches 98; Conservative 10; Mismatches 13; Indels 4; Gaps 3;


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Db      1  EVOLVESGGGLVQPGKSLRLSCAASGFTFSYAMSMVROAPGKGLEWYXAIISGSGSTYY 60
Oy      1  EVOLVESGGGLVQPGKSLRLSCAASGFTFDDYAMHMVROAPGKGLEWYSAITWNSGHIDY 60

Db      61  ADSVKGRTTISRDKSKNTLYLQMSLRADETAVYYCAKGGVLYGSGSYHMFDPWGQGTLL 120
Oy      61  ADSVKGRTTISRDKSKNTLYLQMSLRADETAVYYCAK--VSYLESTAS-S-IDYWGQGTLL 116

Db      121 VTSS 125
Oy      117 VTSS 121

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CDR3

Search completed: Thu Sep 2 11:15:08 1999
 Job time : 22 secs.

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 W P E S R E L I
 (TM)

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 Distribution rights by Oxford Molecular Ltd

March pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:12:42 1999; MasPar time 7.58 Seconds
 Modular output not generated. 639.582 Million cell updates/sec

Title: >US-08-599-226-2
 Description: (1-121) from US08599226.pep
 Perfect Score: 872
 Sequence: 1 EVOLVESGGGLVOPGSRSLRL.....LSTASLDYWGGLTVTVSS 121

Scoring table:
 PAM 150
 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: PIR60
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 41.669; Variance 106.425; scale 0.392

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Query Match	Length	ID	Description	Pred. No.
1	749	85.9	121	2	S31104	Ig heavy chain (subcl 1.11e-97
2	743	85.2	123	2	S30532	Ig heavy chain V regl 1.03e-96
3	742	85.1	121	2	S31118	Ig heavy chain - huma 1.49e-96
4	740	84.9	128	2	S31595	Ig heavy chain V regl 3.13e-96
5	730	83.7	120	2	S36273	Ig heavy chain V regl 1.27e-94
6	707	81.1	121	2	S19666	Ig heavy chain V regl 6.37e-91
7	698	80.0	140	2	S31686	Ig heavy chain V regl 1.78e-89
8	696	80.0	145	2	S11239	Ig heavy chain V regl 1.78e-89
9	696	79.8	120	2	S44111	Ig heavy chain V-D-J 3.72e-89
10	692	79.4	120	2	S31112	Ig heavy chain - huma 1.63e-88
11	690	79.1	122	2	S31117	Ig heavy chain - huma 3.42e-88
12	687	78.8	123	2	S31114	Ig heavy chain - huma 1.03e-87
13	685	78.6	122	1	M3HUM	Ig heavy chain V-III 2.16e-87
14	679	77.9	98	2	S26927	Ig heavy chain V regl 1.98e-86
15	677	77.6	121	2	S36005	Ig heavy chain V regl 4.15e-86
16	677	77.6	140	2	S70442	Ig mu chain precursor 4.15e-86
17	676	77.6	141	2	S31659	Ig heavy chain V regl 6.00e-86
18	676	77.5	135	2	S31598	Ig heavy chain V regl 6.00e-86
19	675	77.4	133	2	S31510	Ig heavy chain - huma 8.68e-86
20	673	77.2	119	2	S31108	Ig heavy chain - huma 1.81e-85
21	672	77.1	120	1	GIHUB	Ig heavy chain V-III 2.62e-85
22	671	76.9	143	2	S23624	Ig heavy chain V regl 3.80e-85
23	670	76.8	120	2	S36278	Ig heavy chain V regl 5.49e-85

Rank	Score	Query Match	Length	ID	Description	Pred. No.
24	669	76.7	119	2	S31107	Ig heavy chain - huma 7.93e-85
25	669	76.7	119	2	F36005	Ig heavy chain V regl 7.93e-85
26	668	76.6	123	2	PC4281	anti-Ss-A/Ro 60K pep 1.15e-84
27	668	76.6	125	2	S30531	Ig heavy chain V regl 1.15e-84
28	667	76.5	140	2	S31588	Ig heavy chain V regl 1.66e-84
29	666	76.4	119	2	C36005	Ig heavy chain V regl 2.40e-84
30	666	76.4	121	2	I55673	Ig heavy chain - huma 2.40e-84
31	666	76.4	133	2	A49028	Ig heavy chain V-III 2.40e-84
32	665	76.3	100	2	S69896	Ig heavy chain V regl 3.47e-84
33	665	76.3	122	2	S69810	Ig V-D-J region (KR) 3.47e-84
34	664	76.1	139	2	S31674	Ig heavy chain V regl 5.01e-84
35	663	76.0	122	2	E36005	Ig heavy chain V regl 7.25e-84
36	662	75.9	120	2	S48798	Ig heavy chain V regl 1.05e-83
37	659	75.6	123	2	S26794	Ig heavy chain V regl 3.16e-83
38	659	75.6	132	2	S31603	Ig heavy chain V regl 3.16e-83
39	655	75.1	118	2	PH1643	Ig heavy chain V regl 1.38e-82
40	655	75.1	118	2	S31116	Ig heavy chain - huma 1.38e-82
41	655	75.1	151	2	A60943	Ig heavy chain precu 1.38e-82
42	653	74.9	122	2	S20772	Ig heavy chain V regl 2.88e-82
43	651	74.7	144	2	S20782	Ig heavy chain V regl 6.02e-82
44	651	74.7	137	2	S31701	Ig heavy chain V regl 6.02e-82
45	648	74.3	112	2	PH1654	Ig heavy chain V regl 1.82e-81

ALIGNMENTS

RESULT 1
 ENTRY S31104 #type fragment
 TITLE Ig heavy chain (subclass IgM) - human (fragment)
 ORGANISM Homo sapiens #common_name man
 DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

ACCESSIONS
 REFERENCE S31104
 #authors Rapphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
 Eur. J. Immunol. (1992) 22:247-251
 #title Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements.
 #cross-references M01D:92111633
 #accession S31104
 #status preliminary: nucleic acid sequence not shown; translation not shown

CLASSIFICATION
 #superfamily Immunoglobulin V region; immunoglobulin homology
 #heterotetramer; immunoglobulin
 #domain immunoglobulin homology #label IMM
 #length 121 #checksum 6696

KEYWORDS
 #molecule_type mRNA
 #residues 1-121 #label PAA
 #cross-references EMBL:X63080; NID:932646; PID:932647
 #note the nucleotide sequence was submitted to the EMBL Data Library, October 1991

SUMMARY
 Query Match 85.9%; Score 749; DB 2; Length 121;
 Best Local Similarity 85.1%; Pred. No. 1.11e-97;
 Matches 103; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

DB	Score	Length	ID	Description	Pred. No.
DB	1	EVOLVESGGGLVOPGSRSLRLSCAASGFTPDYAMHWROAPGGLMVGISWNSIGY 60			
QY	1	EVOLVESGGGLVOPGSRSLRLSCAASGFTPDYAMHWROAPGGLMVGISWNSIGY 60			
DB	61	ADSVKRFITISRDMAKNSLYIQNNSLRAEDTALYCAKDFVGSQGYFDLMGRGLTVTS 120			
QY	61	ADSVKRFITISRDMAKNSLYIQNNSLRAEDTALYCAKDFVGSQGYFDLMGRGLTVTS 120			
DB	121	S 121			
QY	121	S 121			


```

#residues      1-120 #label GRI
#cross-references EMBL:Z18834; NID:G33116; PID:G939896
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        heterotetramer; immunoglobulin
FEATURE
15-98           #domain immunoglobulin homology #label IMM
SUMMARY         #length 120 #checksum 5179

```

Query Match	83.7%;	Score 730;	DB 2;	Length 120;
Best Local Similarity	84.2%;	Pred. No. 1.27e-94;		
Matches 101; Conservative	9;	Mismatches 10;	Indels 0;	Gaps 0;

[illegible]

ENTRY	RESULT	6
TITLE	S19666	#type complete
ORGANISM	Ig heavy chain V region (VH3DJH4) - human	
DATE	#format_name Homo sapiens #common_name man	
	22-Jan-1993 #sequence_revision 22-Jan-1993	
	08-Sep-1997	#text_change

authors Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.
#journal J. Mol. Biol. (1991) 222:581-597
#title By-passing immunization. Human antibodies from V-gene libraries displayed on phage.

```

#residues      1-121 #label MAR
#cross-references EMBL:X61646; NID:937688; PID:641890; PID:61333369
CLASSIFICATION #superfamily1 immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
15-96
SUMMARY

```

Query Match	81.1%;	Score 707;	DB 2;	Length 121;
Best Local Similarity	77.7%;	Pred. No. 6.37e-91;		
Matches	94;	Conservative	15;	Mismatches 12; Indels 0; Gaps 0;

```
Dd      61 ADVYAGRTTISRDNKSNLTLYLQNMNSLRADPDVAYYYCAKGTSSGMMGFDDMGOGLTVTS    120
Oy      61 ADVYBGRRTISRDNKANSLYLQNMNSLRADPDVAYYYCAKATSVLSSTASSLDTWGGOTLVTS    120
Oy      1 EVOLVESGGCGLVOPGRSLRSLCAASGFEFDDYAMHWVQAQKGRLIEWVASITNWSGHIDY    60
Oy      1 OVOLIIVSGGGVWOPGRSLRSLCAASGFEFTSSYGNNHWVQAQKLEIWAYAITYGSNKYY    60
```

Db	121 S 121
	—
QY	121 S 121

RESULT	7
ENTRY	S31686
TITLE	Ig heavy chain v region - human (fragment)
ORGANISM	Homo sapiens
DATE	22-Nov-1993
	#type fragment
	#formal_name Homo sapiens
	#common_name man
	#sequence_revision 10-NOV-1995
	#text_change

#accessions 331686
 #reference 331585
 #authors Cuisinier, A.M.; Gauthier, L.; Boudit, L.; Fougereau, M.;
 Tonneille, C.
 #submission submitted to the EMBL Data Library, June 1992

Accession	Gene	Accession	Gene
U00000	16S ribosomal RNA	U00000	16S ribosomal RNA
U00001	23S ribosomal RNA	U00001	23S ribosomal RNA
U00002	5S ribosomal RNA	U00002	5S ribosomal RNA
U00003	5.8S ribosomal RNA	U00003	5.8S ribosomal RNA
U00004	16S ribosomal RNA	U00004	16S ribosomal RNA
U00005	23S ribosomal RNA	U00005	23S ribosomal RNA
U00006	5S ribosomal RNA	U00006	5S ribosomal RNA
U00007	5.8S ribosomal RNA	U00007	5.8S ribosomal RNA
U00008	16S ribosomal RNA	U00008	16S ribosomal RNA
U00009	23S ribosomal RNA	U00009	23S ribosomal RNA
U00010	5S ribosomal RNA	U00010	5S ribosomal RNA
U00011	5.8S ribosomal RNA	U00011	5.8S ribosomal RNA
U00012	16S ribosomal RNA	U00012	16S ribosomal RNA
U00013	23S ribosomal RNA	U00013	23S ribosomal RNA
U00014	5S ribosomal RNA	U00014	5S ribosomal RNA
U00015	5.8S ribosomal RNA	U00015	5.8S ribosomal RNA
U00016	16S ribosomal RNA	U00016	16S ribosomal RNA
U00017	23S ribosomal RNA	U00017	23S ribosomal RNA
U00018	5S ribosomal RNA	U00018	5S ribosomal RNA
U00019	5.8S ribosomal RNA	U00019	5.8S ribosomal RNA
U00020	16S ribosomal RNA	U00020	16S ribosomal RNA
U00021	23S ribosomal RNA	U00021	23S ribosomal RNA
U00022	5S ribosomal RNA	U00022	5S ribosomal RNA
U00023	5.8S ribosomal RNA	U00023	5.8S ribosomal RNA
U00024	16S ribosomal RNA	U00024	16S ribosomal RNA
U00025	23S ribosomal RNA	U00025	23S ribosomal RNA
U00026	5S ribosomal RNA	U00026	5S ribosomal RNA
U00027	5.8S ribosomal RNA	U00027	5.8S ribosomal RNA
U00028	16S ribosomal RNA	U00028	16S ribosomal RNA
U00029	23S ribosomal RNA	U00029	23S ribosomal RNA
U00030	5S ribosomal RNA	U00030	5S ribosomal RNA
U00031	5.8S ribosomal RNA	U00031	5.8S ribosomal RNA
U00032	16S ribosomal RNA	U00032	16S ribosomal RNA
U00033	23S ribosomal RNA	U00033	23S ribosomal RNA
U00034	5S ribosomal RNA	U00034	5S ribosomal RNA
U00035	5.8S ribosomal RNA	U00035	5.8S ribosomal RNA
U00036	16S ribosomal RNA	U00036	16S ribosomal RNA
U00037	23S ribosomal RNA	U00037	23S ribosomal RNA
U00038	5S ribosomal RNA	U00038	5S ribosomal RNA
U00039	5.8S ribosomal RNA	U00039	5.8S ribosomal RNA
U00040	16S ribosomal RNA	U00040	16S ribosomal RNA
U00041	23S ribosomal RNA	U00041	23S ribosomal RNA
U00042	5S ribosomal RNA	U00042	5S ribosomal RNA
U00043	5.8S ribosomal RNA	U00043	5.8S ribosomal RNA
U00044	16S ribosomal RNA	U00044	16S ribosomal RNA
U00045	23S ribosomal RNA	U00045	23S ribosomal RNA
U00046	5S ribosomal RNA	U00046	5S ribosomal RNA
U00047	5.8S ribosomal RNA	U00047	5.8S ribosomal RNA
U00048	16S ribosomal RNA	U00048	16S ribosomal RNA
U00049	23S ribosomal RNA	U00049	23S ribosomal RNA
U00050	5S ribosomal RNA	U00050	5S ribosomal RNA
U00051	5.8S ribosomal RNA	U00051	5.8S ribosomal RNA
U00052	16S ribosomal RNA	U00052	16S ribosomal RNA
U00053	23S ribosomal RNA	U00053	23S ribosomal RNA
U00054	5S ribosomal RNA	U00054	5S ribosomal RNA
U00055	5.8S ribosomal RNA	U00055	5.8S ribosomal RNA
U00056	16S ribosomal RNA	U00056	16S ribosomal RNA
U00057	23S ribosomal RNA	U00057	23S ribosomal RNA
U00058	5S ribosomal RNA	U00058	5S ribosomal RNA
U00059	5.8S ribosomal RNA	U00059	5.8S ribosomal RNA
U00060	16S ribosomal RNA	U00060	16S ribosomal RNA
U00061	23S ribosomal RNA	U00061	23S ribosomal RNA
U00062	5S ribosomal RNA	U00062	5S ribosomal RNA
U00063	5.8S ribosomal RNA	U00063	5.8S ribosomal RNA
U00064	16S ribosomal RNA	U00064	16S ribosomal RNA
U00065	23S ribosomal RNA	U00065	23S ribosomal RNA
U00066	5S ribosomal RNA	U00066	5S ribosomal RNA
U00067	5.8S ribosomal RNA	U00067	5.8S ribosomal RNA
U00068	16S ribosomal RNA	U00068	16S ribosomal RNA
U00069	23S ribosomal RNA	U00069	23S ribosomal RNA
U00070	5S ribosomal RNA	U00070	5S ribosomal RNA
U00071	5.8S ribosomal RNA	U00071	5.8S ribosomal RNA
U00072	16S ribosomal RNA	U00072	16S ribosomal RNA
U00073	23S ribosomal RNA		

```

#accession      S31686
#status         preliminary
#molecule_type mRNA
#residues       1-140 ##label CUT
#cross-references EMBL:Z14205; NID:g30969; PID:g30970
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        heterotetramer; immunoglobulin
FEATURE

```

34-117	#domain	immunoglobulin	homology	#label	IWM
SUMMARY	#length	140	#checksum	5377	
Query Match	80.0%	Score	698;	DB 2;	length 140;
Best Local Similarity	79.3%	Pred.	1.79e-89;		
Matches	96;	Conservative	13;	Mismatches	12;
				Indels	0;
				Gaps	0;

```

Db 20 EVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMSVVRQAPRGKLEWVAISGGSTYY 79
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTEDDYAMHWVRQAPGKGLEWVAITWNSGHIDY 60

```

D5 S D S Y G R F T I S R D N S K N T L V L Q M N S L R E D T A Y Y C A K P F A G S S P S F D Y W G Q G I L T V S 139
:
61 A D S Y E G R F T I S R D N A K N S L I L Q M N S L R E D T A Y Y C A K V S Y L S T A S S L D Y W G Q G I L T V S 120

Db	140 S 140
QY	121 S 121

RESULT	8
ENTRY	S11239
TITLE	Ig heavy chain V region - human (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 08-Sep-1997

#cross-references MUID:90370490
 HIV-1 - gp41.
 H- and L-chains of a human monoclonal antibody specific to
 Nucleotide sequences of the cDNAs encoding the V-regions of
 the
 Nucleic Acids Res. (1990) 18:4927
 Felgenhauer, M.; Kohl, J.; Rueker, F.
 51139
 51139
 51139
 #authors
 #journal
 #title
 ACCESSIONS
 REFERENCE

```
##status      preliminary
##molecule_type  mRNA
##residues     1-145 #label FEL
```

CLASSIFICATION	#superfamily Immunoglobulin V region; Immunoglobulin
KEYWORDS	heterotrimer; Immunoglobulin
FEATURE	
34.117	
SUMMARY	#domain immunoglobulin homology #label IMM
	#length 145 #checksum 3310
Query Match	80.08; Score 698; DB 2; Length 145;

Db	20	EVOLVESGGGLVQPGKSLRLSCAASGFTFNDYAMHWYOAPEGKLEWVSGISWSSSIGY	79
Matches	98;	Conservative 13; Mismatches 10; Indels 5; Gaps 3,	

D_b

80 ADVYKRETTISRDNKKNSLYIQNNSLAEEDMALYYCYKGADYDSDGGFYFAVDPMWOGT 139
||| ||| ||| ||| ||| ||| ||| | : : : |||
61 ADSEVGRRTISRDKNKSLSYLQNNSSLRAEDTAAYVCARK--SYLSTAS--SLDY--WGOGT 115

QY	116	LVTSS	121	:
RESULT	9			

RESULT

```

ENTRY      S44111      #type complete
TITLE      Ig heavy chain V-D-J region
ORGANISM   Homo sapiens #common_name man
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
08-Sep-1997

ACCESSIONS
REFERENCE   S44111
AUTHORS    Hawlin, R.E.; Zhu, D.; Ovecko, M.; Winter, G.; Hamblin,
            T.J.; Stevenson, F.K.
SUBMISSION #submitted to the EMBL Data Library, March 1994
DESCRIPTION Idiotypic vaccination against human B-cell lymphoma :rescue
            of variable region gene sequences from biopsy material for
            assembly as single chain tv "personal" vaccine.
            S44111
ACCESSION  #accession
STATUS     ##status
            ##molecule_type DNA
            ##residues 1-120 ##label HAM
CLASSIFICATION
#cross-references EMBL:Z31387; NID:9472965; PID:9940522
FEATURES
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
            heterotetramer; immunoglobulin
SUMMARY    #domain immunoglobulin homology #label IMM
            #length 120 #molecular_weight 13256 #checksum 7849

Query Match      79.8% Score 696; DB 2; Length 120;
Best Local Similarity 80.2% Pred. No. 3,72e-89;
Matches 97; Conservative 10; Mismatches 13; Indels 1; Gaps 1;

Db 1 EVOLVESGGVYVQGGSLRLSCAASGFTPDYMHVRAQPGKGLWYSINMGCSNY 60
    |||||.....|.....|.....|.....|.....|.....|.....|.....|
Oy 1 EVOLVESGGGLVQGRSLRSCAASGFTPDYMHVRAQPGKGLWYSALTWNSGHIDY 60
    |||||.....|.....|.....|.....|.....|.....|.....|.....|
Db 61 ADVVKGRTTISRDNKSNLYLQNSLTEDTALYCAKDD-SGSYPEDYWGQGLTVTS 119
    |||||.....|.....|.....|.....|.....|.....|.....|.....|
Oy 61 ADVSEGRFTISRDNKSNLYLQNSLTAEEDTAYYCAKVSYLSTASLDYWGQGLTVTS 120
    |||||.....|.....|.....|.....|.....|.....|.....|.....|
Db 120 S 120
Oy 121 S 121

RESULT 10
ENTRY    S31112      #type complete
TITLE    Ig heavy chain - human
ORGANISM Homo sapiens #common_name man
DATE     02-Dec-1993 #sequence_revision 26-May-1995 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE S31112
AUTHORS   Raaphorst, F.M.; Timmers, E.; Kentor, M.J.H.; van Tol,
            M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
JOURNAL   Eur. J. Immunol. (1992) 22:247-251
TITLE     Restricted utilization of germ-line V(H)3 genes and short
            diverse third complementarity-determining regions (CDR3) in
            human fetal B lymphocyte immunoglobulin heavy chain
            rearrangements.
            S31112
#cross-references MIMD:92111633
#accession S31112
STATUS    ##status
            ##molecule_type mRNA
            ##residues 1-120 ##label RAA
            ##cross-references EMBL:X62961
            ##note the nucleotide sequence was submitted to the EMBL Data
            Library, October 1991
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
            heterotetramer; immunoglobulin
FEATURES
KEYWORDS   #domain immunoglobulin homology #label IMM
            #length 120 #molecular_weight 12974 #checksum 8808
SUMMARY    Query Match      79.4% Score 692; DB 2; Length 120;
            Best Local Similarity 77.7% Pred. No. 1,63e-88;

```

Matches	4;	Conservative	13;	Mismatches	13;	Indels	1;	Gaps	1;
Db	1	QVQLVSGGCVGPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVAVSYDGSNKRY	60	1	QVQLVSGGCVGPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVAVSYDGSNKRY	60			
Oy	1	EVQLVESGGGLVPGPGRSLRLSCAASGFTDDYAMHWVRQAPGKGLVAVSYDGSNKRY	60	1	EVQLVESGGGLVPGPGRSLRLSCAASGFTDDYAMHWVRQAPGKGLVAVSYDGSNKRY	60			
Db	61	ADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATGVVYVAAT-DYNGOGTLYTVS	119	61	ADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATGVVYVAAT-DYNGOGTLYTVS	119			
Oy	61	ADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATGVVYVAAT-DYNGOGTLYTVS	120	61	ADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATGVVYVAAT-DYNGOGTLYTVS	120			
Db	120	S 120		120	S 120				
Oy	121	S 121		121	S 121				
RESULT	11								
ENTRY	S31117	#type complete							
TITLE	Ig heavy chain - human								
ORGANISM	#formal_name Homo sapiens #common_name man								
DATE	02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999								
ACCESSIONS	S31117								
REFERENCE	S31104								
#authors	Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R.K.B.								
#journal	Eur. J. Immunol. (1995) 22:247-251								
#title	Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements.								
#cross-references	NCBI:92111633								
#accession	S31117								
#status	preliminary; nucleic acid sequence not shown; translation not shown								
#molecule_type	mRNA								
##residues	1-122 ##label RAA								
##cross-references	EMBL:X62967								
##note	The nucleotide sequence was submitted to the EMBL Data Library, October 1991								
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin								
KEYWORDS									
FEATURE									
15-98									
SUMMARY	#domain immunoglobulin homology #label IMM								
	#length 122 #molecular_weight 13664 #checksum 8338								
Query Match	79.1%; Score 690; DB 2; Length 122;								
Best Local Similarity	77.2%; Pred. No. 3,42e-88;								
Matches	95; Conservative 10; Mismatches 15; Indels 3; Gaps 3;								
Db	1	QVQLVSGGCVGPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVAVT-WYDGSNKRY	59	1	QVQLVSGGCVGPGRSLRLSCAASGFTSSYAMHWVRQAPGKGLVAVT-WYDGSNKRY	59			
Oy	1	EVQLVESGGGLVPGPGRSLRLSCAASGFTDDYAMHWVRQAPGKGLVAVTWSNGHIDY	60	1	EVQLVESGGGLVPGPGRSLRLSCAASGFTDDYAMHWVRQAPGKGLVAVTWSNGHIDY	60			
Db	60	YADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATDFAPRNMSHPDYNGOGTLYTV	119	60	YADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATDFAPRNMSHPDYNGOGTLYTV	119			
Oy	61	ADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATDFAPRNMSHPDYNGOGTLYTV	118	61	ADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYVCATDFAPRNMSHPDYNGOGTLYTV	118			
Db	120	VSS 122		120	VSS 122				
Oy	119	VSS 121		119	VSS 121				
RESULT	12								
ENTRY	S31114	#type complete							
TITLE	Ig heavy chain - human								
ORGANISM	#formal_name Homo sapiens #common_name man								
DATE	02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999								
ACCESSIONS	S31114								
REFERENCE	S31104								
#authors	Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R.K.B.								
#journal	Eur. J. Immunol. (1995) 22:247-251								

[illegible]

(TM)

21

5e-46RAT MHC V-BETA-11 (FRA 5.82e-04

OS HOMO SAPIENS (HUMAN).
OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ009526; E1311452; -.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9396 MW; 9063B32A CRC32;
Query Match 45.3%; Score 395; DB 4; Length 82;
Best Local Similarity 70.0%; Pred. No. 3 92e-61;
Matches 56; Conservative 9; Mismatches 12; Indels 3; Gaps 3;
Db 1 YAMHWROAPGKGLWVSID-GAGIDTYAESVGRFTISRDNSKNTLYLQMSLRAED 59
OY 32 YAMHWROAPGKGLWVSALTWNSG-HIDYADSVGRTISRDNAKNSLYLQMSLRAED 90
DB 60 TAVYCAKVDG-VSANSVDY 78
OY 91 TAVYCAKVSYLSTASLDY 110
RESULT 3
ID 075731 PRELIMINARY; PRT: 79 AA.
AC 075731;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).
OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ009528; E1311456; -.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8842 MW; 7C40774F CRC32;
Query Match 44.6%; Score 389; DB 4; Length 79;
Best Local Similarity 74.6%; Pred. No. 8 09e-60;
Matches 50; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Db 1 GATWVROAPGKGLWVSIVSAAGSIHYAKSVGRTISRDNSKNTLYLQMSLRAED 60
OY 33 AMHWVROAPGKGLWVSALTWNSGHIDYADSVGRTISRDNAKNSLYLQMSLRAED 92
DB 61 VYVCAKV 67
OY 93 VYVCAKV 99
RESULT 4
ID 075723 PRELIMINARY; PRT: 78 AA.
AC 075723;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).

OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ009520; E1311440; -.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9075 MW; DFEDD569 CRC32;
Query Match 44.0%; Score 384; DB 4; Length 78;
Best Local Similarity 79.4%; Pred. No. 1.00e-58;
Matches 50; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Db 1 WYRQAPGKGLWVXRISSDESRIYADSVKGRFTISRDNAKNTLYLQMSLRAEDTAVY 60
OY 36 WYRQAPGKGLWVSALTWNSGHIDYADSVGRTISRDNAKNSLYLQMSLRAEDTAVY 95
DB 61 CAR 63
OY 96 CAR 98
RESULT 5
ID 075726 PRELIMINARY; PRT: 77 AA.
AC 075726;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).
OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ009523; E1311446; -.
FT NON_TER 1 1
FT NON_TER 77 77
SQ SEQUENCE 77 AA; 9022 MW; EB7B458D CRC32;
Query Match 43.8%; Score 382; DB 4; Length 77;
Best Local Similarity 72.9%; Pred. No. 2.75e-58;
Matches 51; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
Db 1 YELTWROAPGKGLWVATINDEGEEKYVDSVGRFTISRDATNSLYLQMSLRAEDT 60
OY 32 YAMHWROAPGKGLWVSALTWNSGHIDYADSVGRTISRDNAKNSLYLQMSLRAEDT 91
DB 61 AVYVCAKVS 70
OY 92 AVYVCAKVS 101
RESULT 6
ID 075728 PRELIMINARY; PRT: 77 AA.
AC 075728;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS HOMO SAPIENS (HUMAN).
OC EURAROTIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

OC CATARRHINI; HOMINIDAE; HOMO.

RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.; "Human IgA and IgM secreting intestinal plasma cells carry heavily

RT mutated VH region genes.";

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009525; E1311450; -.

FT NON-TER 1 1

FT NON-TER 77 77

SO SEQUENCE 77 AA; 8925 MW; EA14CFDF CRC32;

Query Match 43.6%; Score 380; DB 4; Length 77;

Best Local Similarity 62.5%; Pred. No. 7.51e-58;

Matches 50; Conservative 17; Mismatches 10; Indels 3; Gaps 2;

DB 1 YMMNVRQAPGKGLGVSVITNGVTFYPSVKGFRFISRDNSRNTLYLQNNSLRAEDT 60

AC 075732; PRELIMINARY; PRT: 82 AA.

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

VH. HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

OC CATARRHINI; HOMINIDAE; HOMO.

RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.; "Human IgA and IgM secreting intestinal plasma cells carry heavily

RT mutated VH region genes.";

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009525; E1311450; -.

FT NON-TER 1 1

FT NON-TER 82 82

SO SEQUENCE 82 AA; 9387 MW; 440D63F2 CRC32;

Query Match 43.3%; Score 378; DB 4; Length 82;

Best Local Similarity 76.1%; Pred. No. 2.05e-57;

Matches 51; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

DB 1 Y-MDWVRQAPGKGLGVSVITNGVTFYPSVKGFRFISRDNSRNTLYLQNNSLRAEDT 58

AC 075727; PRELIMINARY; PRT: 80 AA.

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

VH. HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

OC CATARRHINI; HOMINIDAE; HOMO.

RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.; "Human IgA and IgM secreting intestinal plasma cells carry heavily

RT mutated VH region genes.";

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009524; E1311448; -.

FT NON-TER 1 1

FT NON-TER 80 80

SO SEQUENCE 80 AA; 9351 MW; 63DE158A CRC32;

Query Match 43.2%; Score 377; DB 4; Length 80;

Best Local Similarity 62.2%; Pred. No. 3.39e-57;

Matches 51; Conservative 14; Mismatches 13; Indels 4; Gaps 4;

DB 1 Y-MDWVRQAPGKGLGVSVITNGVTFYPSVKGFRFISRDNSRNTLYLQNNSLRAEDT 59

AC 075719; PRELIMINARY; PRT: 81 AA.

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

VH. HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

OC CATARRHINI; HOMINIDAE; HOMO.

RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.; "Human IgA and IgM secreting intestinal plasma cells carry heavily

RT mutated VH region genes.";

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009516; E1311432; -.

FT NON-TER 1 1

FT NON-TER 81 81

SO SEQUENCE 81 AA; 9074 MW; 288593C4 CRC32;

Query Match 43.0%; Score 375; DB 4; Length 81;

Best Local Similarity 63.8%; Pred. No. 9.27e-57;

Matches 51; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

DB 3 YMMNVRQAPGKGLGVSVITNGVTFYPSVKGFRFISRDNSRNTLYLQNNSLRAEDT 62

AC 075722; PRELIMINARY; PRT: 86 AA.

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

VH. HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

OC CATARRHINI; HOMINIDAE; HOMO.

```

RP      SEQUENCE FROM N.A..
RC      TISSUE=INTESTINE;.
RA      FISCHER M., KUEPPERS R.;
RT      "Human IgA and IgM secreting intestinal plasma cells carry heavily
RT      mutated VH region genes."
RL      SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR      EMBL: AJ009519; E1311438; -.
FT      NON_TER          1
FT      NON_TER          1
SO      SEQUENCE        86 AA; 9769 MW; 5F6AC773 CRC32;

Query Match           42.8%; Score 373; DB 4; Length 86;
Best Local Similarity 62.3%; Pred. No. 2,53e-56;
Matches    48; Conservative   15; Mismatches 14; Indels   0; Gaps   0.

Db      5 MKWVROADFGKLEWVASISGSGVIYIGESVKGRFTVSRDNAKNSLYLENMDLDEDTAV 64
         | | | | | | | | | | : : : | | | | | | | | | | | | | | |
Oy      34 MHWVROAGKGKLEWVASITWNHSHIDYADVSEGRFTISRDNAKNSLYLNQSLAEEDTAV 93
         | | | | | | | | | | : : : | | | | | | | | | | | | | | |
         65 YYCCARDRGAAGAICTDY 81
            | | | | | : : : : |
Oy      94 YYCARVSYLTASSLSLDY 110

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RESULT 11 PRELIMINARY; PRT; 72 AA.
ID 075738 AC 075738:
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH..
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.
RC TISSUE-INTESTINE.
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and IgM secreting intestinal plasma cells carry heavily
RL mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL, AJ009537; F1311470; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 72 AA; 8345 MW; EOFB044A CRC32;

Query Match 42.5%; Score 371; DB 4; Length 72;
Best Local Similarity 71.4%; Pred. No. 6,89e-56;
Matches 50; Conservative 10; Mismatches 9; Indels 1; Gaps 1.

Db 2 AMNWROAPGKLEIVSYIRSTGFYYTDSVRGRFTSSDIANKSVYLQWNSLRDDDTA 61
|:|||||||::|::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 33 AMHWROAPGKCLEVMSAITNMSGHDYADSVEGRFTISRDNAKNSLYIQWSIRAEDTA 92
|::|::|:
Db 62 VYCCARLAY 71
|::|::|:
Qy 93 VYCAK-VSY 101

RESULT 12 PRELIMINARY; PRT; 81 AA.
ID 075721 AC 075721:
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH..
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
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RC	TISSUE=TESTES;
RA	FISCHER M., KUEPPERS R.;
RT	"Human IgA and Igm secreting intestinal plasma cells carry heavily
RT	muted VA region genes."
RL	SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR	EMBL; AJ009518; E1311436; -.
FT	NON_TER 1
FT	NON_TER 81
SO	SEQUENCE 81 AA; 9466 MW; ED58A5B2 CRC32;
 Query Match 42.5%; Score 371; DB 4; Length 81; Best Local Similarity 72.1%; Pred. No. 6,89e+56; Matches 49; Conservative 7; Mismatches 10; Indels 2; Gaps 2;	
Dd	2 YSMNNVROAPQKGLEWWSLIC-TTDRATFYASVSRGFTISRDDAKSLYQMNTSLRDD 60 : : : : : : : : : : : : : : : Oy 32 YAMHNVROAPQKGLEWWSAITMNSGHID-YADSVEGFITSRDNAKNLSLYQNMSLRADD 90 : :
Dd	61 TAVYYCAR 68 :
Oy	91 TAVYYCAK 98

RESULT	13		PRELIMINARY:	PRT:	77 AA.	
ID	075741					
AC	075741.					
DT	01-NOV-1998	(TREMBLREL. 08,	CREATED)			
DT	01-NOV-1998	(TREMBLREL. 08,	LAST SEQUENCE UPDATE)			
DT	01-NOV-1998	(TREMBLREL. 08,	LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).					
GN	VH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA;	VERTEBRATA; MAMMALIA;	EUTHERIA; PRIMATES;			
OC	CATARRHINI; HOMINIDAE; HOMO.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-INTESTINE.					
RA	FISCHER M., KUEPPERS R.;					
RP	TISSUE-INTESTINE.					
RT	"Human Iga and IgM secreting intestinal plasma cells carry heavily					
RL	mutated VH region genes."					
DR	SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.					
EMBL:	AJ009540; E1311476; -.					
FT	NON_TER	1	1			
FT	NON_TER	77	77			
SQ	SEQUENCE	77 AA;	8734 MB;	1c7f9e8e CRC32;		
Query Match		42.4%;	Score 370;	DB 4;	Length 77;	
Best Local Similarity		66.7%;	Pred. No. 1,14e-55;			
Matches	52;	Conservative	12;	Mismatches	12;	
			Indels	2;	Gaps	2;
Dd	2 MSWQAAGKGLGVSGISGSDTYTADSVKGRFTTSRDNSKNLTSLQLNSTAEDTAV	61				
Oy	34 MHMVQAAGKGLGVSAITWN SGHIDYADVSGRFTTSRDNAKNSLYLOHNSLAEDTAV	93				
Dd	62 YYCAR-HYYDS-SPEPDYW	77				
Oy	94 YTCARVSTLSTRASSLDYV	111				
RESULT	14		PRELIMINARY:	PRT:	80 AA.	
ID	075735					
AC	075735.					
DT	01-NOV-1998	(TREMBLREL. 08,	CREATED)			
DT	01-NOV-1998	(TREMBLREL. 08,	LAST SEQUENCE UPDATE)			
DT	01-NOV-1998	(TREMBLREL. 08,	LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).					
GN	VH.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA;	VERTEBRATA; MAMMALIA;	EUTHERIA; PRIMATES;			
OC	CATARRHINI; HOMINIDAE; HOMO.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-INTESTINE.					

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 W P E R E H
 (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:13:15 1999; Maspar time 5.30 Seconds
 Tabular output not generated. 645.271 Million cell updates/sec

Title: >US-08-599-226-2
 Description: (1-121) from US08599226.pap
 Perfect Score: 872
 Sequence: 1 EVOLVESGGGLVQPGKSLRL.....LSTASLDYWGQGLTVVSS 121

Scoring table:
 Gap 11
 PAM 150

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 41.985; Variance 74.241; scale 0.566

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	685	78.6	122	1	HV3G_HUMAN	IG HEAVY CHAIN V-III R 3.03e-127
2	675	77.4	122	1	HV3H_HUMAN	IG HEAVY CHAIN V-III R 6.21e-125
3	672	77.1	120	1	HV3J_HUMAN	IG HEAVY CHAIN V-III R 3.06e-124
4	669	76.7	121	1	HV3J_HUMAN	IG HEAVY CHAIN V-III R 1.51e-123
5	647	74.2	119	1	HV3I_HUMAN	IG HEAVY CHAIN V-III R 1.79e-118
6	632	72.5	116	1	HV3I_HUMAN	IG HEAVY CHAIN V-III R 5.08e-115
7	632	72.5	119	1	HV3L_HUMAN	IG HEAVY CHAIN V-III R 5.08e-115
8	623	71.4	126	1	HV3K_HUMAN	IG HEAVY CHAIN V-III R 5.96e-113
9	621	71.2	122	1	HV3A_HUMAN	IG HEAVY CHAIN V-III R 1.72e-112
10	611	70.1	136	1	HV16_MOUSE	IG HEAVY CHAIN PRECURS 3.39e-110
11	590	67.7	117	1	HV3C_HUMAN	IG HEAVY CHAIN PRECURS 2.21e-105
12	577	66.2	119	1	HV40_MOUSE	IG HEAVY CHAIN V REGIO 2.08e-102
13	572	65.6	119	1	HV3J_MOUSE	IG HEAVY CHAIN V REGIO 2.88e-101
14	571	65.5	114	1	HV3B_HUMAN	IG HEAVY CHAIN V-III R 4.88e-101
15	564	64.7	115	1	HV3F_HUMAN	IG HEAVY CHAIN V-III R 1.93e-99
16	563	64.6	115	1	HV3D_HUMAN	IG HEAVY CHAIN V-III R 3.27e-99
17	562	64.4	142	1	HV01_RAT	IG HEAVY CHAIN PRECURS 5.52e-99
18	561	64.3	119	1	HV3K_HUMAN	IG HEAVY CHAIN V-III R 9.34e-99
19	560	64.2	120	1	HV3E_HUMAN	IG HEAVY CHAIN V-III R 1.38e-98
20	560	64.2	122	1	HV20_MOUSE	IG HEAVY CHAIN V REGIO 1.58e-98
21	555	63.6	119	1	HV3P_HUMAN	IG HEAVY CHAIN V-III R 2.18e-97
22	554	63.5	119	1	HV3M_HUMAN	IG HEAVY CHAIN V-III R 3.68e-97
23	552	63.3	123	1	HV18_MOUSE	IG HEAVY CHAIN V REGIO 1.05e-96

24	549	63.0	117	1	HV02_CANFA	IG HEAVY CHAIN V REGIO 5.07e-96
25	549	63.0	123	1	HV19_MOUSE	IG HEAVY CHAIN V REGIO 5.07e-96
26	547	62.7	116	1	HV05_CARAT	IG HEAVY CHAIN PRECURS 1.45e-95
27	547	62.7	123	1	HV23_MOUSE	IG HEAVY CHAIN V REGIO 1.45e-95
28	546	62.6	122	1	HV21_MOUSE	IG HEAVY CHAIN V REGIO 2.44e-95
29	544	62.4	123	1	HV24_MOUSE	IG HEAVY CHAIN V REGIO 6.96e-95
30	543	62.3	119	1	HV38_MOUSE	IG HEAVY CHAIN V REGIO 1.18e-94
31	543	62.3	123	1	HV22_MOUSE	IG HEAVY CHAIN V REGIO 1.18e-94
32	542	62.2	123	1	HV25_MOUSE	IG HEAVY CHAIN V REGIO 1.98e-94
33	539	61.8	116	1	HV3R_HUMAN	IG HEAVY CHAIN V-III R 9.34e-94
34	539	61.8	117	1	HV17_MOUSE	IG HEAVY CHAIN V REGIO 9.34e-94
35	538	61.7	117	1	HV30_HUMAN	IG HEAVY CHAIN V-III R 1.61e-93
36	534	61.2	98	1	HV57_MOUSE	IG HEAVY CHAIN V REGIO 1.31e-92
37	533	61.1	117	1	HV26_MOUSE	IG HEAVY CHAIN V REGIO 2.20e-92
38	532	61.0	144	1	HV26_MOUSE	IG HEAVY CHAIN PRECURS 3.72e-92
39	531	60.9	117	1	HV54_MOUSE	IG HEAVY CHAIN PRECURS 6.27e-92
40	531	60.9	117	1	HV55_MOUSE	IG HEAVY CHAIN PRECURS 6.27e-92
41	530	60.8	117	1	HV56_MOUSE	IG HEAVY CHAIN V REGIO 1.06e-91
42	525	60.2	118	1	HV39_MOUSE	IG HEAVY CHAIN V REGIO 2.43e-90
43	524	60.1	118	1	HV3V_HUMAN	IG HEAVY CHAIN V-III R 4.10e-90
44	523	60.0	114	1	HV01_CANFA	IG HEAVY CHAIN V REGIO 4.10e-90
45	523	60.0	115	1	HV35_HUMAN	IG HEAVY CHAIN V-III R 4.10e-90

ALIGNMENTS

RESULT 1
 ID HV3G_HUMAN STANDARD: PRT: 122 AA.

AC P01768;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)

DE IG HEAVY CHAIN V-III REGION (CAM).

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]

RP SEQUENCE.

RX MEDIANE; 81013859.

RA LEHMAN D.W.; PUTNAM F.W.;

RT "Amino acid sequence of the variable region of a human mu chain;

RT location of a possible JH segment."

RL PROC. NATL. ACAD. SCI. U.S.A. 77:3239-3243(1980).

CC -1- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH

MACROGLOBULINEMIA.

CC PIR; A02051; M3HGM.

DR PIR; A02051; M3HGM.

DR PIR; A02051; M3HGM.

DR HSSP; P01772; 2162.

KV IMMUNOGLOBULIN V REGION.

FT MOD.RES

FT NON_TER

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

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FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

FT SEQUENCE

Query Match	78.6%	Score 685;	DB 1;	Length 122;
Best Local Similarity	70.5%	Pred. No. 3.03e-127;		
Matches	86;	Conservative	22;	Mismatches 13;
				Indels 1;
				Gaps 1;

DB	1	EVOLVESGGGLVQPGKSLRLSCAASGFTFSNYAMHVRQPPKGLKLEWYAVISGGBKRY 60
QY	1	EVOLVESGGGLVQPGKSLRLSCAASGFTFDYAMHWQAQPKGLEWYSAITWNSGHIDY 60
DB	61	ASVYGRFTISDPSKREYLYLQMSLRARVAVYICADRPYGYRPAFTWGGGLTVV 120
QY	61	ADVSGRFTISDPSKREYLYLQMSLRARVAVYICADRPYGYRPAFTWGGGLTVV 119
DB	121	SS 122
QY	120	SS 121
RESULT 2		
ID	HV3H_HUMAN	STANDARD: PRT: 122 AA.
AC	P01769;	

[illegible]

```

RP      SEQUENCE: 79124695.
RX      MEDLINE;
RA      CHIU Y.-Y.H., LOPEZ DE CASTRO J.A., POLJAK R.J.;
RT      "Amino acid sequence of the VH region of human myeloma
RL      cryoglobulinoglobulin IgG H1."
RL      BIOCHEMISTRY 18:553-560(1979).
CC      -I THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
DR      PIR: A02054; GIDUHL.
DR      PRAM; PEO0047; 1g; 1.
DR      HSSP; P01772; 2IG2.
RW      IMMUNOGLOBULIN V REGION.
FT      MOD_RES          1
FT      NON_TER         121    121
SQ      SEQUENCE       121 AA; 13566 MW; 8E91B7EC CRC32;

Query Match           76.7%; Score 669; DB 1; Length 121;
Best Local Similarity 71.3%; Fred. No. 1.51e-123;
Matches   87; Conservative 20; Mismatches 13; Indels 2; Gaps 2

Db      1 QVLTQAGGGVOPGRSLRLSCIASGFETSYNGAHWRQAPGKLEWAVI-WYNGSRTY 59
        :|:::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|
Qy      1 EQVLVESGGGLVPGRSRLRSCASGTFEDDYAAHWWRQAPGKLEWVSALTW-NSGHID 59
        ::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Db      60 YDSYSKGFPTISRDNSKRTLYIMANSRTEDTAVAYICARDDILITAFSDIWGGGLVTY 119
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy      60 YADSEGRFTISRDAKSKNTYLQNMSLRAEDETVAYICAKVSYLSTASSLDYWGGGLVTY 119
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||

Db      120 SS 121
Qy      120 SS 121

RESULT 5
AC      HV31_HUMAN          STANDARD;             PRT;              119 AA.
ID      P01770;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE      IG HEAVY CHAIN V-II REGION (NIE).
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CARNIVORINII; HOMINIDAE; HOMO.
RN      [1]
RP      SEQUENCE.
RX      MEDLINE; 77070269.
RA      PONSINGL H., HILSCHMANN N.;
RT      "The role of antibody structure. The primary structure of a
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[illegible]

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Db      1 EVQVYESGGDLYQPERSR.LRLSCAASGFEFBGLTWTWRQAPGKGLEWYANKRZGSZBY 60
        |E|V|Q|V|Y|E|S|G|G|D|Y|Q|P|E|R|S|R|L|S|C|A|S|G|F|E|F|B|G|L|T|W|T|W|R|Q|A|P|G|K|G|L|E|W|Y|A|N|K|R|Z|G|S|Z|B|Y|
Qy      1 EVQVYESGGGLVQPERSR.LRLSCAASGFEFFDDYANHWYRQAPGKGLEWYSAITWNSGHIDY 60
        |E|V|Q|V|Y|E|S|G|G|L|V|Q|P|E|R|S|R|L|S|C|A|S|G|F|E|F|D|D|Y|A|N|H|W|Y|R|Q|A|P|G|K|G|L|E|W|Y|S|A|I|T|W|N|S|G|H|I|D|Y|

Db      61 VDSVYGRFTISRDNAKNSLYLQMSLSLRVEDYALYYCAR-GW--GGG-DYWGCGTLTVTS 115
        |V|D|S|V|Y|G|R|F|T|I|S|R|D|N|A|K|N|S|Y|L|Q|M|S|L|S|R|V|E|D|Y|A|L|Y|Y|C|A|R|-|G|W|-|-|G|G|G|-|D|Y|W|G|C|G|T|L|T|V|T|S|
Qy      61 ADSVYGRFTISRDNAKNSLYLQMSLSLRVEDYAVYYCAVSVLSYSLASSLDYWGCGTLTVTVS 120
        |A|D|S|V|Y|G|R|F|T|I|S|R|D|N|A|K|N|S|Y|L|Q|M|S|L|S|R|V|E|D|Y|A|V|Y|Y|C|A|V|S|V|L|S|Y|S|L|A|S|S|L|D|Y|W|G|C|G|T|L|T|V|T|S|

Db      116 T 116
        |T|
Qy      121 S 121

RESULT 7
ID      HV3L_HUMAN          STANDARD;          PRT;          119 AA.
AC      P01773;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE      IG HEAVY CHAIN V-III REGION (BDR).
OS      HOMO SAPIENS (HUMAN).
OC      EDUAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
CN      [1]
RP      SEQUENCE (MYELOMA PROTEIN BDR).
RX      MEDLINE: 79151016.
RA      PUTNAM F.W., LIO Y.-S.V., LOW T.L.K.;
RT      "Primary structure of a human IgM1 immunoglobulin. IV. Streptococcal
RT      IgM1 protease, digestion, Fab and Fc fragments, and the complete
RT      amino acid sequence of the alpha 1 heavy chain.";
RL      J. BIOL. CHEM. 254:2865-2874(1979).
DR      PIR: A02056; ALHDBR.
DR      PIR: PRO0047; Ig; 1.
DR      HSSP: P01772; 2IG2.
RW      IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT      MOD_RES          1          PYRROLIDONE CARBOXYLIC ACID.
FT      DISULFID        22          96
FT      CARBOHYD        28          28
FT      NON_TER         119        119
SQ      SEQUENCE 119 AA; 12981 MW; 323A4FE1 CRC32;

Query Match          72.5%; Score 632; DB 1; Length 119;
Best Local Similarity 65.8%; Pred. No. 5,08e-115;
Matches 79; Conservative 27; Mismatches 12; Indels 2; Gaps 1

Db      1 QVQVYESGGGYQAGTSLRLSCTISAEFLSYDANHWYRQAPGKGLZVVALISYGSBTYY 60
        |Q|V|Q|V|Y|E|S|G|G|Y|Q|A|G|T|S|R|L|S|C|T|I|S|A|E|F|L|S|Y|D|A|N|H|W|Y|R|Q|A|P|G|K|G|L|Z|V|V|A|L|I|S|Y|G|S|B|T|Y|Y|
Qy      1 EVQVYESGGGLVQPERSR.LRLSCAASGFEFFDDYANHWYRQAPGKLEWYSAITWNSGHIDY 60
        |E|V|Q|V|Y|E|S|G|G|L|V|Q|P|E|R|S|R|L|S|C|A|S|G|F|E|F|D|D|Y|A|N|H|W|Y|R|Q|A|P|G|K|L|E|W|Y|S|A|I|T|W|N|S|G|H|I|D|Y|

Db      61 ADSVYGRFTISRBLSKBLLYLZMKTLTREDYAVYYCAKL--IAYAGTBBFAGCGTLTVTS 118
        |A|D|S|V|Y|G|R|F|T|I|S|R|B|L|S|K|B|L|Y|L|Z|M|K|T|L|T|R|E|D|Y|A|V|Y|Y|C|A|K|L|-|-|I|A|Y|A|G|T|B|B|F|A|G|C|G|T|L|T|V|T|S|
Qy      61 ADSVYGRFTISRDNAKNSLYLQMSLSLRVEDYAVYYCAKVSLSYSLASSLDYWGCGTLTVTVS 120
        |A|D|S|V|Y|G|R|F|T|I|S|R|D|N|A|K|N|S|Y|L|Q|M|S|L|S|R|V|E|D|Y|A|V|Y|Y|C|A|K|V|S|L|S|Y|S|L|A|S|S|L|D|Y|W|G|C|G|T|L|T|V|T|S|

RESULT 8
ID      HV3L_HUMAN          STANDARD;          PRT;          126 AA.
AC      P01772;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE      IG HEAVY CHAIN V-III REGION (KOL).
OS      HOMO SAPIENS (HUMAN).
OC      EDUAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
CN      [1]
RP      SEQUENCE, AND DISULFIDE BONDS.
RX      MEDLINE: 83289131.
RA      SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;
RT      "Three-dimensional structure determination of antibodies. Primary
RT      structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",
RL      HOPPE-SELYER S Z. PHYSIOL. CHEM. 364:713-747(1983).
CN      [2]

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FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
SO SEQUENCE 136 AA: 15071 MW: 24BFD28 CRC32:
Query Match
Best Local Similarity 68.1%; Score 611; DB 1; Length 136;
Matches 84; Conservative 19; Mismatches 16; Indels 3; Gaps 3;
Db 17 DVALYESGGGLVQPGSRKLSCAASGFTFFSSGMMWVROAPKGLGEMVAYISSGSTLAY 76
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLVESGGGLVQPGSRIRLSCAASGFTFDDYAMHWVROAPKGLGEMVSAITWNSGHIDY 60
17 ADVYAGREFTISDRNKNLTFLQMTLSRSDDTAMMYCARBNGN-pv-YANDYAGGOSTVTV 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADVYAGREFTISDRNKNNSLYLQMNLSLRADVIAYVYCAK-VSYLSTASSLIDYGGGLTVTV 119
Db 135 SS 136
||
QY 120 SS 121
RESULT 11
ID HV3C_HUMAN STANDARD: PRT: 117 AA.
AC P01764:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-II REGION (VH26).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81101090.
RA MATTHYSSENS G., RABBITTS T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region."
RL PROC. NATL. ACAD. SCI. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
R EMBL: J00236; G553412; -.
R EMBL: M35415; G553422; -.
R PIR: A02047; H3H026.
R PIR: PF00047; I9; 1.
DR IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-II REGION (VH26).
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12582 MW: 15A21B2A CRC32:
Query Match
Best Local Similarity 83.7%; Score 590; DB 1; Length 117;
Matches 82; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Db 20 EVOLIESGGGLVQPGSRIRLSCAASGFTFFSSYAMSWVROAPKGLGEMVSAISGSGSTYY 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVOLYESGGGLVQPGSRIRLSCAASGFTFDDYAMHWVROAPKGLGEMVSAITWNSGHIDY 60
Db 80 GDSVAGREFTISDRNKNLTFLQMNLSLRADVIAYVYCAK 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADVYAGREFTISDRNKNNSLYLQMNLSLRADVIAYVYCAK 98
RESULT 12
ID HVAO_MOUSE STANDARD: PRT: 119 AA.
AC P01810:

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DE 21-JUL-1986 (REL. 01, CREATED)
DE 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (J539).
OS MUS MUSCULUS (MOUSE).
OC EUDARCTA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ROENTLIA; SCUROGNATHI; MORIDAE; MURINAE; MUS.
RN [1]
RP PRELIMINARY SEQUENCE.
RX MEDLINE; 79223895.
RA RAO D.N., RUDIKOFF S., KRUTZSCH H., POTTER M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL PROC. NATL. ACAD. SCI. U.S.A. 76:2890-2894 (1979).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE; 88217852.
RA SUH S.W., BHAT T.N., NAVIA M.A., COHEN G.H., RAO D.N., RUDIKOFF S.,
RA DAVIES D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT study at 2.6-A resolution."
RL PROTEINS 1:74-80 (1986).
CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS
CC GALACTAN.
DR PIR: A02080; AVMSJ5.
DR PDB: 2FBJ; 15-OCT-90.
DR PFAM: PF00047; 19; 1.
KW IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
FT NON_TER 119 119
FT STRAND 3 7
FT TURN 10 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURN 101 103
FT STRAND 104 108
FT STRAND 112 116
SQ SEQUENCE 119 AA; 13240 MW; 6892320D CRC32;

Query Match 66.2%; Score 577; DB 1; Length 119;
Best Local Similarity 66.1%; Pred. No. 2,08e-102;
Matches 80; Conservative 19; Mismatches 19; Indels 3; Gaps 2.

Db 1 EVKLLESGGLVOPGGSILKISCAASGFDFSKYWNVRAOPAGKLEWIGEIHPDSGTINY 60
||:|||||:|||||:|||||:| | | | | | | | | | | | | | | | | | | | | |
Oy 1 EVQLVESGGGLVQPGSRSLRISCAASGETFPDYAHHWVRAOPAGKLEWVSAITWNSCHIDY 60
||:|||||:|||||:|||||:| | | | | | | | | | | | | | | | | | | | | |

Db 61 TPSLKDKTIIIRDNAAKNSLYLQMSKVSSEDTALYYCARLHYIGY-NA--YWGQGLTVTS 117
||:|:|||||:|||||:|||||:| | | | | | | | | | | | | | | | | | | | | |
Oy 61 ADSEVGRFTIRDNAAKNSLYLQMNLSRAEDTAYVYCAKVSYLSYASSLDYWGQGLTVTS 120
||:|:|||||:|||||:|||||:| | | | | | | | | | | | | | | | | | | | | |

Db 118 A 118
Oy 121 S 121

RESULT 13
ID HV37.MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DE 21-JUL-1986 (REL. 01, CREATED)
DE 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

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Thu Sep 2 11:09:22 1999; MasPar time 9.64 Seconds

DIQMTQSPSSLSASVGDRVT...CQRYNRAPTYEGQGTKEIK 107

Gap 11

I:sp_ar

13:sp_vertebrate 14:sp_virus

and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
	1	516	68.6		130	11	P80913	IG KAPPA CHAIN V REGIO	4.01e-90
	2	322	42.8		100	4	Q15353	V KAPPA (FRAGMENT)	1.31e-46
	3	301	40.0		50	4	Q15353	DNA REARRANGED BY A T	4.75e-42
	4	218	29.0		145	4	Q16237	VPRE-B PROTEIN.	1.50e-24
	5	181	24.1		133	7	Q31178	MHC CLASS II I-A-BETA	3.90e-17
	6	162	21.5		135	4	O99602	TRGV4F PROTEIN (FRAGE	1.81e-13
	7	162	21.5		509	11	O08907	SHAP IMMUNOLOGICAL-I1	1.80e-13
	8	161	21.4		513	11	P97797	BHN SUBSTRATE-1 PRECR	2.80e-13
	9	160	21.3		132	7	Q31175	MHC CLASS II I-A-ALPHA	4.35e-13
	10	160	21.3		137	7	Q31181	MHC CLASS II I-A-ALPHA	4.35e-13
	11	156	20.7		509	11	O35924	PROTEIN TYROSINE PHOS	2.43e-12
	12	155	20.6		123	11	Q61243	SHS20 PROTEIN PRECURSO	3.79e-12
	13	148	19.7		132	7	Q31177	MHC CLASS II I-A-ALPHA	7.60e-11
	14	145	19.4		117	11	O61863	INTEGRAL MEMBRANE PROT	1.77e-10
	15	145	19.3		120	7	Q31212	TRANSMEMBRANE PROTEIN	2.71e-10
	16	144	19.1		503	4	P78324	SHP SUBSTRATE-1 PRECR	4.13e-10
	17	141	18.8		288	4	O00517	HPD-1.	1.45e-09
	18	139	18.5		117	7	Q31278	RAT MHC V-BETA-11 (FRA	3.35e-09
	19	139	18.5		134	7	Q31180	MHC CLASS II I-A-BETA	3.35e-09
	20	139	18.5		291	11	O88556	INHIBITORY RECEPTOR SH	3.35e-09

21	139	8.5	509.11	088555	INHIBITORY RECEPTOR SH	3.35e-09
22	134	17.8	100.6	076524	SURROGATE LIGHT CHAIN	2.65e-08
23	134	17.8	398.4	000241	SIGNAL-REGULATORY PROT	2.65e-08
24	131	17.4	135.7	031174	MHC CLASS II I-A-ALPHA	9.02e-08
25	128	17.0	509.11	P97170	SHC SUBSTRATE-1 PRECUR	3.04e-07
26	125	16.6	418.11	070426	SIGNAL REGULATORY PROT	1.01e-06
27	123	16.4	82.4	075732	IG HEAVY CHAIN VARIABLE	2.25e-06
28	122	16.2	122.4	099604	TIGV9 (FRAGMENT)	3.34e-06
29	122	16.2	122.4	099603	TIGV9 (FRAGMENT)	3.34e-06
30	120	16.0	89.7	095578	CLASS II MAJOR HISTOC	7.34e-06
31	119	15.8	506.6	046631	MYD-1 ANTIGEN PRECURSO	1.09e-05
32	118	15.7	85.4	075724	IG HEAVY CHAIN VARIABLE	1.61e-05
33	118	15.7	118.7	031176	MHC CLASS II I-A-ALPHA	1.61e-05
34	116	15.4	113.3	090532	NOVEL ANTIGEN RECEPTOR	3.49e-05
35	113	15.0	78.4	075739	IG HEAVY CHAIN VARIABLE	1.11e-04
36	112	14.9	235.13	090770	CD8 ALPHA CHAIN PRECUR	1.62e-04
37	111	14.8	72.4	015638	CD8 ALPHA CHAIN PRECUR	2.36e-04
38	109	14.5	506.6	046632	MYD-1 ANTIGEN PRECURSO	5.03e-04
39	108	14.4	167.13	F79985	CD8 ALPHA CHAIN (FRAGM	7.31e-04
40	106	14.1	16.1	079461	LIGHT-CHAIN COMPLEMENTA	1.54e-03
41	106	14.1	16.14	079455	LIGHT-CHAIN COMPLEMENTA	1.54e-03
42	106	14.1	16.14	079456	LIGHT-CHAIN COMPLEMENTA	1.54e-03
43	106	14.1	16.14	079453	LIGHT-CHAIN COMPLEMENTA	1.54e-03
44	106	14.1	97.4	043324	RHEUMATOID FACTOR RF-E	1.54e-03
45	105	14.0	397.6	009261	CD4 (CD4) (FRAGMENT)	2.22e-03

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	130 AA.
ID	P80913;			
AC	P80913;			
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)			
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V REGION PRECURSOR.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;			
OC	SCIUROGNATHI; MORIDAE; MORINAE; MUS.			
RP	(1)			
RP	SEQUENCE FROM N.A.			
RA	JANON K.;			
RL	SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; J79906; E269393; ALT TERM.			
KM	IMMUNOGLOBULIN V REGION; SIGNAL.			
FT	SIGNAL. 1 22 POTENTIAL.			
FT	CHAIN 23 130 IG KAPPA CHAIN V REGION.			
SQ	SEQUENCE 130 AA; 14124 MW; 1DC6F7D9 CRC32;			
Query Match		68.6%;	Score 516;	DB 11; Length 130;
Best Local Similarity		63.9%;	Pred. No. 4,01e-90;	
Matches	69;	Conservative	23;	Mismatches 15; Indels 1; Gaps 1
Dy	23 QIVLTSPALMAGNSLGERVTMTCTNASSVSSSYLHWTQOKPSSPKIMITYISNLSAGVP 82			
Qy	1 DIQMTSPSSLSASVGDRTYITICRASOGIRN-YLAWQOKPGAKPRLIYASTLOSQVP 59			
Dy	83 ARSSGSGSCTSYLTSSMEADATYYCHQYHRFPPTFGGTRKLE 130			
Qy	60 SRSSGSGSCTDFTLTLSLQPDVATYYCQYNNAPFTFGGTRKLE 107			
RESULT	2	PRELIMINARY:	PRT:	100 AA.
ID	Q15535			
AC	Q15535;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)			
DE	V KAPPA (FRAGMENT).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;			
OC	CATARRHINI; HOMINIDAE; HOMO.			
IN	(1)			

RP SEQUENCE FROM N.A.
RA KATO S., TACHIBANA K., TAKAYAMA N., KATARA H., YOSHIDA M.C.,
RA TAKANO T.;
RT "Genetic recombination in a chromosomal translocation t(2;8)
RT (p11;q24) of a Burkitt's lymphoma cell line, KOB101.";
RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D90161; D1014896; -.
DR PFAM: PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 100 AA; 10871 MW; 06A1440D CRC32;
Query Match 42.8%; Score 322; DB 4; Length 100;
Best Local Similarity 53.8%; Pred. No. 1.31e-46;
Matches 50; Conservative 18; Mismatches 20; Indels 5; Gaps 3;
Db 1 DVMYTOPPLSYTPPGAPASISCKSIQSLHSDGKTYLXXLQKPGSPOLLIEVSRRF 60
QY 1 D1QMTGSPSSLSASVGDVITTCRASGIGI-R-N--YLAWYQKPGKAPKLLIYAASLTQ 55
QY 61 SGVPRFSGSGGTDFTLKISRVEAEDVGVYCC 93
QY 56 SGVPRFSGSGGTDFTLKISRVEAEDVGVYCC 88

RESULT 3
ID Q15533 PRELIMINARY; PRT; 50 AA.
AC Q15533;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DNA REARRANGED BY A T(2;8) TRANSLOCATION LEADING TO BURKITT'S
DE LYMPHOMA IN THE CELL LINE JI (CLONE JIP).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA KLOBECK H.G.;
RL SUBMITTED (AUG-1987) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 36-50 FROM N.A.
RX MEDLINE; 87259967.
RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
RT "N segment insertion and region-directed somatic hypermutation in a
RT kappa gene of a t(2;8) chromosomal translocation.";
RL NUCLEIC ACIDS RES. 15:4877-4888(1987).
DR EMBL: X05929; E12675; -.
FT CHAIN 1
FT NON_TER 50 AA; 5486 MW; 65586C19 CRC32;
SQ SEQUENCE 50 AA; 5486 MW; 65586C19 CRC32;
Query Match 40.0%; Score 301; DB 4; Length 50;
Best Local Similarity 89.4%; Pred. No. 4.75e-42;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 4 D1QMTGSPSSLSASVGDVITTCRASGIGI-R-N--YLAWYQKPGKAPKLL 50
QY 1 D1QMTGSPSSLSASVGDVITTCRASGIGI-R-N--YLAWYQKPGKAPKLL 47

RESULT 4
ID Q16237 PRELIMINARY; PRT; 145 AA.
AC Q16237;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE VPRE-B PROTEIN.
GN VPRE-B.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95021318.

RA GUELPA-FONTLUPT V., BOSSY D., ALZARI P., FUMOUX F., FOUGEREAU M.,
RA SCHIFF C.;
RT "The human pre-B cell receptor: structural constraints for a
RT tentative model of the pseudo-light (psl L) chain.";
RL MOL. IMMUNOL. 31:1099-1108(1994).
DR EMBL: S74019; G693811; -.
DR PFAM: PF00047; 1g; 1.
SQ SEQUENCE 145 AA; 16605 MW; 7E7002CB CRC32;
Query Match 29.0%; Score 218; DB 4; Length 145;
Best Local Similarity 40.4%; Pred. No. 1.50e-24;
Matches 40; Conservative 22; Mismatches 28; Indels 9; Gaps 8;
Db 24 HOPPAMSSAAGTIRLCTLRNDHDIGVSVYQOQPGHPFLRYFSQSDKSGQPGV 83
QY 6 QSPSSLSASVGDVITTC--RASGIRNY-LAWYQKPGKAPKLLIYAASLTQSG-V 58
QY 84 PPRPSSKDVARNRGYISLQPEDEAMYYCAMGARS 122
QY 59 PSRPSGS-GSGTDFT-LTISLQPEDEVATYYCORYNAP 95

RESULT 5
ID Q31178 PRELIMINARY; PRT; 133 AA.
AC Q31178;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MHC CLASS II I-A-BETA mRNA
DE (H-2B), 5' END, HYBRIDOMA DA.33.C2 PRECURSOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIDROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87224052.
RA SPINELLA D.G., HANSEN T.H., WALSH W.D., BEHKE M.A., TILLINGHAFT J.P.,
RA CHOU H.S., WHITELEY P.J., KAPP J.A., PIERCE C.W., SHEVACH E.M.,
RA LOH D.Y.;
RT "Receptor diversity of insulin-specific T cell lines from C57BL
RT (H-2b) mice.";
RL J. IMMUNOL. 138:3991-3995(1987).
DR EMBL: M16679; G199470; -.
DR PFAM: PF00047; 1g; 1.
KW SIGNAL; MHC.
FT SIGNAL 1
FT CHAIN 20
FT NON_TER 133
FT NON_TER 133
SQ SEQUENCE 133 AA; 15124 MW; 51D600EF CRC32;
Query Match 24.1%; Score 181; DB 7; Length 133;
Best Local Similarity 31.9%; Pred. No. 3.90e-17;
Matches 36; Conservative 30; Mismatches 38; Indels 9; Gaps 8;
Db 20 NTKITGSPRYLLIGRANK-SLECEOHLG-HNAMYWKQSAKEPPEFLYNLQOLINRETV 77
QY 1 D1QMTGSPSSLSASVGDVITTCRASGIGI-R-N--YLAWYQKPGKAPKLLIYAASLTQSG-V 58

Db 78 PSRPIPCDSSKLLHISAVDPEDSNVYFCASQDRAQONTLYFGAGRTLSV 130
QY 59 PSRPSGS-GSGTDFT-LTISLQPEDEVATYYCORY-NRAP-YT--FGGKRVKI 106

RESULT 6
ID Q99602 PRELIMINARY; PRT; 135 AA.
AC Q99602;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TRGVAF PROTEIN (FRAGMENT).
GN TRGVAF.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

Query Match	Best Local	Similarity	27.4%	Score 161:	DB 11:	Length 513:
Matches	27:	Conservative	30:	Mismatches 36:	Indels 5:	Gaps 5:
Db	33	ELKATQPEKSVSAAGSTVLNCTITSLVGPDKWRG-VGOS-RLIYSFTGEHPPRV 90				
Oy	1	DIGNQTPSSSLASVSGVRVITTCGASGIR-NIYLAQOQKRPKLLIYAASILQ-SGV 58				
Db	91	TNVS DATRRNNDFSIINISVTPEDACTYCVKFKCP 128				

[illegible]

Query Match	Similarity	26.1%	Score	160	DB 7	Length	137
Best Local	Similarity	26.1% <td>Pred. No.</td> <td>4.33e-13<td></td><td></td><td></td></td>	Pred. No.	4.33e-13 <td></td> <td></td> <td></td>			
Matches	25	Conservative	32	Mismatches	27	Indels	5
DB	85	GYDASREKKSFSFLTVTSQAQKNAVFLC	113				
QY	61	RFSGS-GSGTDFLTLSLQPEDVATYYC	88				
RESULT	11	PRELIMINARY	PRT	509	AA		
ID	035924						
AC	035924						
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)					
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)					
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)					
DE	PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR (P84).						
GN	PTPNS1.						
OS	MUS MUSCULUS (MOUSE).						
OC	EUFAROTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;						
CC	SCUROGNATHI; MORIDAE; MORINAE; MUS.						
RN	[1]						
RA	SEQUENCE FROM N.A.						
RA	MEDLINE; 98012243.						
RA	COUJ S., WENG W., OLINSKY S., ISHMAD P., MI Z., HEMPEL J., WATKINS S., LAEENUDR C.F., NARAYANAN V.;						
RT	"The murine p84 neutral adhesion molecule is SHPS-1, a member of the phosphatase-binding protein family."						
RL	J. NEUROSCI. 17:8702-8710(1997).						
DR	EMBL; U89694; G2580535; -						
DR	MGI; MGI:108563; PTPNS1.						
DR	PFAM; PF00047; 1g; 3.						
RT	SIGNAL.						
FT	CHAIN	1	31	POTENTIAL.			
FT	CHAIN	32	509	P84.			
SEQ	SEQUENCE	509	AA; 56056	MM; 3A781050	CRC32;		
Query Match	Similarity	20.7%	Score	156	DB 11	Length	509
Best Local	Similarity	27.6%	Pred. No.	2.46e-12			
Matches	27	Conservative	29	Mismatches	37	Indels	5
DB	33	ELKATQPEKSVVAGDSTVNCNLTSLTPGPIKWRG-VGOS-RLTIYSFTGEHPRV	90				
QY	1	DIDQMSSSSLSASVGDVITTCRASQIR-NYLAWQKRGKAPKLLIYASTLQ-SGV	58				
DB	91	RNVSDTKRNNMDSIRISNVPEDAGTYVCVKGFRGS	128				
QY	59	PSRFSGS-SGTDFTLTSSLOPEDVATYYCQRYNRP	95				
RESULT	12	PRELIMINARY	PRT	123	AA		
ID	061243						
AC	061243						
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)					
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1999	(TREMBLREL. 09, LAST ANNOTATION UPDATE)					
DE	BHS20 PROTEIN PRECURSOR.						
GN	VPREB3.						
OS	MUS MUSCULUS (MOUSE).						
OC	EUFAROTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;						
CC	SCUROGNATHI; MORIDAE; MORINAE; MUS.						
RN	[1]						
RA	SEQUENCE FROM N.A.						
RA	STRAIN-BALB/C;						
RA	MEDLINE; 93259124.						
RA	SHIRASAWA T., OHNISHI K., HAGIWARA S., SHIENOTO K., TAKEBE Y., RAJEWSKY K., TAKEMORI T.;						
RT	"A novel gene product associated with mu chains in immature B cells."						
RT	EMBO J. 12:1827-1834(1993).						

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WIREH

(TM)

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MSearch protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:08:53 1999; Maspar time 4.82 Seconds
Distribution output not generated. 628.059 Million cell updates/sec

Title: >US-08-599-226-1
Description: (1.107) from US08599226.pep
Perfect Score: 752
Sequence: 1 DIQMTPSSLSASVGDRTV.....CQRNRPAPYFGGCTKYEIK 107

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: swiss-prot37
trwswsprot

Statistics: Mean 40.589; Variance 67.765; scale 0.599

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	642	85.4	108	1	KVIB_HUMAN	IG KAPPA CHAIN V-I REG	2.16e-125
2	640	85.1	108	1	KVIO_HUMAN	IG KAPPA CHAIN V-I REG	6.65e-125
3	636	84.6	108	1	KVIL_HUMAN	IG KAPPA CHAIN V-I REG	6.31e-124
4	635	84.4	108	1	KVIO_HUMAN	IG KAPPA CHAIN V-I REG	1.11e-123
5	635	84.4	108	1	KVIR_HUMAN	IG KAPPA CHAIN V-I REG	1.11e-123
6	635	84.4	108	1	KVIR_HUMAN	IG KAPPA CHAIN V-I REG	1.11e-123
7	633	84.2	129	1	KVIL_HUMAN	IG KAPPA CHAIN PRECURS	3.41e-123
8	631	83.9	108	1	KVIL_HUMAN	IG KAPPA CHAIN V-I REG	1.05e-122
9	627	83.4	108	1	KVIN_HUMAN	IG KAPPA CHAIN V-I REG	9.93e-122
10	624	83.0	108	1	KVID_HUMAN	IG KAPPA CHAIN V-I REG	5.36e-121
11	622	82.7	107	1	KVID_HUMAN	IG KAPPA CHAIN V-I REG	1.65e-120
12	622	82.7	108	1	KVIF_HUMAN	IG KAPPA CHAIN V-I REG	1.65e-120
13	620	82.4	108	1	KVIE_HUMAN	IG KAPPA CHAIN V-I REG	5.07e-120
14	619	82.3	108	1	KVIG_HUMAN	IG KAPPA CHAIN V-I REG	8.88e-120
15	617	82.0	108	1	KVIM_HUMAN	IG KAPPA CHAIN V-I REG	2.73e-119
16	615	81.8	108	1	KVIE_HUMAN	IG KAPPA CHAIN V-I REG	8.39e-119
17	612	81.4	108	1	KVIE_HUMAN	IG KAPPA CHAIN V-I REG	4.51e-118
18	604	80.3	108	1	KVIA_HUMAN	IG KAPPA CHAIN V-I REG	4.01e-116
19	604	80.3	129	1	KVIX_HUMAN	IG KAPPA CHAIN PRECURS	4.01e-116
20	603	80.2	108	1	KVIX_HUMAN	IG KAPPA CHAIN V-I REG	7.02e-116
21	600	79.8	108	1	KVIR_HUMAN	IG KAPPA CHAIN V-I REG	3.77e-115
22	587	78.1	109	1	KVIT_HUMAN	IG KAPPA CHAIN V-I REG	5.46e-112
23	580	77.1	108	1	KVSI_MOUSE	IG KAPPA CHAIN V-V REG	2.73e-110

24	578	76.9	117	1	KVIJ_HUMAN	IG KAPPA CHAIN PRECURS	8.36e-110
25	572	76.1	117	1	KVIL_HUMAN	IG KAPPA CHAIN PRECURS	2.39e-108
26	559	74.3	129	1	KV3H_HUMAN	IG KAPPA CHAIN PRECURS	3.37e-105
27	556	73.9	108	1	KVED_MOUSE	IG KAPPA CHAIN V-V REG	1.79e-103
28	551	73.3	108	1	KV3L_MOUSE	IG KAPPA CHAIN V-V REG	2.90e-103
29	551	73.3	108	1	KV3L_MOUSE	IG KAPPA CHAIN V-V REG	2.90e-103
30	550	73.1	109	1	KV3L_HUMAN	IG KAPPA CHAIN V-I REG	5.07e-103
31	550	73.1	129	1	KV3M_HUMAN	IG KAPPA CHAIN PRECURS	5.07e-103
32	549	73.0	108	1	KV5O_MOUSE	IG KAPPA CHAIN V-V REG	8.84e-103
33	548	72.9	108	1	KV3L_MOUSE	IG KAPPA CHAIN PRECURS	1.54e-102
34	547	72.7	109	1	KV3L_HUMAN	IG KAPPA CHAIN V-I REG	2.69e-102
35	546	72.6	108	1	KV5N_MOUSE	IG KAPPA CHAIN V-V REG	4.69e-102
36	546	72.6	108	1	KV5N_MOUSE	IG KAPPA CHAIN V-V REG	4.69e-102
37	545	72.5	109	1	KV3D_HUMAN	IG KAPPA CHAIN V-I REG	8.19e-101
38	544	72.3	108	1	KV3A_HUMAN	IG KAPPA CHAIN V-I REG	1.43e-101
39	536	71.3	108	1	KV5P_MOUSE	IG KAPPA CHAIN V-V REG	1.22e-99
40	535	71.1	114	1	KV4A_HUMAN	IG KAPPA CHAIN V-IV REG	2.13e-99
41	534	71.0	108	1	KV5U_MOUSE	IG KAPPA CHAIN V-V REG	3.70e-99
42	533	70.9	108	1	KV5J_MOUSE	IG KAPPA CHAIN V-V REG	6.46e-99
43	533	70.9	108	1	KV5Q_MOUSE	IG KAPPA CHAIN V-V REG	6.46e-99
44	532	70.7	108	1	KV5T_MOUSE	IG KAPPA CHAIN V-V REG	1.13e-98
45	531	70.6	109	1	KV3E_HUMAN	IG KAPPA CHAIN V-III R	1.96e-98

ALIGNMENTS

RESULT ID	1	Query Match	85.4%	Score 642	DB 1	Length 108
AC	P01594	STANDARD				
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)					
DE	IG KAPPA CHAIN V-I REGION (AU).					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;					
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.					
RN	[1]					
RP	SEQUENCE.					
RX	MEDLINE: 72189444.					
RA	SCHIECHL H., HILSCHMANN N.;					
RT	"Rule of antibody structure. The primary structure of a monoclonal					
RT	immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones					
RT	protein Au).";					
RL	HOPPE-SEYLER S Z. PHYSIOL. CHEM. 353:345-370(1972).					
RN	[2]					
RP	X-RAY CRYSTALLOGRAPHY.					
RX	MEDLINE: 77022433.					
RA	FEHLHAMMER H., SCHIEFER M., EPP O., COLMAN P.M., LATMAN E.E.,					
RA	SCHWAGER P., STEIGEMANN W., SCHRAMM H.J.;					
RT	"The structure determination of the variable portion of the					
RT	Bence-Jones protein Au.";					
RL	BIOPHYS. STRUCT. MECH. 1:139-146(1975).					
CC	-1- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR					
CC	REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF					
CC	THE KAPPA CHAIN REL.					
CC	-1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.					
DR	PIR: A01862; KIHOUU.					
DR	PFAM: PF00047; 19; 1.					
DR	HSSP: P01607; 1REI.					
KW	IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN.					
FT	DOMAIN 1	23				
FT	DOMAIN 2	34				
FT	DOMAIN 3	35				
FT	DOMAIN 4	49				
FT	DOMAIN 5	56				
FT	DOMAIN 6	57				
FT	DOMAIN 7	58				
FT	DOMAIN 8	97				
FT	DOMAIN 9	107				
FT	DISULFID	23				
FT	NON_TER	108				
FT	SEQUENCE	108 AA; 11939 MW; B455AF00 CRC32;				

Best Local Similarity 83.2%; Pred. No. 2,16e-125;
Matches 89; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Db 1 DIOMTOSPSLSASVGDRTVITTCRASODISDYLMWYQOKPGKAPKLLIYASNLGSGVPS 60
QY 1 DIOMTOSPSLSASVGDRTVITTCRASOGIRNRYLAWYQOKPGKAPKLLIYASNLGSGVPS 60
Db 61 RFGSGSGTDFLTLLISLOPEDVATYTCORYNRAPYTFGGGTKEIK 107
QY 61 RFGSGSGTDFLTLLISLOPEDVATYTCORYNRAPYTFGGGTKEIK 107

RESULT 2
ID KY10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (REL.).
DE HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE.
RX MEDLINE: 76023758.
RA PALM W., HILSCHMANN N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";
RT HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 356:167-191(1975).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE: 76039968.
RA EPP O., LATTMAN E.E., SCHIEFER M., HUBER R., PALM W.;
RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Rel refined at 2.0-A resolution.";
RT BIOCHEMISTRY 14:4943-4952(1975).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01873; KIHORE.
DR PDB; 1REI; 17-FEB-84.
DR PRAM; PFO0047; 19; 1.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 50 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 98 107 FRAMEWORK 4.
FT NON_TER 23 88
FT STRAND 108 108
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 45 49
FT STRAND 50 52
FT STRAND 53 54
FT STRAND 55 57
FT STRAND 60 61
FT STRAND 62 67
FT STRAND 68 69
FT STRAND 70 75
FT STRAND 80 82
FT STRAND 85 90
FT STRAND 98 98

FT STRAND 102 106
SQ SEQUENCE 108 AA; 11902 MW; D08F51A4 CRC32;

Query Match
Best Local Similarity 83.0%; Score 640; DB 1; Length 108;
Matches 88; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Db 1 DIOMTOSPSLSASVGDRTVITTCRASODIIRKYLWYQOKPGKAPKLLIYASNLGSGVPS 60
QY 1 DIOMTOSPSLSASVGDRTVITTCRASOGIRNRYLAWYQOKPGKAPKLLIYASNLGSGVPS 60
Db 61 RFGSGSGTDFLTLLISLOPEDVATYTCORYNRAPYTFGGGTKEIK 106
QY 61 RFGSGSGTDFLTLLISLOPEDVATYTCORYNRAPYTFGGGTKEIK 106

RESULT 3
ID KY11_HUMAN STANDARD; PRT; 108 AA.
AC P01604;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (KUE).
DE HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE.
RX MEDLINE: 79237924.
RA EULITZ M., KLEY H.-P., ZEITLER H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";
RT HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 360:725-734(1979).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01870; KIHORE.
DR PRAM; PFO0047; 19; 1.
DR HSSP; P01607; 1REI.
KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 35 FRAMEWORK 2.
FT DOMAIN 4 49 FRAMEWORK 3.
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DOMAIN 98 107 BY SIMILARITY.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; AA801BE9 CRC32;

Query Match
Best Local Similarity 81.3%; Pred. No. 6,31e-124;
Matches 87; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Db 1 DIOMTOSPSLSASVGDRTVITTCRASOSINIMILAWYQOKPGKAPKLLIYASTLETGVP 60
QY 1 DIOMTOSPSLSASVGDRTVITTCRASOGIRNRYLAWYQOKPGKAPKLLIYASTLETGVP 60
Db 61 RFGSGSGTDFLTLLISLOPEDVATYTCORYNRAPYTFGGGTKEIK 107
QY 61 RFGSGSGTDFLTLLISLOPEDVATYTCORYNRAPYTFGGGTKEIK 107

RESULT 4
ID KY10_HUMAN STANDARD; PRT; 108 AA.
AC P01609;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (SCW).
DE HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]
 RP SEQUENCE.
 RX MEDLINE: 75059271.
 RA ELLITZ M., HILSCHMANN N.;
 RT "The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scv.), II: The chymotryptic peptides and the complete amino acid sequence."
 RL HOPPE-SELYER S. Z. PHYSIOL. CHEM. 355:842-866(1974).
 CC -1- THE C REGION OF THE CHAIN HAS THE INV (1,2) MARKER.
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01875; KIHUSM.
 DR PFAM: PF00047; 19; 1.
 DR HSSP: P01607; 1REI.
 KM IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 34 FRAMEWORK 2.
 FT DOMAIN 3 35 49 FRAMEWORK 3.
 FT DOMAIN 4 50 56 FRAMEWORK 4.
 FT DOMAIN 5 57 88 FRAMEWORK 5.
 FT DOMAIN 6 89 97 FRAMEWORK 6.
 FT DOMAIN 7 98 107 FRAMEWORK 7.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11764 MW; 66DABC95 CRC32;
 Query Match 84.4%; Score 635; DB 1; Length 108;
 Best Local Similarity 80.4%; Pred. No. 1,11e-123;
 Matches 86; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 Db 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 QY 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 Db 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 QY 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 RESULT 5
 ID KY1V_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (WEA).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OS PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 [1]
 SEQUENCE.
 RX MEDLINE: 83273707.
 RA GONTI F., FRANGIONE B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33."
 RL PROC. NATL. ACAD. SCI. U.S.A. 80:4837-4841(1983).
 CC -1- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.
 CC PIR: A01876; KIHUWE.
 DR PFAM: PF00047; 19; 1.
 DR HSSP: P80362; 1WTL.
 KM IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 24 34 FRAMEWORK 2.
 FT DOMAIN 3 35 49 FRAMEWORK 3.
 FT DOMAIN 4 50 56 FRAMEWORK 4.
 FT DOMAIN 5 57 88 FRAMEWORK 5.
 FT DOMAIN 6 89 97 FRAMEWORK 6.
 FT DOMAIN 7 98 107 FRAMEWORK 7.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; B8ADA251 CRC32;

Query Match 84.4%; Score 635; DB 1; Length 108;
 Best Local Similarity 84.1%; Pred. No. 1,11e-123;
 Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 Db 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 QY 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 Db 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 QY 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 RESULT 6
 ID KY1V_HUMAN STANDARD; PRT; 108 AA.
 AC P04430;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (BAN).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OS PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 [1]
 SEQUENCE.
 RX MEDLINE: 86174817.
 RA DWULET F.E., O'CONNOR T.P., BENSON M.D.;
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN)."
 RL MOL. IMMUNOL. 23:73-78(1986).
 DR PIR: A01878; KIHUSM.
 DR PFAM: PF00047; 19; 1.
 DR HSSP: P80362; 1WTL.
 KM IMMUNOGLOBULIN V REGION; AMYLOID.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 24 34 FRAMEWORK 2.
 FT DOMAIN 3 35 49 FRAMEWORK 3.
 FT DOMAIN 4 50 56 FRAMEWORK 4.
 FT DOMAIN 5 57 88 FRAMEWORK 5.
 FT DOMAIN 6 89 97 FRAMEWORK 6.
 FT DOMAIN 7 98 107 FRAMEWORK 7.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 0D44DA0A CRC32;
 Query Match 84.4%; Score 635; DB 1; Length 108;
 Best Local Similarity 85.0%; Pred. No. 1,11e-123;
 Matches 91; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
 Db 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 QY 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 1 DIQNTGSSSLASVSGDGVITTCRASQDINRYKQADNPIFGGTREK 107
 Db 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 QY 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 61 RFSGSGGTDFLTITSLQPEDVATYCCQYNSPYFGGTREK 107
 RESULT 7
 ID KY1V_HUMAN STANDARD; PRT; 129 AA.
 AC P04431;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OS PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE: 85014148.
 RA KLOBECK H.G., COMRIANO G., ZACHAU H.G.;
 RT "Immunoglobulin genes of the kappa light chain type from two human

RT Lymphoid cell lines are closely related.";
 RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
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 CC EMBL: X00965; G296684; ALT_TERM.
 DR PIR: A01883; KIHU00.
 DR PFAM: PF00047; 1g; 1.
 DR HSSP: P01607; 1REI.
 KM IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (WALKER).
 FT DOMAIN 23 45 FRAMEWORK 1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 120 129 FRAMEWORK 4.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14069 MW; 99925172 CRC32;
 Query Match 84.2%; Score 633; DB 1; Length 129;
 Best Local Similarity 86.0%; Pred. No. 3,4e-123;
 Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 Db 23 DIQWTGSPSSLSASVGBRVITTCRASQSSISYLMWYQOKPKAKPLIYASLSQSVTS 82
 QY 1 DIQWTGSPSSLSASVGBRVITTCRASQSSISYLMWYQOKPKAKPLIYASLSQSVTS 60
 Db 83 RFSGSGSGTDFLTITSLQPEDSATYTCQOQSSTLITFGGTRLEIK 129
 QY 61 RFSGSGSGTDFLTITSLQPEDSATYTCQOQSSTLITFGGTRLEIK 107
 RESULT 8
 ID KVIH_HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 RT IG KAPPA CHAIN V-I REGION (HAD).
 RL HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 71032830.
 RA WATANABE S., HILSCSMANN N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups.";
 RL HOPPE-SEILER S. Z. PHYSIOL. CHEM. 351:1291-1295(1970).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PFAM: PF00047; 1g; 1.
 DR HSSP: P80362; 1MTL.
 KM IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.

FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; C8A2EE86 CRC32;
 Query Match 83.9%; Score 631; DB 1; Length 108;
 Best Local Similarity 84.1%; Pred. No. 1.05e-122;
 Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 Db 1 DIQWTGSPSSLSASVGBRVITTCRASQSSISYLMWYQOKPKAKPLIYASLSQSVTS 60
 QY 1 DIQWTGSPSSLSASVGBRVITTCRASQSSISYLMWYQOKPKAKPLIYASLSQSVTS 60
 Db 61 RFSGSGSGTDFLTITSLQPEDSATYTCQOQNTPTSPFGGTRVEIK 107
 QY 61 RFSGSGSGTDFLTITSLQPEDSATYTCQOQNTPTSPFGGTRVEIK 107
 RESULT 9
 ID KVIH_HUMAN STANDARD; PRT; 108 AA.
 AC P01606;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 RT IG KAPPA CHAIN V-I REGION (OU).
 RL HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 70201507.
 RA KOHLER H., SHIMIZU A., PUTNAM F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 RT chains.";
 RL SCIENCE 169:56-59(1970).
 CC -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
 CC PIR: A01872; KIHU00.
 DR PFAM: PF00047; 1g; 1.
 DR HSSP: P01607; 1REI.
 KM IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11777 MW; 4B089785 CRC32;
 Query Match 83.4%; Score 627; DB 1; Length 108;
 Best Local Similarity 72.9%; Pred. No. 9.93e-122;
 Matches 78; Conservative 20; Mismatches 9; Indels 0; Gaps 0;
 Db 1 DIQWTGSPSSLSASVGBRVITTCRASQSSISYLMWYQOKPKAKPLIYASLSQSVTS 60
 QY 1 DIQWTGSPSSLSASVGBRVITTCRASQSSISYLMWYQOKPKAKPLIYASLSQSVTS 60
 Db 61 RFSGSGSGTDFLTITSLQPEDSATYTCQOQNTPTSPFGGTRLEIK 107
 QY 61 RFSGSGSGTDFLTITSLQPEDSATYTCQOQNTPTSPFGGTRLEIK 107
 RESULT 10
 ID KVIH_HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 RT IG KAPPA CHAIN V-I REGION (WAT).
 RL HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE: 95086080.
 RA HUANG D.-B., CHANG C.-H., AINSWORTH C., BRUENGER A.T., EULITZ M.,
 RA SOLOMON A., STEVENS F.J., SCHIFFER M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers.";
 RL BIOCHEMISTRY 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE: 81267384.
 RA STEVENS F.J., WESTHOLM F.A., PANAGIOTPOULOS N., SCHIFFER M.,
 RA POPP R.A., SOLOMON A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein Mat.";
 RL J. MOL. BIOL. 147:185-193(1981).
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 PDB: 1MTL; 01-NOV-94.
 PFAM: PF00047; 19; 1.
 IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT CONFLICT 30 31
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; 41A2388C CRC32;
 Query Match 83.0%; Score 624; DB 1; Length 108;
 Best Local Similarity 80.4%; Pred. No. 5.36e-121;
 Matches 86; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 DB 1 DIOMTSPSTLSASVGDRAVITTCRASQDINTYNNMFOQRGQAPKYLITGASILESGVPS 60
 QY 1 DIOMTSPSTLSASVGDRAVITTCRASQDINTYNNMFOQRGQAPKYLITGASILESGVPS 60
 DB 61 RFGSSSGTDFLTITSLDPEVATYTCORYNAPYFGGTVEIK 107
 QY 61 RFGSSSGTDFLTITSLDPEVATYTCORYNAPYFGGTVEIK 107
 RESULT 11
 KVID_HUMAN STANDARD; PRT; 107 AA.
 P01596;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (CAR).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 75075135.
 RA MILSTEIN C.P., DEVERSON E.V.;
 RT "Primary structure of kappa light chain from a human myeloma
 RT protein.";
 RL EUR. J. BIOCHEM. 49:377-391(1974).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PFAM: PF00047; 19; 1.
 DR HSSP: P80362; 1MTL.
 KM IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
 FT CARBOHYD 28 28
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; 04B9E9ED CRC32;

Query Match 82.7%; Score 622; DB 1; Length 107;
 Best Local Similarity 79.4%; Pred. No. 1.65e-120;
 Matches 85; Conservative 14; Mismatches 7; Indels 1; Gaps 1;
 DB 1 DIOMTSPSTLSASVGDRAVITTCRASQDINTYNNMFOQRGQAPKYLITGASILESGVPS 60
 QY 1 DIOMTSPSTLSASVGDRAVITTCRASQDINTYNNMFOQRGQAPKYLITGASILESGVPS 60
 DB 61 RFGSSSGTDFLTITSLDPEVATYTCORYNAPYFGGTVEIK 106
 QY 61 RFGSSSGTDFLTITSLDPEVATYTCORYNAPYFGGTVEIK 107
 RESULT 12
 KVID_HUMAN STANDARD; PRT; 108 AA.
 P01598;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (EU).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 71064023.
 RA GOTTLIEB P.D., CUNNINGHAM B.A., RUTISHAUSER U., EDELMAN G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
 RT acid sequence of the light chain.";
 RL BIOCHEMISTRY 9:3155-3161(1970).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE: 71064027.
 RA GALL W.E., EDELMAN G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Interchain disulfide bonds.";
 RL BIOCHEMISTRY 9:3188-3196(1970).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PFAM: PF00047; 19; 1.
 DR HSSP: P01607; 1REI.
 KM IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11788 MW; 9AF455E5 CRC32;
 Query Match 82.7%; Score 622; DB 1; Length 108;
 Best Local Similarity 81.3%; Pred. No. 1.55e-120;
 Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
 DB 1 DIOMTSPSTLSASVGDRAVITTCRASQDINTYNNMFOQRGQAPKYLITGASILESGVPS 60
 QY 1 DIOMTSPSTLSASVGDRAVITTCRASQDINTYNNMFOQRGQAPKYLITGASILESGVPS 60
 DB 61 RFGSSSGTDFLTITSLDPEVATYTCORYNAPYFGGTVEIK 107
 QY 61 RFGSSSGTDFLTITSLDPEVATYTCORYNAPYFGGTVEIK 107
 RESULT 13
 KVID_HUMAN STANDARD; PRT; 108 AA.
 P01608;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (ROY).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 [1]
 RP SEQUENCE.
 RX MEDLINE: 68362076.
 RA HILSCHMANN N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)."
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 348:1077-1080(1967).
 RN [2]
 RP REVISIONS TO 39 AND 41.
 RA HILSCHMANN N., BARNIKOL H.U., HESS M., LANGER B., PONTING H.,
 STEINMETZ-KAYNE M., SUTER L., WATANABE S.;
 RL (IN) FRANK F., SHUGAR D. (EDS.);
 RL GAMMA GLOBULINS: STRUCTURE AND FUNCTION, PP.57-74, ACADEMIC PRESS,
 NEW YORK (1969).
 -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 -1- THIS IS A BENCE-JONES PROTEIN.
 PIR: A01874; KIHURY.
 PFAM: PF00047; 19; 1.
 DR HSSP: P80362; 1WTI.
 KM IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 FRAMEWORK 2.
 FT DOMAIN 35 49 FRAMEWORK 3.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SO SEQUENCE 108 AA; 11782 MW; 98778875 CRC32;
 Query Match 82.4%; Score 620; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 5,07e-120;
 Matches 85; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
 Db 1 DIQNTGSSLSASVSGRVITTCRASGIDISFLNMWQKPKAPKRLIYDASKLEAGVPS 60
 QY 1 DIQNTGSSLSASVSGRVITTCRASGIDISFLNMWQKPKAPKRLIYDASKLEAGVPS 60
 61 RFSGSGGTDEFTLTISLQPEDVATYTCQRYNRPATYFGGKTVEIK 107
 QY 61 RFSGSGGTDEFTLTISLQPEDVATYTCQRYNRPATYFGGKTVEIK 107
 RESULT 14
 ID KVIU_HUMAN STANDARD; PRT; 108 AA.
 AC P01599;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (GAL).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 [1]
 RP SEQUENCE.
 RX MEDLINE: 75059122.
 RA LAURE C.J., WATANABE S., HILSCHMANN N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin gal.), I. The amino acid sequence of the L-chain of
 kappa-type, subgroup I."
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1503-1504(1973).
 -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
 PIR: A01667; KIHUGL.
 PFAM: PF00047; 19; 1.
 DR HSSP: P01607; 1REI.
 KM IMMUNOGLOBULIN V REGION.

FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SO SEQUENCE 108 AA; 11814 MW; CCAEAD2 CRC32;
 Query Match 82.3%; Score 619; DB 1; Length 108;
 Best Local Similarity 86.0%; Pred. No. 8.88e-120;
 Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 Db 1 DIQNTGSSLSASVSGRVITTCRASGIDISFLNMWQKPKAPKRLIYDASKLEAGVPS 60
 QY 1 DIQNTGSSLSASVSGRVITTCRASGIDISFLNMWQKPKAPKRLIYDASKLEAGVPS 60
 61 RFSGSGGTDEFTLTISLQPEDVATYTCQRYNRPATYFGGKTVEIK 107
 QY 61 RFSGSGGTDEFTLTISLQPEDVATYTCQRYNRPATYFGGKTVEIK 107
 RESULT 15
 ID KVIU_HUMAN STANDARD; PRT; 108 AA.
 AC P01605;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (LAI).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 [1]
 RP SEQUENCE.
 RX MEDLINE: 77038198.
 RA CAPRA J.D., KLAPPER D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
 RT specificities."
 RL SCAND. J. IMMUNOL. 5:677-684(1976)
 -1- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
 CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
 CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 PIR: A01871; KIHURY.
 PFAM: PF00047; 19; 1.
 DR HSSP: P01607; 1REI.
 KM IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SO SEQUENCE 108 AA; 11834 MW; 22228B0C CRC32;
 Query Match 82.0%; Score 617; DB 1; Length 108;
 Best Local Similarity 82.2%; Pred. No. 2.73e-119;
 Matches 88; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 Db 1 DIQNTGSSLSASVSGRVITTCRASGIDISFLNMWQKPKAPKRLIYDASKLEAGVPS 60
 QY 1 DIQNTGSSLSASVSGRVITTCRASGIDISFLNMWQKPKAPKRLIYDASKLEAGVPS 60
 61 RFSGSGGTDEFTLTISLQPEDVATYTCQRYNRPATYFGGKTVEIK 107
 QY 61 RFSGSGGTDEFTLTISLQPEDVATYTCQRYNRPATYFGGKTVEIK 107

• Fri Sep 3 09:52:42 1999

US-08-599-226-1.rsp

Page 7

Search completed: Thu Sep 2 11:09:05 1999
Job time : 12 secs.

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 (TM)

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:08:12 1999; Maspar time 7.06 Seconds
 606.945 Million cell updates/sec
 Molecular output not generated.

Title: >US-08-599-226-1
 Description: (1-107) from US08599226.pep
 Sequence: 1 DIQMTQSPSSLSASVGDRTV.....CORYNRAPYTFGGTKVEIK 107

Scoring table: PAM 150
 GAP 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r60
 1:ipr1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 40.209; Variance 100.321; scale 0.401

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	694	92.3	131	2	S40352	1.01e-91
2	683	90.8	107	2	S36275	6.53e-90
3	660	87.8	127	2	S40367	3.93e-86
4	653	86.8	123	2	S40331	5.53e-85
5	653	86.8	125	2	S40333	5.53e-85
6	653	86.8	132	2	S40334	5.53e-85
7	649	86.3	124	2	S40336	5.51e-84
8	648	86.2	108	2	I39154	3.66e-84
9	647	86.0	108	2	B49047	5.33e-84
10	644	85.6	129	2	S40369	1.66e-83
11	642	85.4	108	1	K1HUAU	3.52e-83
12	641	85.2	108	1	S30521	5.14e-83
13	639	85.0	107	2	S36264	1.09e-82
14	639	85.0	117	2	S46371	1.09e-82
15	637	84.7	129	2	S52792	1.09e-82
16	635	84.4	95	2	PH0863	4.94e-82
17	635	84.4	107	2	S40366	4.94e-82
18	635	84.4	108	1	K1HUME	4.94e-82
19	635	84.4	108	1	K1HUNB	4.94e-82
20	635	84.4	108	1	S46372	4.94e-82
21	634	84.3	108	2	S34007	7.20e-82
22	634	84.3	129	2	S52789	7.20e-82
23	633	84.2	129	1	K1HUMK	1.05e-81

24	633	84.2	129	2	S52793	Ig kappa chain V regl	1.05e-81
25 <td>632 <td>84.0 <td>132 <td>2 <th>S38646</th> <th>Ig kappa chain V regl</th> <th>1.53e-81</th> </td></td></td></td>	632 <td>84.0 <td>132 <td>2 <th>S38646</th> <th>Ig kappa chain V regl</th> <th>1.53e-81</th> </td></td></td>	84.0 <td>132 <td>2 <th>S38646</th> <th>Ig kappa chain V regl</th> <th>1.53e-81</th> </td></td>	132 <td>2 <th>S38646</th> <th>Ig kappa chain V regl</th> <th>1.53e-81</th> </td>	2 <th>S38646</th> <th>Ig kappa chain V regl</th> <th>1.53e-81</th>	S38646	Ig kappa chain V regl	1.53e-81
26 <td>631 <td>83.9 <td>108 <td>1 <th>K1HUMU</th> <th>Ig kappa chain V-I re</th> <th>2.23e-81</th> </td></td></td></td>	631 <td>83.9 <td>108 <td>1 <th>K1HUMU</th> <th>Ig kappa chain V-I re</th> <th>2.23e-81</th> </td></td></td>	83.9 <td>108 <td>1 <th>K1HUMU</th> <th>Ig kappa chain V-I re</th> <th>2.23e-81</th> </td></td>	108 <td>1 <th>K1HUMU</th> <th>Ig kappa chain V-I re</th> <th>2.23e-81</th> </td>	1 <th>K1HUMU</th> <th>Ig kappa chain V-I re</th> <th>2.23e-81</th>	K1HUMU	Ig kappa chain V-I re	2.23e-81
27 <td>630 <td>83.8 <td>107 <td>2 <th>S36269</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td></td></td></td>	630 <td>83.8 <td>107 <td>2 <th>S36269</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td></td></td>	83.8 <td>107 <td>2 <th>S36269</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td></td>	107 <td>2 <th>S36269</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td>	2 <th>S36269</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th>	S36269	Ig kappa chain V regl	3.25e-81
28 <td>630 <td>83.8 <td>108 <td>2 <th>S44122</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td></td></td></td>	630 <td>83.8 <td>108 <td>2 <th>S44122</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td></td></td>	83.8 <td>108 <td>2 <th>S44122</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td></td>	108 <td>2 <th>S44122</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th> </td>	2 <th>S44122</th> <th>Ig kappa chain V regl</th> <th>3.25e-81</th>	S44122	Ig kappa chain V regl	3.25e-81
29 <td>630 <td>83.8 <td>109 <td>2 <th>S31998</th> <th>Ig kappa chain - huma</th> <th>3.25e-81</th> </td></td></td></td>	630 <td>83.8 <td>109 <td>2 <th>S31998</th> <th>Ig kappa chain - huma</th> <th>3.25e-81</th> </td></td></td>	83.8 <td>109 <td>2 <th>S31998</th> <th>Ig kappa chain - huma</th> <th>3.25e-81</th> </td></td>	109 <td>2 <th>S31998</th> <th>Ig kappa chain - huma</th> <th>3.25e-81</th> </td>	2 <th>S31998</th> <th>Ig kappa chain - huma</th> <th>3.25e-81</th>	S31998	Ig kappa chain - huma	3.25e-81
30 <td>629 <td>83.6 <td>125 <td>2 <th>S40349</th> <th>Ig kappa chain V-I re</th> <th>4.74e-81</th> </td></td></td></td>	629 <td>83.6 <td>125 <td>2 <th>S40349</th> <th>Ig kappa chain V-I re</th> <th>4.74e-81</th> </td></td></td>	83.6 <td>125 <td>2 <th>S40349</th> <th>Ig kappa chain V-I re</th> <th>4.74e-81</th> </td></td>	125 <td>2 <th>S40349</th> <th>Ig kappa chain V-I re</th> <th>4.74e-81</th> </td>	2 <th>S40349</th> <th>Ig kappa chain V-I re</th> <th>4.74e-81</th>	S40349	Ig kappa chain V-I re	4.74e-81
31 <td>629 <td>83.2 <td>108 <td>2 <th>S19674</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td></td></td></td>	629 <td>83.2 <td>108 <td>2 <th>S19674</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td></td></td>	83.2 <td>108 <td>2 <th>S19674</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td></td>	108 <td>2 <th>S19674</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td>	2 <th>S19674</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th>	S19674	Ig kappa chain V regl	1.47e-80
32 <td>626 <td>83.2 <td>108 <td>2 <th>S40330</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td></td></td>	626 <td>83.2 <td>108 <td>2 <th>S40330</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td></td>	83.2 <td>108 <td>2 <th>S40330</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td>	108 <td>2 <th>S40330</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td>	2 <th>S40330</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th>	S40330	Ig kappa chain V-I re	1.47e-80
33 <td>626 <td>83.2 <td>122 <td>2 <th>S40314</th> <th>Ig kappa chain - huma</th> <th>1.47e-80</th> </td></td></td></td>	626 <td>83.2 <td>122 <td>2 <th>S40314</th> <th>Ig kappa chain - huma</th> <th>1.47e-80</th> </td></td></td>	83.2 <td>122 <td>2 <th>S40314</th> <th>Ig kappa chain - huma</th> <th>1.47e-80</th> </td></td>	122 <td>2 <th>S40314</th> <th>Ig kappa chain - huma</th> <th>1.47e-80</th> </td>	2 <th>S40314</th> <th>Ig kappa chain - huma</th> <th>1.47e-80</th>	S40314	Ig kappa chain - huma	1.47e-80
34 <td>626 <td>83.2 <td>123 <td>2 <th>S40313</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td></td></td>	626 <td>83.2 <td>123 <td>2 <th>S40313</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td></td>	83.2 <td>123 <td>2 <th>S40313</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td>	123 <td>2 <th>S40313</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td>	2 <th>S40313</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th>	S40313	Ig kappa chain V-I re	1.47e-80
35 <td>626 <td>83.2 <td>126 <td>2 <th>S40335</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td></td></td>	626 <td>83.2 <td>126 <td>2 <th>S40335</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td></td>	83.2 <td>126 <td>2 <th>S40335</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td></td>	126 <td>2 <th>S40335</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th> </td>	2 <th>S40335</th> <th>Ig kappa chain V-I re</th> <th>1.47e-80</th>	S40335	Ig kappa chain V-I re	1.47e-80
36 <td>626 <td>83.2 <td>127 <td>2 <th>S11240</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td></td></td></td>	626 <td>83.2 <td>127 <td>2 <th>S11240</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td></td></td>	83.2 <td>127 <td>2 <th>S11240</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td></td>	127 <td>2 <th>S11240</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th> </td>	2 <th>S11240</th> <th>Ig kappa chain V regl</th> <th>1.47e-80</th>	S11240	Ig kappa chain V regl	1.47e-80
37 <td>625 <td>83.1 <td>109 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td></td></td>	625 <td>83.1 <td>109 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td></td>	83.1 <td>109 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td>	109 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td>	1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th>	K1HURU	Ig kappa chain V-I re	2.14e-80
38 <td>625 <td>83.1 <td>120 <td>2 <th>S46370</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td></td></td>	625 <td>83.1 <td>120 <td>2 <th>S46370</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td></td>	83.1 <td>120 <td>2 <th>S46370</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td>	120 <td>2 <th>S46370</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td>	2 <th>S46370</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th>	S46370	Ig kappa chain V-I re	2.14e-80
39 <td>625 <td>83.1 <td>139 <td>2 <th>S40365</th> <th>Ig kappa chain - huma</th> <th>2.14e-80</th> </td></td></td></td>	625 <td>83.1 <td>139 <td>2 <th>S40365</th> <th>Ig kappa chain - huma</th> <th>2.14e-80</th> </td></td></td>	83.1 <td>139 <td>2 <th>S40365</th> <th>Ig kappa chain - huma</th> <th>2.14e-80</th> </td></td>	139 <td>2 <th>S40365</th> <th>Ig kappa chain - huma</th> <th>2.14e-80</th> </td>	2 <th>S40365</th> <th>Ig kappa chain - huma</th> <th>2.14e-80</th>	S40365	Ig kappa chain - huma	2.14e-80
40 <td>625 <td>83.1 <td>141 <td>2 <th>S49134</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td></td></td>	625 <td>83.1 <td>141 <td>2 <th>S49134</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td></td>	83.1 <td>141 <td>2 <th>S49134</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td></td>	141 <td>2 <th>S49134</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th> </td>	2 <th>S49134</th> <th>Ig kappa chain V-I re</th> <th>2.14e-80</th>	S49134	Ig kappa chain V-I re	2.14e-80
41 <td>624 <td>83.0 <td>107 <td>2 <th>S36262</th> <th>Ig kappa chain V regl</th> <th>3.12e-80</th> </td></td></td></td>	624 <td>83.0 <td>107 <td>2 <th>S36262</th> <th>Ig kappa chain V regl</th> <th>3.12e-80</th> </td></td></td>	83.0 <td>107 <td>2 <th>S36262</th> <th>Ig kappa chain V regl</th> <th>3.12e-80</th> </td></td>	107 <td>2 <th>S36262</th> <th>Ig kappa chain V regl</th> <th>3.12e-80</th> </td>	2 <th>S36262</th> <th>Ig kappa chain V regl</th> <th>3.12e-80</th>	S36262	Ig kappa chain V regl	3.12e-80
42 <td>622 <td>82.7 <td>108 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>6.62e-80</th> </td></td></td></td>	622 <td>82.7 <td>108 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>6.62e-80</th> </td></td></td>	82.7 <td>108 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>6.62e-80</th> </td></td>	108 <td>1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>6.62e-80</th> </td>	1 <th>K1HURU</th> <th>Ig kappa chain V-I re</th> <th>6.62e-80</th>	K1HURU	Ig kappa chain V-I re	6.62e-80
43 <td>622 <td>82.7 <td>109 <td>2 <th>S31978</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td></td></td></td>	622 <td>82.7 <td>109 <td>2 <th>S31978</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td></td></td>	82.7 <td>109 <td>2 <th>S31978</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td></td>	109 <td>2 <th>S31978</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td>	2 <th>S31978</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th>	S31978	Ig kappa chain - huma	6.62e-80
44 <td>622 <td>82.7 <td>129 <td>2 <th>S40317</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td></td></td></td>	622 <td>82.7 <td>129 <td>2 <th>S40317</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td></td></td>	82.7 <td>129 <td>2 <th>S40317</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td></td>	129 <td>2 <th>S40317</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th> </td>	2 <th>S40317</th> <th>Ig kappa chain - huma</th> <th>6.62e-80</th>	S40317	Ig kappa chain - huma	6.62e-80
45 <td>621 <td>82.6 <td>109 <td>2 <th>S31981</th> <th>Ig kappa chain - huma</th> <th>9.65e-80</th> </td></td></td></td>	621 <td>82.6 <td>109 <td>2 <th>S31981</th> <th>Ig kappa chain - huma</th> <th>9.65e-80</th> </td></td></td>	82.6 <td>109 <td>2 <th>S31981</th> <th>Ig kappa chain - huma</th> <th>9.65e-80</th> </td></td>	109 <td>2 <th>S31981</th> <th>Ig kappa chain - huma</th> <th>9.65e-80</th> </td>	2 <th>S31981</th> <th>Ig kappa chain - huma</th> <th>9.65e-80</th>	S31981	Ig kappa chain - huma	9.65e-80

ALIGNMENTS

RESULT 1

ENTRY 1
 TITLE S40352 #type complete
 ORGANISM Ig kappa chain V-J-C region - human
 DATE 19-May-1994 #sequence_revision 26-May-1995 #text_change 20-Mar-1998

ACCESSIONS
 REFERENCE S40352
 #authors Klein, R.; Jaenichen, R.; Zachau, H.G.
 #journal Eur. J. Immunol. (1993) 23:3248-3271
 #title Expressed human immunoglobulin chl genes and their hypermutation.
 #accession S40352
 #status Preliminary; translation not shown
 #molecule_type mRNA
 #residues 1-131 #label KLE
 #cross-references EMBL:X72462; NID:q441392; PID:q441393
 CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 131 #molecular-weight 14265 #checksum 1902

Query Match 92.3%; Score 694; DB 2; Length 131;
 Best Local Similarity 92.5%; Pred. No. 1.01e-91;
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 21 DIQMTQSPSSLSASVGNRVITTCASGIGISNYLAWYQKFGKVLIIYASTQSGVPS 80
 |||||||
 Qy 1 DIQMTQSPSSLSASVGNRVITTCASGIGIRNYLAWYQKFGKVLIIYASTQSGVPS 60
 |||||||
 Db 81 RFSSGGTDFSLTSSLOPEDVATYCCORYNAPYTFGGTKVEIK 127
 |||||||
 Qy 61 RFSSGGTDFSLTSSLOPEDVATYCCORYNAPYTFGGTKVEIK 107
 |||||||

RESULT 2

ENTRY 2
 TITLE S36275 #type fragment
 ORGANISM Ig lambda chain V region (clone alpha-F0G1-A4) - human
 DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

ACCESSIONS
 REFERENCE S36275
 #authors Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; Balcer, M.; Holliger, K.P.; Gorlick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter, G.

#journal EMBO J. (1993) 12:725-734
#title Human anti-self antibodies with high specificity from phage
#display libraries.
#cross-references MUID:93178448
#accession S36275
#status preliminary; nucleic acid sequence not shown
#molecule-type mRNA
#residues 1-107 #label GRI
#cross-references EMBL:X18827; NID:g939416; PID:g939909
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 107 #checksum 8985

Query Match 90.8%; Score 683; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 6,53e-90;
Matches 99; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 1 DIOMTQSPSSLSASVGDVVTTCRASQGISNLTAWYQOKPGKAPKLLIYAASLQSGVPS 60
1 DIOMTQSPSSLSASVGDVVTTCRASQGISNLTAWYQOKPGKAPKLLIYAASLQSGVPS 60
61 RFSGSGCTDFTLTITSSLOPEDVATYYCQQRNRPATYFGGQTKVEIK 106
61 RFSGSGCTDFTLTITSSLOPEDVATYYCQQRNRPATYFGGQTKVEIK 107

RESULT 3
ENTRY S40367 #type complete
TITLE Ig kappa chain V-J-C region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-May-1994 #sequence_revision 26-May-1995 #text_change 20-Mar-1998

ACCESSIONS S40367
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40367
#status preliminary; translation not shown
#molecule-type mRNA
#residues 1-127 #label KLE
#cross-references EMBL:X72477
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 127 #molecular-weight 13919 #checksum 8394

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Best Local Similarity 89.8%; Pred. No. 3,93e-86;
Matches 97; Conservative 5; Mismatches 4; Indels 2; Gaps 2;

Db 18 DIOMTQSPSSLSASVGDVVTTCRASQGISNLTAWYQOKPGKAPKLLIYAASLQSGVPS 77
1 DIOMTQSPSSLSASVGDVVTTCRASQGISNLTAWYQOKPGKAPKLLIYAASLQSGVPS 77
61 RFSGSGCTDFTLTITSSLOPEDVATYYCQQRNRPATYFGGQTKVEIK 124
61 RFSGSGCTDFTLTITSSLOPEDVATYYCQQRNRPATYFGGQTKVEIK 107

RESULT 4
ENTRY S40331 #type complete
TITLE Ig kappa chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 08-Sep-1997

ACCESSIONS S40331
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40331

#status preliminary; translation not shown
#molecule-type mRNA
#residues 1-123 #label KLE
#cross-references EMBL:X72441; NID:g441350; PID:g441351
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 123 #molecular-weight 13353 #checksum 3925

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Best Local Similarity 88.8%; Pred. No. 5,53e-85;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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1 DIOMTQSPSSLSASVGDVVTTCRASQGISNLTAWYQOKPGKAPKLLIYAASLQSGVPS 60
61 RFSGSGCTDFTLTITSSLOPEDVATYYCQQRNRPATYFGGQTKVEIK 123
61 RFSGSGCTDFTLTITSSLOPEDVATYYCQQRNRPATYFGGQTKVEIK 107

RESULT 5
ENTRY S40333 #type complete
TITLE Ig kappa chain V-J region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-May-1994 #sequence_revision 26-May-1995 #text_change 20-Mar-1998

ACCESSIONS S40333
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40333
#status preliminary; translation not shown
#molecule-type mRNA
#residues 1-125 #label KLE
#cross-references EMBL:X72443; NID:g441354; PID:g441355
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 125 #molecular-weight 13633 #checksum 5223

Query Match 86.8%; Score 653; DB 2; Length 125;
Best Local Similarity 86.0%; Pred. No. 5,53e-85;
Matches 92; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Db 19 DIOMTQSPSSLSASVGDVVTTCRASQGISNLTAWYQOKPGKAPKLLIYAASLQSGVPS 78
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61 RFSGSGCTDFTLTITSSLOPEDVATYYCQQRNRPATYFGGQTKVEIK 107

RESULT 6
ENTRY S40334 #type complete
TITLE Ig kappa chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 16-Aug-1996

ACCESSIONS S40334
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40334
#status preliminary; translation not shown
#molecule-type mRNA
#residues 1-132 #label KLE
#cross-references EMBL:X72444
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

QY 61 RFGSGSGCTDFTLTILSIQLPEDVATYYCQRINRAPYTFGGGTKEIK 107

Search completed: Thu Sep 2 11:08:34 1999
Job time : 22 secs.

Job time : 22 secs.

RESULT	14
NUMBER	

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ORGANISM		ig formal_name Homo sapiens #common_name man
DATE		27-Jan-1995 #sequence_rev1stion 01-Sep-1995 #text_change

ACCESSIONS
REFERENCE

150

546369

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MUSE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MUSCH_PP protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 11:10:01 1999; Maspar time 2.89 Seconds
Molecular output not generated. 376,184 Million cell updates/sec

Title: >US-08-599-226-1
Description: (1-107) from US08599226.pep
Perfect Score: 752
Sequence: 1 DIOMTQSPSSLSASVGDRTV.....CORYNRAPYTFGQTRVEIK 107

Scoring table: PAM 150
Gap 11

Searched: 106580 segs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
LITSA_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 27.430; Variance 140.190; scale 0.196

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	687	91.4	109	2	US-07-934- Sequence 3, Applicatio	2.14e-46
2	687	91.4	109	3	PCT-US93-0 Sequence 3, Applicatio	2.14e-46
3	682	90.7	107	2	US-07-934- Sequence 18, Applicati	5.51e-46
4	682	90.7	107	3	PCT-US93-0 Sequence 18, Applicati	5.51e-46
5	680	90.4	107	2	US-08-899- Sequence 84, Applicati	8.05e-46
6	680	90.4	107	3	PCT-US95-0 Sequence 84, Applicati	8.05e-46
7	680	90.4	107	2	US-08-899- Sequence 84, Applicati	8.05e-46
8	680	90.4	107	1	US-08-276- Sequence 84, Applicati	8.05e-46
9	674	89.6	107	1	US-08-276- Sequence 82, Applicati	2.51e-45
10	674	89.6	107	2	PCT-US95-0 Sequence 82, Applicati	2.51e-45
11	674	89.6	107	3	US-08-899- Sequence 82, Applicati	2.51e-45
12	674	89.6	107	2	US-08-899- Sequence 82, Applicati	2.51e-45
13	663	88.2	106	1	US-08-276- Sequence 85, Applicati	2.01e-44
14	663	88.2	106	2	US-08-899- Sequence 85, Applicati	2.01e-44
15	663	88.2	106	3	PCT-US95-0 Sequence 85, Applicati	2.01e-44
16	663	88.2	106	2	US-08-899- Sequence 85, Applicati	2.01e-44
17	662	88.0	108	2	US-08-378- Sequence 85, Applicati	2.43e-44
18	660	87.8	107	2	US-08-477- Sequence 14, Applicati	3.54e-44
19	660	87.8	107	2	US-08-082- Sequence 13, Applicati	3.54e-44
20	660	87.8	107	2	US-08-107- Sequence 13, Applicati	3.54e-44
21	660	87.8	107	2	US-08-646- Sequence 149, Applicati	3.54e-44
22	660	87.8	107	2	US-08-477- Sequence 13, Applicati	3.54e-44
23	660	87.8	107	2	US-08-318- Sequence 6, Applicatio	3.54e-44

24	660	87.8	107	1	US-08-488- Sequence 149, Applicat	3.54e-44
25	660	87.8	107	2	US-08-472- Sequence 13, Applicati	3.54e-44
26	656	87.2	106	2	US-08-899- Sequence 83, Applicati	7.54e-44
27	656	87.2	106	3	PCT-US95-0 Sequence 83, Applicati	7.54e-44
28	656	87.2	106	2	US-08-899- Sequence 83, Applicati	7.54e-44
29	656	87.2	106	1	US-08-276- Sequence 83, Applicati	7.54e-44
30	656	87.2	108	2	US-08-378- Sequence 16, Applicati	7.54e-44
31	651	86.6	111	2	US-08-137- Sequence 67, Applicati	1.94e-43
32	651	86.6	111	2	US-08-436- Sequence 67, Applicati	1.94e-43
33	651	86.6	126	2	US-08-137- Sequence 71, Applicati	1.94e-43
34	651	86.6	126	2	US-08-436- Sequence 71, Applicati	1.94e-43
35	647	86.0	107	3	PCT-US93-0 Sequence 17, Applicati	4.13e-43
36	647	86.0	107	2	US-07-934- Sequence 17, Applicati	4.13e-43
37	647	86.0	108	2	US-08-379- Sequence 29, Applicati	6.03e-43
38	645	85.8	106	3	PCT-US95-0 Sequence 101, Applicat	6.03e-43
39	645	85.8	106	2	US-08-899- Sequence 101, Applicat	6.03e-43
40	645	85.8	106	1	US-08-276- Sequence 101, Applicat	6.03e-43
41	645	85.8	106	2	US-08-899- Sequence 101, Applicat	6.03e-43
42	642	85.4	107	2	US-08-899- Sequence 104, Applicat	1.06e-42
43	642	85.4	107	1	US-08-276- Sequence 104, Applicat	1.06e-42
44	642	85.4	107	2	US-08-899- Sequence 104, Applicat	1.06e-42
45	642	85.4	107	3	PCT-US95-0 Sequence 104, Applicat	1.06e-42

ALIGNMENTS

RESULT 1
ID US-07-934-373C-3 STANDARD: PRT: 109 AA.
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AC
DT
XX
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Sequence 3, Application US/07934373C
DE
CC Sequence 3, Application US/07934373C
CC Patent No. 5821337
CC GENERAL INFORMATION:
CC APPLICANT: Paul J. Carter
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 1 DNA Way
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WinPatIn (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/934,373C
CC FILING DATE: 21-Aug-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05126
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/715272
CC FILING DATE: 14-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER: 40,378
CC REFERENCE/DOCKET NUMBER: P0709P2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 650/225-1994
CC TELEFAX: 650/952-9881
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:

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CC LENGTH: 109 amino acids
CC TYPE: Amino acid
CC TOPOLOGY: Linear
SQ SEQUENCE 109 AA; 11850 MW; 69772 CN;

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Best Local Similarity 90.7%; Pred. No. 2,14e-46;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY      1 DIQMTSPSSLSASVGDRTVTTCRASQGVIRNYLWYQQPKKAPKLIIYAASSIENGSPS 60
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        61 RFSGSGCTDEFTLTISLPEDFATYYCQCNLSLPYFGGTKEIK 107
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PCT-US93-07832-3    STANDARD:      CDR2
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XX Sequence 3, Application PC/TUS9307832
DX
DT
CC Sequence 3, Application PC/TUS9307832
CC GENERAL INFORMATION:
CC APPLICANT: Genentech, Inc.
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 40
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/07832
CC FILING DATE: 19930820
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/715272
CC FILING DATE: 14-JUN-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05126
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/934373
CC FILING DATE: 21-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME:
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 709P2PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE:
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 109 AA; 11850 MW; 69772 CN;

Query Match          91.4%; Score 687; DB 3; Length 109;
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Best Local Similarity 90.7%: Pred No. 2,14e-46; Indels 0; Gaps 0;
Matches 97; Conservative 5; Mismatches 5;

Db      1 DIOMTQSPSSLSASVGDVRVTITCRASODVSSYLAWYQQRPGKAPKLIIYAASSLESQVPS 60
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Qy      1 DIOMTQSPSSLSASVGDVRVTITCRASGIRINRYLAWYQQRPGKAPKLIIYAASTIQSVPS 60
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||

Db      61 RFSSSGSGTDFTLTISLSLOPEDVATYYCCQYNLSPTFFGGGTVEIK 107
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||
Qy      61 RFSSSGSGTDFTLTISLSLOPEDVATYYCORNAPNAPYTFGGGTVEIK 107
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RESULT      3 CDR3
ID US-07-934-373C-18 STANDARD: PRT: 107 AA.
AC xxxxxx
XX
DX Sequence 18, Application US/07934373C
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CC Sequence 18, Application US/07934373C
CC Patent No. 582137
CC GENERAL INFORMATION:
CC APPLICANT: Paul J. Carter
CC APPLICANT: Leonard G. Presta
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 1 DNA Way
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Winpatin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/934, 373C
CC FILING DATE: 21-Aug-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05126
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/715272
CC FILING DATE: 14-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER: 40,378
CC REFERENCE/DOCKET NUMBER: P0709P2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 650/225-1994
CC TELEFAX: 650/952-9881
CC INFORMATION FOR SEQ ID NO: 18:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC type: Amino Acid
CC TOPOLOGY: Linear
CC CC
SQ SEQUENCE 107 AA; 11629 MW; 67250 CN;

Query Match 90.7%; Score 682; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 5.51e-46;
Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db      1 DIOMTQSPSSLSASVGDVRVTITCRASOISISYLAWYQQRPGKAPKLIIYAASSLESQVPS 60
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||
Qy      1 DIOMTQSPSSLSASVGDVRVTITCRASGIRINRYLAWYQQRPGKAPKLIIYAASTIQSVPS 60
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||

Db      61 RFSSSGSGTDFTLTISLSLOPEDVATYYCOQYNLSPTFFGGGTVEIK 107
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Qy      61 RFSSSGSGTDFTLTISLSLOPEDVATYYCORNAPNAPYTFGGGTVEIK 107
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QY 61 RFGSGSGTDFLTLLISSLOPEDVATYCCORYNRAPYTFGGGTVEIK 107
C D R 3

RESULT 4
ID PCT-US93-07832-18 STANDARD; PRT: 107 AA.

AC xxxxxx

Sequence 18, Application PC/TUS9307832

Sequence 18, Application PC/TUS9307832

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: palin (genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07832

FILING DATE: 19930820

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/115272

FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373

FILING DATE: 21-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 709P2PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE 107 AA: 11629 MW: 67250 CN:

Query Match 90.7%; Score 682; DB 3; Length 107;

Best Local Similarity 91.6%; Pred. No. 5.51e-46;

Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

DB 1 DIOMTSPSSLSASVGDRTVITCRASOSISNTLAWYQOKPGKAPKLLIYAASLSGSPS 60
QY 1 DIOMTSPSSLSASVGDRTVITCRASOSISNTLAWYQOKPGKAPKLLIYAASLSGSPS 60
DB 61 RFGSGSGTDFLTLLISSLOPEDVATYCCORYNRAPYTFGGGTVEIK 107
QY 61 RFGSGSGTDFLTLLISSLOPEDVATYCCORYNRAPYTFGGGTVEIK 107
C D R 3

RESULT 5
ID PCT-US95-08743-84 STANDARD; PRT: 107 AA.

XX
AC xxxxxx

Sequence 84, Application PC/TUS9508743

Sequence 84, Application PC/TUS9508743

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08743

FILING DATE: 11-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/276,852

FILING DATE: 18-JUL-1994

INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 107 AA: 11532 MW: 65997 CN:

Query Match 90.4%; Score 680; DB 3; Length 107;

Best Local Similarity 93.3%; Pred. No. 8.05e-46;

Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

DB 1 ELTQSPSSLSASVGDRTVITCRASOSISNTLAWYQOKPGKAPKLLIYAASLSGSPSRF 60
QY 3 QMOTSPSSLSASVGDRTVITCRASOSISNTLAWYQOKPGKAPKLLIYAASLSGSPSRF 62
DB 61 SSGSGSGTDFLTLLISSLOPEDVATYCCORYNRAPYTFGGGTVEIK 105
QY 63 SSGSGSGTDFLTLLISSLOPEDVATYCCORYNRAPYTFGGGTVEIK 107
C D R 3

RESULT 6
ID US-08-899-575-84 STANDARD; PRT: 107 AA.

AC xxxxxx

Sequence 84, Application US/08899575

Sequence 84, Application US/08899575

Patent No. 5804440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESSES:

ADDRESS: The Scripps Research Institute, Office of

ADDRESS: Patent Counsel

STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 84:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 107 AA; 11532 MW; 65997 CN;

Query Match 90.4%; Score 680; DB 2; Length 107;
Best Local Similarity 93.3%; Pred. No. 8.05e-46;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 ELTSPSLASVGDRTITCRASGINSYLAWQKRGKVPKLLIYAASLQSGVPSRF 60
QY :::
OY 3 QMTSPSLASVGDRTITCRASGINSYLAWQKRGKVPKLLIYAASLQSGVPSRF 62

Db 61 SSGSGTDFLTLLISLQPEDVATYCCQKYNAPRTFGQGTVEIK 105
OY :::
OY 63 SSGSGTDFLTLLISLQPEDVATYCCQKYNAPRTFGQGTVEIK 107

RESULT 7
ID US-08-899-575-84 STANDARD: PRT; 107 AA.
XX xxxxxx
AC xxxxxx

Sequence 84, Application US/08899575
DE Patent No. 5770440
CC Sequence 84, Application US/08899575
CC Patent No. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 84:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 107 AA; 11532 MW; 65997 CN;

Query Match 90.4%; Score 680; DB 2; Length 107;
Best Local Similarity 93.3%; Pred. No. 8.05e-46;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 ELTSPSLASVGDRTITCRASGINSYLAWQKRGKVPKLLIYAASLQSGVPSRF 60
QY :::
OY 3 QMTSPSLASVGDRTITCRASGINSYLAWQKRGKVPKLLIYAASLQSGVPSRF 62

Db 61 SSGSGTDFLTLLISLQPEDVATYCCQKYNAPRTFGQGTVEIK 105
OY :::
OY 63 SSGSGTDFLTLLISLQPEDVATYCCQKYNAPRTFGQGTVEIK 107

RESULT 8
ID US-08-276-852-84 STANDARD: PRT; 107 AA.
XX xxxxxx
AC xxxxxx
DT xxxxxx
DX xxxxxx

Sequence 84, Application US/08276852
DE Patent No. 5652138
CC Sequence 84, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible

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CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/276,852
CC      FILING DATE: 18-JUL-1994
CC      CLASSIFICATION: 514
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/178,302
CC      FILING DATE: 30-SEP-1993
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/954,148
CC      FILING DATE: 30-SEP-1992
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Fitting, Thomas
CC      REGISTRATION NUMBER: 34,163
CC      REFERENCE/DOCKET NUMBER: SCRI452P
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 619-554-2937
CC      TELEFAX: 619-554-6312
CC      INFORMATION FOR SEQ ID NO: 84:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 107 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 107 AA; 11532 MW; 65997 CN;
SQ
Query Match          90.4%; Score 680; DB 1; Length 107;
Best Local Similarity 93.3%; Pred. No. 8,056-46;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0
Db 1 ELTQSPSSLASVGDRTVITCRASGGSINLYAMTQQKPKVILITAASTLQSGVSRF 60
QY 3 QMTQSPSSLASVGRVYITCRASGGSINLYAMTQQKPKVILITAASTLQSGVSRF 62
Db 61 SSGSGGTDFLTLSLQPEDEVATYCYCKYNSAPRTFGGTVEIK 105
QY 63 SSGSGGTDFLTLSLQPEDEVATYCYCKYNSAPRTFGGTVEIK 107
                                CDR3
RESULT 9          STANDARD: PRT; 107 AA.
ID 1 US-08-276-852-82
AC xxxxxx
MC
DT
XX
Sequence 82, Application US/08276852
Sequence 82, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 NO. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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CC CC APPLICATION NUMBER: US/08/276,852
CC CC FILING DATE: 18-JUL-1994
CC CC CLASSIFICATION: 514
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: US 08/178,302
CC CC FILING DATE: 30-SEP-1993
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: US 07/954,148
CC CC FILING DATE: 30-SEP-1992
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Fitting, Thomas
CC CC REGISTRATION NUMBER: 34,163
CC CC REFERENCE/DOCKET NUMBER: SCRI452P
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: 619-554-2937
CC CC TELEFAX: 619-554-6312
CC CC INFORMATION FOR SEQ ID NO: 82:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 107 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC SEQUENCE 107 AA; 11570 MW; 65513 CN;

SQ Query Match 89.6%; Score 674; DB 1; Length 107;
SQ Best Local Similarity 91.4%; Pred. No. 2,51e-45;
SQ Matches 96; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 1 ELTQSPSSLASVCDRYVTTCRASQGISNTLAWYQOKFGKVPRLTYASTLQPGVPSRF 60
Qy 3 QMTQSPSSLASVGDRTYITTCRASQGISNTLAWYQOKFGKVPRLTYASTLQSGVPSRF 62
Db 61 SGGSGGTDFTLTITLISLPEDVATYYCQRYNSAPRTFEGQGTVEIK 105
Qy 63 SGGSGGTDFTLTITLISLPEDVATYYCQRYNSAPRTFEGQGTVEIK 107

RESULT 10 STANDARD; PRT: 107 AA.
ID PCT-US95-08743-82
XX AC xxxxxx
XX DE
XX SEQUENCE 82, Application PC/TUS9508743
XX CC GENERAL INFORMATION:
XX CC APPLICANT:
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US95/08743
XX CC FILING DATE: 11-JUL-1995
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC INFORMATION FOR SEQ ID NO: 82:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 107 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 107 AA; 11570 MW; 65513 CN;

Query Match 89.6%; Score 674; DB 3; Length 107;
Best Local Similarity 91.4%; Pred. No. 2,51e-45;

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Db 1 ELTQSPSSLSASVGRVITTCRASGGINNYLAWYQOKPGKAPRLIYAASTLQSGVPSRF 60
OY 3 OMTQSPSSLSASVGRVITTCRASGGINNYLAWYQOKPGKAPRLIYAASTLQSGVPSRF 62
Db 61 SSGSGCTDFTLTITSSLPEDVATYYCQKYNAPRTFGCGTKVEIK 105
OY 63 SSGSGCTDFTLTITSSLPEDVATYYCQKYNAPRTFGCGTKVEIK 107

RESULT 13

ID US-08-276-852 STANDARD; PRT: 106 AA.

AC XXXXXX

Sequence 85, Application US/08276852

Sequence 85, Application US/08276852
Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276, 852

FILING DATE: 18-JUL-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178, 302

FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954, 148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCRI452P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 106 AA: 11406 MW: 64692 CN:

Query Match 88.2%; Score 663; DB 1; Length 106;

Best Local Similarity 88.6%; Pred. No. 2, 01e-44;

Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPSSLSASVGRVITTCRASGGINNYLAWYQOKPGKAPRLIYAASTLQSGVPSRF 60
OY 3 OMTQSPSSLSASVGRVITTCRASGGINNYLAWYQOKPGKAPRLIYAASTLQSGVPSRF 62

Db 61 SSGSGCTDFTLTITSSLPEDVATYYCQKYNAPRTFGCGTKVEIK 105
OY 63 SSGSGCTDFTLTITSSLPEDVATYYCQKYNAPRTFGCGTKVEIK 107

RESULT 14

ID US-08-899-575-85 STANDARD; PRT: 106 AA.

AC XXXXXX

Sequence 85, Application US/08899575

Sequence 85, Application US/08899575
Patent No. 5804440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899, 575

FILING DATE: 24-JUL-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/276, 852

FILING DATE: 18-JUL-1994

APPLICATION NUMBER: US 08/178, 302

FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954, 148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCRI452P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 106 AA: 11406 MW: 64692 CN:

Query Match 88.2%; Score 663; DB 2; Length 106;

Best Local Similarity 88.6%; Pred. No. 2, 01e-44;

Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPSSLSASVGRVITTCRASGGINNYLAWYQOKPGKAPRLIYAASTLQSGVPSRF 60
OY 3 OMTQSPSSLSASVGRVITTCRASGGINNYLAWYQOKPGKAPRLIYAASTLQSGVPSRF 62

WISREK (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MSearch.p protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:07:16 1999; Maspar time 7.80 Seconds
291.807 Million cell updates/sec

ular output not generated.

Title: >US-08-599-226-1
Description: (1-107) from US08599226.pep
Perfect Score: 752
Sequence: 1 DIQMTGPSLSLSASVGDRTV.....CQRVNRAPYFGGGRKVEIK 107

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7
8:part8 9:part10 10:part11 11:part12 12:part13 13:part14
14:part15 15:part16 16:part17 17:part18 18:part19
19:part20 20:part21 21:part22 22:part23 23:part24
24:part25 25:part26 26:part27 27:part28 28:part29
29:part30 30:part31 31:part32 32:part33 33:part34
34:part35 35:part36 36:part37 37:part38 38:part39
39:part39

Statistics: Mean 29.465; Variance 153.837; scale 0.192

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	752	100.0	107 27	W27568	Anti-TNF-alpha antilo	7.87e-50
2	682	90.7	108 37	W70622	Human consensus frame	3.33e-44
3	681	90.6	109 9	R47041	Sequence of the conse	4.01e-44
4	680	90.4	107 10	W01263	VL region of HIV neut	4.83e-44
5	680	90.4	107 10	R54305	Anti-HIV gp120 immuno	4.83e-44
6	674	89.6	107 19	W01261	VL region of HIV neut	1.46e-43
7	674	89.6	107 10	R54303	Anti-HIV gp120 immuno	1.46e-43
8	673	89.5	107 6	R30770	Consensus humanised m	1.76e-43
9	667	88.7	107 39	W87455	Humanised anti-alpha-	5.32e-43
10	667	88.7	109 8	R40956	Human germ-line gene	5.32e-43
11	665	88.4	109 6	R30764	Consensus humanised a	7.70e-43
12	665	88.4	109 25	W27543	Human Ab light chain	7.70e-43
13	663	88.2	106 10	R54306	Anti-HIV gp120 immuno	1.11e-42
14	663	88.2	107 19	W01264	VL region of HIV neut	1.11e-42
15	660	87.8	107 7	R38592	Human lambda light ch	1.94e-42
16	660	87.8	107 31	W58492	Human kappa light cha	1.94e-42

17	656	87.2	106 19	W01262	VL region of HIV neut	4.06e-42
18	656	87.2	106 10	R54304	Anti-HIV gp120 immuno	4.06e-42
19	655	87.1	107 37	W70630	Humanised murine anti	4.88e-42
20	655	87.1	107 38	W86804	Variable light domain	4.88e-42
21	654	87.0	132 23	W22842	Human anti-tumour ant	5.87e-42
22	652	86.7	108 33	W62017	Light chain variable	8.48e-42
23	652	86.7	108 33	W63529	Humanised MHM24 light	8.48e-42
24	651	86.6	107 38	W86805	Variable light domain	1.02e-41
25	651	86.6	107 37	W70625	Humanised murine anti	1.02e-41
26	651	86.6	126 6	R29015	pUC-RV1-PMA.	1.02e-41
27	651	86.6	126 6	R29013	pUC-RV1-PMA.	1.02e-41
28	649	86.3	108 14	R65163	Human REI monoclonal	1.48e-41
29	648	86.2	107 25	W16649	Anti-cancer specific	1.77e-41
30	648	86.2	108 37	W70618	Anti-VEGF humanised a	1.77e-41
31	645	85.8	106 19	W01280	VL region of HIV neut	3.08e-41
32	645	85.8	106 19	R54257	Anti-HIV gp120 immuno	3.08e-41
33	645	85.8	129 35	W70379	Anti-human CD23 SE8 m	3.08e-41
34	644	85.6	108 24	W15524	Anti-TGF beta-2 scfv	3.71e-41
35	644	85.6	110 37	W70673	Anti-VEGF humanised a	3.71e-41
36	644	85.6	237 37	W70703	Protein encoded by Fa	3.71e-41
37	642	85.4	106 18	R88847	Human antibody IM9 1i	5.36e-41
38	642	85.4	107 19	W01283	VL region of HIV neut	5.36e-41
39	642	85.4	107 10	R54260	Anti-HIV gp120 immuno	5.36e-41
40	641	85.2	110 37	W70687	Anti-VEGF humanised a	6.45e-41
41	641	85.2	107 15	W70677	Human REI antibody 1i	7.76e-41
42	640	85.1	108 5	R81329	Human REI antibody 1i	7.76e-41
43	640	85.1	108 5	R81329	Human REI antibody 1i	7.76e-41
44	639	85.0	113 3	R13311	Light chain variable	9.32e-41
45	639	85.0	127 1	P90938	Humanised light chain	9.32e-41

ALIGNMENTS

CD responsive 117

RESULT 1
ID W27568 standard: Protein; 107 AA.
AC W27568;
DE 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain variable region.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody;
KW light chain; variable region; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELM-1;
KW keloid formation; scar tissue formation; pyrexia; HVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-AI.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Iadkovsky B,
PI Menkovich JA, McGuinness BF, Roberts AJ, Sakorafas P,
PI Seifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI; 97-415302/38.
DR N-PSDB; T88403.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PT Claim 15, Page 75; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC U929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerostis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 107 AA;

Query Match 100.0%; Score 752; DB 27; Length 107;
 Best Local Similarity 100.0%; Pred. No. 7, 87e-50;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 d1gmtpspaslaasvgtvltcrasqglnyawyqkpgkpklllyaaaslesgyps 60
 1 DIQMTQSPSSLSASVGDRTITCRASGIRNLTARYOQKPKGAPKLLITAASTLQSGVPS 60
 Oy 61 rfsgsgsgtdftltisslqpedvatycqyrnrapytfggqtkveik 107
 61 RFSGSGSGTDFLTITISSLPEDVATYCCORYNRAPYTFGGQTKVEIK 107

RESULT 2
 ID W70622 standard; peptide: 108 AA.

DE 27-JAN-1999 (first entry)
 AC W70622;
 DE Human consensus framework hum kappa1 for light kappa subgroup 1.
 KW Light variable domain; murine; humanised antibody; anti-VEGF antibody;
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
 KW VEGF-induced angiogenesis; tumour; retinal disorder;
 KW age-related macular degeneration; diabetic retinopathy;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease;
 KW Human consensus framework hum kappa1; light kappa subgroup 1.
 OS Homo sapiens.
 PV M09845331-A2.
 PD 15-OCT-1998;
 PF 03-APR-1998; U06604.
 PR 06-AUG-1997; US-908469.
 PR 07-APR-1997; US-833504.
 PA (GETH) GENENTECH INC.
 PI Baca M, Chen YM, Lowman HB, Presta LG, Wells JA;
 DR WPL: 96-568337/48.

DE New humanised antibody with affinity for vascular endothelial growth
 factor - for treatment of tumours, retinal disease and other
 PT angiogenic states, also related nucleic acid, vectors and
 PT transformed cells

Example 1: fig 1B: 100pp; English.

The present sequence represents the human consensus framework hum kappa1
 for light kappa subgroup 1. The sequence is used to humanise the variable
 CC light domain of the murine anti-vascular endothelial growth factor
 CC (anti-VEGF) antibody A4.6.1. The humanised antibodies are used to
 CC inhibit VEGF-induced angiogenesis, particularly for treating or
 CC preventing tumours (of any type) and retinal disorders (e.g. age-related
 CC macular degeneration or diabetic retinopathy). They can also be used to
 CC treat other conditions that involve angiogenesis, e.g. rheumatoid
 CC arthritis, psoriasis, atherosclerosis, Grave's disease, etc.
 SO Sequence 108 AA;

Query Match 90.7%; Score 682; DB 37; Length 108;
 Best Local Similarity 91.6%; Pred. No. 3, 33e-44;
 Matches 96; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 1 d1gmtpspaslaasvgtvltcrasqglnyawyqkpgkpklllyaaaslesgyps 60
 1 DIQMTQSPSSLSASVGDRTITCRASGIRNLTARYOQKPKGAPKLLITAASTLQSGVPS 60
 Oy 61 rfsgsgsgtdftltisslqpedvatycqyrnrapytfggqtkveik 107
 61 RFSGSGSGTDFLTITISSLPEDVATYCCORYNRAPYTFGGQTKVEIK 107

RESULT 3
 ID R47041 standard; peptide: 109 AA.
 AC R47041;
 DE 02-SEP-1994 (first entry)
 DE Sequence of the consensus antibody variable domain of the light
 DE chain.
 KW Monoclonal antibody; light chain; variable domain; consensus.
 OS Synthetic.
 PN W09404679-A.
 PD 03-MAR-1994.
 PF 20-AUG-1993; U07832.
 PR 21-AUG-1992; US-934373.
 PA (GETH) GENENTECH INC.
 PI Carter PJ, Presta LG;
 DR WPL: 94-083196/10.
 DE Preparation of improved humanised antibodies - by comparison of
 PT consensus and import complementarity determining regions and
 PT framework region sequences, e.g. to humanise murine
 PS Claim 16; Page 108; 126pp; English.
 CC The consensus variable domain sequences are derived from the most
 CC abundant subclasses in the sequence compilation of Kabat et al.,
 CC Sequences of Proteins of Immunological Interest, National
 CC Institutes of Health, Bethesda MD (1987), namely, VL-kappa
 CC subgroup I and VH group III. In such 166 gamma-1 human consensus
 CC sequences, the VL consensus domain has the AA sequence in R47041,
 CC and the VH consensus domain has the AA sequence in R47042.
 SO Sequence 109 AA;

Query Match 90.6%; Score 681; DB 9; Length 109;
 Best Local Similarity 89.7%; Pred. No. 4, 01e-44;
 Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 1 d1gmtpspaslaasvgtvltcrasqglnyawyqkpgkpklllyaaaslesgyps 60
 1 DIQMTQSPSSLSASVGDRTITCRASGIRNLTARYOQKPKGAPKLLITAASTLQSGVPS 60
 Oy 61 rfsgsgsgtdftltisslqpedvatycqyrnrapytfggqtkveik 107
 61 RFSGSGSGTDFLTITISSLPEDVATYCCORYNRAPYTFGGQTKVEIK 107

RESULT 4
 ID W01263 standard; protein: 107 AA.

DE 28-JAN-1997 (first entry)
 AC W01263;
 DE VL region of HIV neutralising Mab, clone b14.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW Virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT region 1..21
 FT /label= FR1
 FT region 22..32
 FT /label= CDRI
 FT region 33..47
 FT /label= FR2
 FT region 48..54
 FT /label= CDR2
 FT region 55..86
 FT /label= FR3
 FT region 87..95
 FT /label= CDR3
 FT region 96..107
 FT /label= FR4

PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbais CP, Burton DR, Lerner RA;
 DR WPL: 96-179601/18.

PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
PT passive immunotherapy and detection of HIV infection.
PS Example; Fig 11; 366pp; English.
CC The sequences given in W01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the Jk1
CC gene clone, b14. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/mL, and
CC binds mature gp120 preferentially over the precursor gp160. The Mab
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

Query Match	90.48;	Score 680;	DB 19;	Length 107;
Best Local Similarity	93.38;	Pred. No. 4.83e-44;		
Matches	98;	Conservative	3;	Mismatches 4;
			Indels 0;	Gaps 0

1 elcspsspsasavgdvlttccraasglsnylawqdkpkykpklllyaaatlqsgvprf 60
 2 :::::|||||
 3 QMTGSPSSLSASGKRVITTCRASGIRNYLAWQKGRKAPKRLIIAASTLDSGVSNF 62
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CDR3

RESULT 5
ID R54305 standard; protein; 107 AA. CDR3
AC R54305:
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region b1.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
OS Homo sapiens.
FH Key Location/Qualifiers
FT region 1..21
FT region /label= FR1
FT region 22..32
FT region /label= CDR1
FT region 33..47
FT region /label= FR2
FT region 48..54
FT region /label= CDR2
FT region 55..86
FT region /label= FR3
FT region 87..95
FT region /label= CDR3
FT region 96..107
FT region /label= FR4
PN MO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; 009328.
PR 30-SEP-1992; US-954148.
PA (SCRI) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA:
WPI; 94-13516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 176; 248pp: English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC distictonic vector to produce a library of firegments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54305 is from a gp120-
CC specific clone.
SQ Sequence 107 AA:

Query Match	90.48;	Score 680;	DB 10;	Length 107;
Best Local Similarity	93.38;	Pred. No. 4.83e-44;		
Matches	98;	Conservative	3;	Mismatches 4; Indels 0; Gaps 0

61	ggagsgatdcttcttsttqpsdvatlytgcqaynaaprttfgtggctveak	105
Dd	1 elqpspsstasasvqgdvtvtcttcrasglsinylawqkqkqkvpklllyaaactlsgvysr	6
63	sgsgsgtdpflrttssldqpdvartttcqrnrnprrtffgggltveak	107
Qy	3 qmngpspsstasasvqgdvrttcrasglsinylawqkqkqkvpklllyaaactlsgvysr	6
Dd		

CDR3

ID	RESULT	6
AC	W01261 standard; Protein; 107 AA.	
AC	W01261:	
DT	28-JAN-1997 (first entry)	
DE	VL region of HIV neutralising Mab, clone b1.	
KM	Heavy chain; light chain; variable region; VH: monoclonal antibody;	
KM	Mab; HIV: human immunodeficiency virus; glycoprotein; gp120; clone;	
KM	virus infectivity assay; precursor gp160; immunocompetence; human;	
OS	anti-HIV antibody; detection; HIV infection.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	region	1..21
FT	region	/label= FR1
FT	region	22..32
FT	region	/label= CDR1
FT	region	33..47
FT	region	/label= FR2
FT	region	48..54
FT	region	/label= CDR2
FT	region	55..86
FT	region	/label= FR3
FT	region	87..95
FT	region	/label= CDR3
FT	region	96..107
FT	region	/label= FR4
PN	W0602273-A1.	
PD	01-FEB-1996.	
PF	11-JUL-1995; U08743.	
PR	18-JUL-1994; US-276852.	
PA	(SCRI) SCRIPPS RES INST.	
PI	Barbas CF, Burton DR, Lerner RA;	
PI	WPI: 96-179601/18.	
PT	Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in	
PT	passive immuno:therapy and detection of HIV infection.	
PS	Example; Fig 11; 366pp; English.	
CC	The sequences given in W01261-92 represent the light chain variable	
CC	regions (VL) of a series of monoclonal antibodies (Mab's) which are	
CC	immunoreactive with HIV glycoprotein gp120 and are capable of	
CC	neutralising HIV. This sequence represents the sequence of the JKL	
CC	gene clone, b1. A Mab containing this VL sequence has the capacity	
CC	to reduce HIV infectivity titre in an in vivo virus infectivity assay	
CC	by 50 % at a concentration of less than 700 ng of antibody/ml, and	
CC	binds mature gp120 preferentially over the precursor gp160. The Mab	
CC	antibody and in the detection of a human anti-HIV	
CC	antibody and in the detection of HIV infection.	
CC	Sequence 107 AA;	
SO		
Query Match	89.6%; Score 674; DB 19; Length 107;	
Best Local Similarity	91.4%; Pred. No. 1,46e-43;	
Matches	96; Conservative 5; Mismatches 4; Indels 0; Gaps 0;	
D0	1 eltspsalsasvgydyrttceraaglsnylawyqgkpgkvrlllyaaatlqgvpsrf 60	
QY	3 QMTSPSLSASVGDRTYITICRASQGRNRYLAWYQGRKPKLLIYAASLTGSPSRF 62	
D0	61 sgsgsgtdftllslslqpedvaytycgkynsapttfsgqtkvlekl 105	
Y	63 SGSSSGTDFTLTISLQPEDVAYTYCGRKNAPTYTSGTKVLEKL 107	

Query match	89.68;	Score 674;	DB 19;	Length 107
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[illegible]

CDR

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RESULT 7
ID R54303 standard; protein; 107 AA.
AC R54303;
DE 10-NOV-1994 (first entry)
DT Anti-HIV gp120 immunoglobulin light chain variable region b1.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
OS variable region; framework; complementarity determining region.
FH Homo sapiens.
FH Key Location/Qualifiers
FT region 1..21
FT FT /label= FR1
FT region 22..32
FT FT /label= CDRL
FT region 33..47
FT FT /label= FR2
FT region 48..54
FT FT /label= CDR2
FT region 55..86
FT FT /label= FR3
FT region 87..95
FT FT /label= CDR3
FT FT /label= FR4
FT region 96..107
FT FT /label= FR4

PN W09407922-A.
PD 14-APR-1994.
PE 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PR (SCRI ) SCRIPPS RES INST.
PA Barbas CF, Burton DR, Lerner RA;
PI WPJ; 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PT Example; Page 175; 248pp; English.
PS Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54303 is from a gp120-
CC specific clone.
SQ Sequence 107 AA;

Query Match 89.6%; Score 674; DB 10; Length 107;
Best Local Similarity 91.4%; Pred. No. 1,466-43;
Matches 96; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 1 eltsqpslisaavqdrvtlcrasqslansylawyqgkpgkvpriilyaaatlpgyvsrf 60
::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 3 QMTQSPFSLISAVSGRVTITCRASGGINNYLAWTQOKRGAAPKILITAASTLQSGVSRF 62

Db 61 sgsqsgldfcltlslslqpedvaelycyqkynsaaprtffgsgtkvkl 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 63 SSGSGGTDFTLTILSLQPEDVATYCCQAYKNAPYFGGTRVEIK 107

RESULT 8
ID R30770 standard; protein; 107 AA.
AC R30770;
DE 12-MAY-1993 (first entry)
DT Consensus humanised murine anti-CD3 MAb UCHL1 VL domain huki.
KW Humanisation; rapid; monoclonal antibody; muxCD3; light chain.
OS Synthetic.
PN W09222853-A.
PD 23-DEC-1992.
PE 15-JUN-1992; U05126.
PE 14-JUN-1991; US-715272.
PA (GETH ) GENENTECH INC.
PI Carter PJ, Presta LG;

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PR WPI: 93018139/02.
PR Humanisation of antibodies - by molecular modelling of the variable
PR domains and alteration by gene conversion mutagenesis
PS Disclosure; Fig 5; 126pp; English.
PS The sequence is that of a consensus sequence huki of the most
CC abundant human subgroups, namely VL K 1 upon which is based the
CC humanised variants of the light chain variable domain of murine
CC anti-CD3 monoclonal antibody UCART1 (mucCD3, Shalaby 1992).
SO Sequence 107 AA;

Query Match      89.5%; Score 673; DB 6; Length 107;
Best Local Similarity 90.7%; Pred. No. 1,76e-43;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 1 d1gmtbpslmsavgdvlttcragslsnylwygkpkapklillyaassleagvps 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 1 D10MTQSSSSIASVGRVITTCRASGIRNYILAWYQOKPGKAPKLITVYASTQSCVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 rfsgsgsgtdftlyslqpedfctlyccqynslpwffggtkvrlk 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 61 RFSGSGSGTDFTLTISLQPEDVATVYICORNPAPYTFGGGTVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
ID W87455 standard; Protein; 107 AA.
AC W87455;
DT 15-MAR-1999 (first entry)
DE Humanised anti-alpha-v beta-3 Mab D12HZREI VL.
KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12HZREI.
OS Homo sapiens.
OS Synthetic.
FH Key
FT Region Location/Qualifiers
FT Region 24..34 /label= CDR1
FT Region 50..56 /label= CDR2
FT Region 89..97 /label= CDR3
FT Region /label= CDR3

PN W09840488-A1.
PD 17-SEP-1998.
PF 12-MAR-1998; U04987.
PR 12-MAR-1997; US-039609.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PI Johanson KO, Jonak ZL, Taylor AH;
PI WPI: 99-034590/03.
PI New anti alpha-v beta-3 vitronectin receptor antibodies - used for
PI immunotherapeutic treatment of e.g. diabetic retinopathy ,
PI inflammatory disorders, atherosclerosis, restenosis, cancers or
PI osteoporosis
PS Claim 6; Page 65-66; 97pp; English.
PS This is the amino acid sequence of the light chain variable region
CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
CC monoclonal antibody D12HZREI. It is based on the VL sequence
CC (see W84096) of human REI kappa chain framework, with
CC complementarity determining regions (CDRs) from the murine
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC D12 (see W84093). Humanised antibodies of the invention can be
CC used for passive immunotherapy of disorders mediated by the alpha-v
CC beta-3 receptor. e.g. cardiovascular or angiogenic-related
CC disorders, such as angiogenesis associated with diabetic
CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
CC disorders, macular degeneration, rheumatoid arthritis and cancer,
CC e.g. solid tumour metastasis, and diseases where bone resorption is
CC associated with pathology such as osteoporosis, hyperparathyroidism,
CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
CC produced by bone metastasis, bone loss due to immobilisation or sex
CC hormone deficiency. They can also be used for targeted drug

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CC therapy, and for detection and diagnosis.
SQ Sequence 107 AA;

Query Match 88.7%; Score 667; DB 39; Length 107;
Best Local Similarity 86.9%; Pred. No. 5,32e-43;
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

DB 1 d1qmtgspsslsasvgrvtltccasgqdl1kylmwygqkpgkpklllyeasniqayvps 60
|||||
OY 1 DIQMTQSPSSLSASVGRVITTCRASGGINRYLAWYQOKPKAKRLIYAASITQSGVPS 60
|||||
61 rfsgsgsgtdftltlsslpqdefatlycqqynslpytfggskvlelk 107
|||||
OY 61 RFSGSGSGTDFTLTSSLQPEDVATYYCQRNRPAPYFGGSKTVEIK 107
|||||

RESULT 10
ID R40956 standard; protein; 109 AA.

AC R40956;
25-FEB-1994 (first entry)
Human germ-line gene HK137 antibody light (kappa) chain.
humanised antibody; human germ-line; light chain; variable region;
framework region; reshaped antibody; CDR-grafted antibody;
KW Complementarity determining region; immuno silent.
OS Homo sapiens.

FT Key location/Qualifiers
FT region 1..23 /label= FR1
FT /note= "framework region"
FT region 24..34 /label= CDR1
FT region 35..49 /label= FR2
FT /note= "framework region"
FT region 50..56 /label= CDR2
FT region 57..88 /label= FR3
FT /note= "framework region"
FT region 89..97 /label= CDR3
FT region 98..109 /label= FR4
FT /note= "framework region"

PN WO9317105-A.
PD 02-SEP-1993.
PE 19-FEB-1993; G00363.
19-FEB-1992; GB-003459.
(SCOR-) SCOTGEN LTD.
Carr EJ, Harris WJ, Winter GP;
WPI: 93-288411/36.
New altered antibodies with reduced immune responses - have
germ-line aminoacid residues replacing somatically mutated
PT residues

PS Example 3: Fig 4b; 53pp; English.
CC A humanised antibody comprised CDRs originally from a mouse Mab
CC REV19 specific for Respiratory Syncytial Virus transplanted onto
CC heavy and light chain V region domains derived from NEMM and REI
CC myeloma proteins, respectively. The framework regions of this
CC CDR-grafted antibody were converted to the germ-line equivalent.
CC For conversion of the K-chain, the germ-line light chain VK137
CC (R40956) was used. Germ-line framework regions are those present in
CC immature B cells, i.e. prior to any somatic mutation which takes
CC place during maturation. Unlike mutations in the CDRs, any mutation
CC in framework regions does not affect affinity for an antigen and is
CC therefore essentially random. The mutation may, however, cause the
CC "self" antibody to be recognised as "foreign" and conversion to the
CC unmutated germ-line sequence renders the framework regions "immuno
CC silent".
SQ Sequence 109 AA;

Query Match 88.7%; Score 667; DB 8; Length 109;
Best Local Similarity 90.7%; Pred. No. 5,32e-43;

Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

DB 1 d1qmtgspsslsasvgrvtltccasgdl1kylmwygqkpgkpklllyeasniqayvps 60
|||||
OY 1 DIQMTQSPSSLSASVGRVITTCRASGGINRYLAWYQOKPKAKRLIYAASITQSGVPS 60
|||||
61 rfsgsgsgtdftltlsslpqdefatlycqqynslpytfggskvlelk 107
|||||
OY 61 RFSGSGSGTDFTLTSSLQPEDVATYYCQRNRPAPYFGGSKTVEIK 107
|||||

RESULT 11
ID R30764 standard; protein; 109 AA.

AC R30764;
12-MAY-1993 (first entry)
DE Consensus humanised antibody light chain variable domain.
KW Humanisation; rapid; muMab4D5; monoclonal antibody; murine.
OS Mus musculus.

PN WO9222653-A.
PD 23-DEC-1992.
PF 15-JUN-1992; US-715272.
PR 14-JUN-1991; US-715272.
PA (GETH) GENENTECH INC.
PI Carter PJ, Presta LG;
DR WPI: 93-018139/02.
PT Humanisation of antibodies - by molecular modelling of the variable
PT domains and alteration by gene conversion mutagenesis
PS Disclosure; Page 8; 12pp; English.
CC The sequence is that of a consensus humanised antibody light chain
CC variable domain of murine monoclonal antibody muMab4D5 which can
CC be used in the preparation of humanised antibodies.
SQ Sequence 109 AA;

Query Match 88.4%; Score 665; DB 6; Length 109;
Best Local Similarity 88.8%; Pred. No. 7,70e-43;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

DB 1 d1qmtgspsslsasvgrvtltccasgdl1kylmwygqkpgkpklllyeasniqayvps 60
|||||
OY 1 DIQMTQSPSSLSASVGRVITTCRASGGINRYLAWYQOKPKAKRLIYAASITQSGVPS 60
|||||
61 rfsgsgsgtdftltlsslpqdefatlycqqynslpytfggskvlelk 107
|||||
OY 61 RFSGSGSGTDFTLTSSLQPEDVATYYCQRNRPAPYFGGSKTVEIK 107
|||||

RESULT 12
ID W27543 standard; Protein; 109 AA.

AC W27543;
DE 22-JAN-1998 (first entry)
DE Human Ab light chain variable region V-kappa-1 consensus.
KW Human; antibody; preparation; library; V-kappa-1; variable region;
KW light chain; consensus.
OS Homo sapiens.

PN WO9708320-A1.
PD 06-MAR-1997.
PF 19-AUG-1996; E03647.
PR 18-AUG-1995; EP-113021.
PA (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.
PI Ge L, Irag V, Knaaplik A, Moroney S, Peck P, Plueckthun A;
DR WPI: 97-179277/16.
DR N-PSDB; T87938.
PT Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
PS Example 1: Fig 3A; 436pp; English.
CC The present sequence is the human antibody light chain
CC variable region synthetic kappa sequence V-kappa-1, used in the
CC preparation of a human derived antibody gene library.
SQ Sequence 109 AA;

Query Match 88.4%; Score 665; DB 25; Length 109;
Best Local Similarity 90.7%; Pred. No. 7,70e-43;


```

FT /note-"residue conserved in less than 50% of the
FT known sequences of hL2"
FT misc_difference 53
FT /note-"residue conserved in less than 50% of the
FT known sequences of hL2"
FT misc_difference 55
FT /note-"residue conserved in less than 50% of the
FT known sequences of hL2"
FT misc_difference 70
FT /note-"residue conserved in less than 50% of the
FT known sequences of hL2"
FT misc_difference 92..94
FT /note-"residues conserved in less than 50% of the
FT known sequences of hL2"
FT misc_difference 96
FT /note-"residue conserved in less than 50% of the
FT known sequences of hL2"
PN WO9311794-A.
PD 24-JUN-1993.
PD 14-DEC-1992: U10906.
PD 13-DEC-1991: US-808464.
PI (XOMA ) XOMA CORP.
PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
DR WPI; 93-213827/26.
PT Antibodies prep. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Claim 2: Page 93; 160pp; English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (hK1 - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 -
CC R38592, hL3 - R38593, hL6 - R38594, hK4 - R38595, hL4 - R38596,
CC and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
CC hH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 107 AA;

```

```

Query Match 87.8%: Score 660: DB 7: Length 107;
Best Local Similarity 87.9%: Pred. No. 1.94e-42;
Matches 94: Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 dlmqtgspsslsasvgrvltcraasqisxylxwqgkpkapkllyaaasxlsgvps 60
1 DIQMTGSPSSLSASVGRVITTCRASGIRNYLAWYQKPKAPKLILYAASTIQSGVPS 60
Db 61 rfsgsgsgxtfltlslslpedefatyycqgyxxxpxtfgqgtkveik 107
61 RFSGSGSGTDFLTLLISLQPEDVATYYCQRYNRPATYFGQGTVEIK 107

```

Search completed: Thu Sep 2 11:07:52 1999
 Job time : 36 secs.

CAR

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 W P E R E H
 (TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Sep 2 12:00:31 1999; Maspar time 3.37 Seconds
 56,731 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-599-226-21
 Description: (1-9) from US08599226.pep
 Perfect Score: 59
 Sequence: 1 OKNSAAYS 9

Scoring table:
 PAM 150
 Gap 15

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

a.geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 15.444; Variance 49.479; scale 0.312

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	59	100.0	9	27	W27580	Anti-TNF-alpha antibo
2	54	91.5	9	27	W27570	Anti-TNF-alpha antibo
3	54	91.5	9	27	W27574	Anti-TNF-alpha antibo
4	53	89.8	9	27	W27577	Anti-TNF-alpha antibo
5	52	88.1	9	27	W27576	Anti-TNF-alpha antibo
6	50	84.7	9	27	W27573	Anti-TNF-alpha antibo
7	50	84.7	9	27	W27582	Anti-TNF-alpha antibo
8	49	83.1	9	27	W27578	Anti-TNF-alpha antibo
9	49	83.1	9	27	W27575	Anti-TNF-alpha antibo
10	49	83.1	9	27	W27571	Anti-TNF-alpha antibo
11	48	81.4	9	27	W27579	Anti-TNF-alpha antibo
12	46	78.0	9	27	W27585	Anti-TNF-alpha antibo
13	46	78.0	9	27	W27583	Anti-TNF-alpha antibo
14	46	78.0	9	27	W27584	Anti-TNF-alpha antibo
15	46	78.0	107	27	W27568	Anti-TNF-alpha antibo
16	45	76.3	193	25	W24877	Diphtheria toxin frag

17	45	76.3	452	37	W80217	48 kDa modified diph
18	45	76.3	475	27	W34056	Modified diphtheria t
19	45	76.3	475	3	R15148	Ro/SSA autoantigen.
20	45	76.3	480	37	W80218	51 kDa modified diph
21	45	76.3	518	8	R40208	Sequence of geneical
22	45	76.3	528	8	R44892	Diphtheria toxin (del
23	45	76.3	532	8	R44890	Diphtheria toxin (del
24	45	76.3	533	8	R44898	Diphtheria toxin (del
25	45	76.3	533	8	R44897	Diphtheria toxin (del
26	45	76.3	533	8	R44893	Diphtheria toxin (del
27	45	76.3	533	8	R44902	Diphtheria toxin (del
28	45	76.3	533	8	R44889	Diphtheria toxin (del
29	45	76.3	533	8	R44895	Diphtheria toxin (del
30	45	76.3	533	8	R44891	Diphtheria toxin (del
31	45	76.3	533	8	R44896	Diphtheria toxin (del
32	45	76.3	533	8	R44901	Diphtheria toxin (del
33	45	76.3	534	37	W80216	Native diphtheria tox
34	45	76.3	535	28	W46448	Antino acid sequence o
35	45	76.3	535	8	R44888	Wild-type diphtheria
36	45	76.3	535	17	R86825	Diphtheria toxin.
37	45	76.3	535	17	P90181	Cross-reactive materi
38	45	76.3	535	17	R86826	Diphtheria toxin (mut
39	45	76.3	535	25	W24876	Diphtheria toxin.
40	45	76.3	560	2	P70597	Modified diphtheria t
41	45	76.3	560	2	P60516	Tox228 diphtheria tox
42	45	76.3	567	2	R06607	Gly(158) Diphtheria t
43	45	76.3	619	2	R26486	Hybrid protein DAB86
44	45	76.3	671	37	W68500	Hybrid receptor toxin
45	45	76.3	676	1	P93172	Quarter-length hybrid

ALIGNMENTS

RESULT 1
 AC W27580 standard; peptide: 9 AA.
 AC W27580;
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disorder; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW peridontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN M09729131-A1.
 PD 14-APR-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manukovich JA, McGuiness BT, Roberts AJ, Sakorats P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20, page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption diseases,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).

CC Sequence 9 AA:

Query Match 100.0%; Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.90e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsaaps 9
 QY 1 QKNSAAPS 9

RESULT 2
 ID W2570 standard; peptide; 9 AA.

AC W2570; 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BANDT) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 67; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 91.5%; Score 54; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.74e+01;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsaaps 9
 QY 1 QKNSAAPS 9

RESULT 3
 ID W2574 standard; peptide; 9 AA.

AC W2574; 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BANDT) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 91.5%; Score 54; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.74e+01;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsaaps 9
 QY 1 QKNSAAPS 9

RESULT 4
 ID W2577 standard; peptide; 9 AA.

AC W2577; 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA.

Query Match 89.8%; Score 53; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3.50e+01;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsapy 9
 |||||:
 1 OKINSAIVS 9

Yy 1 OKINSAIVS 9

RESULT 5
 ID W27576 standard; peptide: 9 AA.
 AC W27576:
 DE 19-MAR-1998 (first entry)
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA.

PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA.

Query Match 88.1%; Score 52; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 4.47e+01;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsapy 8
 |||||:
 1 OKINSAIV 8

Yy 1 OKINSAIV 8

RESULT 6
 ID W27573 standard; peptide: 9 AA.
 AC W27573:
 DE 19-MAR-1998 (first entry)
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA.

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 84.7%; Score 50; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.26e+01;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|:|:
 QY 1 QKYNMAYS 9

RESULT 7
 ID W27582 standard; peptide: 9 AA.
 AC W27582;
 DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PI 09-FEB-1996; US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Markovich JA, McGulness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 84.7%; Score 50; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.26e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|:|:
 QY 1 QKYNMAYS 9

RESULT 8
 ID W27578 standard; peptide: 9 AA.
 AC W27578;
 DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PI 09-FEB-1996; US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Markovich JA, McGulness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 83.1%; Score 49; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 9.23e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|:|:
 QY 1 QKYNMAYS 9

RESULT 9

ID W27575 standard; peptide: 9 AA.

AC W27575; 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PA 09-FEB-1996: US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI MPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20: Page 69; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Kof rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

CC Sequence 9 AA;

SQ

Query Match 83.1%; Score 49; DB 27; Length 9;

Best Local Similarity 66.7%; Pred. No. 9.23e+01;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkyrapt 9

OY 1 OKXNSAAYS 9

RESULT 10

ID W27571 standard; peptide: 9 AA.

AC W27571; 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; inflammatory bone disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PA 09-FEB-1996: US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI MPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20: Page 68; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Kof rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

CC Sequence 9 AA;

SQ

Query Match 83.1%; Score 49; DB 27; Length 9;

Best Local Similarity 66.7%; Pred. No. 9.23e+01;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkyrapt 9

OY 1 OKXNSAAYS 9

RESULT 11

ID W27579 standard; peptide: 9 AA.

AC W27579; 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; inflammatory bone disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PA 09-FEB-1996: US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI MPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20: Page 68; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Kof rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

CC Sequence 9 AA;

SQ

Query Match 83.1%; Score 49; DB 27; Length 9;

Best Local Similarity 66.7%; Pred. No. 9.23e+01;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkyrapt 9

OY 1 OKXNSAAYS 9

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC U937 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, allergy, multiple
 CC spondylitis, osteoarthritis, gouty arthritis, rheumatoid
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 SQ Sequence 9 AA;

Query Match 81.4%; Score 48; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.17e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkyrnapyn 9
 ||| | | | |
 Qy 1 OKYNSAAYS 9

RESULT 12
 ID W27585 standard; peptide: 9 AA.
 AC W27585;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Menkovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 72: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC U937 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 SQ Sequence 9 AA;

Query Match 78.0%; Score 46; DB 27; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.88e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkyrnapyn 9
 | | | | | | |
 Qy 1 OKYNSAAYS 9

RESULT 13
 ID W27583 standard; peptide: 9 AA.
 AC W27583;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Menkovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 72: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC U937 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, allergy, multiple
 CC spondylitis, osteoarthritis, gouty arthritis, rheumatoid
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 SQ Sequence 9 AA;

Query Match 78.0% Score 46; DB 27; Length 9;
Best Local Similarity 66.7% Pred. No. 1.88e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkytsapyt 9
| | | | |
1 OKYNSAAYS 9

RESULT 14
ID W27584 standard; peptide: 9 AA.
AC W27584;
DE 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN MO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BAD1) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PI WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 72; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 78.0% Score 46; DB 27; Length 9;
Best Local Similarity 55.6% Pred. No. 1.88e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkyrppyt 9
| | | | |
1 OKYNSAAYS 9

RESULT 15
ID W27568 standard; protein: 107 AA.
AC W27568;

DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain variable region.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody;
KW light chain; variable region; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN MO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BAD1) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PI WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 15; Page 75; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 107 AA;

Query Match 78.0% Score 46; DB 27; Length 107;
Best Local Similarity 55.6% Pred. No. 1.88e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 89 qkyrppyt 97
| | | | |
1 OKYNSAAYS 9

Search completed: Thu Sep 2 12:00:50 1999
Job time : 19 secs.

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CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 20 AA; 2244 MW; 2009 CN;

Query Match 76.3%; Score 45; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.02e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 9 KYDAAGS 16
11::111
QY 2 KYNAAVS 9

RESULT 2 STANDARD; PRT; 193 AA.
ID US-08-564-972-8

AC xxxxxx

DE Sequence 8, Application US/08564972

CC Sequence 8, Application US/08564972

CC Patent No. 5843462

CC GENERAL INFORMATION:

CC APPLICANT: CONTI-FINE, B. M.

CC TITLE OF INVENTION: DIPHTHERIA TOXIN EPTOPES

CC NUMBER OF SEQUENCES: 79

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Schwegman, Lundberg, Woessner & Riuth, P.A.

CC STREET: P.O. Box 2938

CC CITY: Minneapolis

CC STATE: MN

CC COUNTRY: USA

CC ZIP: 55402

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC OPERATING SYSTEM: IBM compatible

CC SOFTWARE: FASTSEQ Version 1.5

CC CURRENT APPLICATION DATA:

CC FILING DATE: 30-NOV-1995

CC CLASSIFICATION: 424

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER:

CC FILING DATE:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Woessner, Warren D

CC REGISTRATION NUMBER: 30,440

CC REFERENCE/DOCKET NUMBER: 600.344US1

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 612-339-0331

CC TELEFAX: 612-339-3061

CC TELEX:

CC INFORMATION FOR SEQ ID NO: 8:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 193 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC ANTI-SENSE: NO

CC FRAGMENT TYPE: N-terminal

CC ORIGINAL SOURCE:

CC SEQUENCE 193 AA; 21164 MW; 184975 CN;

Query Match 76.3%; Score 45; DB 2; Length 193;

Best Local Similarity 62.5%; Pred. No. 1.02e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 59 KYDAAGS 66
11::111
QY 2 KYNAAVS 9

RESULT 3 STANDARD; PRT; 194 AA.
ID US-08-466-604-27

AC xxxxxx

DE Sequence 27, Application US/08466604

CC Sequence 27, Application US/08466604

CC Patent No. 5843776

CC GENERAL INFORMATION:

CC APPLICANT: TAMAOKI, TAIRI

CC TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN

CC NUMBER OF SEQUENCES: 46

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

CC STREET: 699 PRINCE STREET

CC CITY: ALEXANDRIA

CC STATE: VA

CC COUNTRY: USA

CC ZIP: 2213-1404

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/466,604

CC FILING DATE: 06-JUN-1995

CC CLASSIFICATION: 435

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US 08/148,058

CC FILING DATE: 04-NOV-1993

CC ATTORNEY/AGENT INFORMATION:

CC NAME: MOOI, LESLIE A.

CC REGISTRATION NUMBER: 37,047

CC REFERENCE/DOCKET NUMBER: 028722-125

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415-854-8275

CC TELEFAX: 415-854-7400

CC INFORMATION FOR SEQ ID NO: 27:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 194 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 194 AA; 21235 MW; 187002 CN;

Query Match 76.3%; Score 45; DB 2; Length 194;
Best Local Similarity 62.5%; Pred. No. 1.02e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 60 KYDAAGS 67
11::111
QY 2 KYNAAVS 9

RESULT 4 STANDARD; PRT; 194 AA.
ID US-08-478-042-27

AC xxxxxx

DE Sequence 27, Application US/08478042
 CC
 CC Sequence 27, Application US/08478042
 CC Patent No. 5807738
 CC GENERAL INFORMATION:
 CC APPLICANT: TAMAOKI, TAIKI
 CC APPLICANT: NAKABAYASHI, HIDEKAZU
 CC TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
 CC NUMBER OF SEQUENCES: 46
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 CC STREET: 699 PRINCE STREET
 CC CITY: ALEXANDRIA
 CC STATE: VA
 CC COUNTRY: USA
 CC ZIP: 22313-1404
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/478,042
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/148,058
 CC FILING DATE: 04-NOV-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: MOOI, LESLIE A.
 CC REGISTRATION NUMBER: 37,047
 CC REFERENCE//DOCKET NUMBER: 028722-126
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-854-7400
 CC TELEFAX: 415-854-8275
 CC INFORMATION FOR SEQ ID NO: 27:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 194 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 194 AA; 21235 MW; 187002 CN;
 SQ
 Query Match 76.3%; Score 45; DB 2; Length 194;
 Best Local Similarity 62.5%; Pred. NO.1.02e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0
 Db 60 KYDAGYS 67
 ||:|:|
 Oy 2 KYSNAYS 9
 RESULT 5 STANDARD: PRT; 194 AA.
 ID US-08-645-215-27
 AC xxxxxx
 XX
 XX
 DE Sequence 27, Application US/08645215
 CC
 CC Sequence 27, Application US/08645215
 CC Patent No. 5827686
 CC GENERAL INFORMATION:
 CC APPLICANT: TAMAOKI, TAIKI
 CC APPLICANT: NAKABAYASHI, HIDEKAZU
 CC TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
 CC TITLE OF INVENTION: MAMMALIAN CELLS
 CC NUMBER OF SEQUENCES: 46
 CC CORRESPONDENCE ADDRESS:
 CC

CC ADDRESS: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
CC STREET: 699 PRINCE STREET
CC CITY: ALEXANDRIA
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/645,215
CC FILING DATE: 13-MAY-1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/148,058
CC FILING DATE: 04-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: MOOI, LESLIE A. 37,047
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 028722-135
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-854-7400
CC TELEFAX: 415-854-8275
CC INFORMATION FOR SEQ ID NO: 27:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 194 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 194 AA: 21235 MW; 187002 CN;

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Query Match          76.3%; Score 45; DB 2; Length 194;
Best Local Similarity 62.5%; Pred.No. 1.02e+02;
Matches      5; Conservative      3; Mismatches      0; Indels      0; Gaps      0

Db      60 KYDAAGYS 67
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QY      2 KYNSAAYS 9

RESULT        6
XX US-08-148-058A-27 STANDARD; PRT; 194 AA.
XX AC xxxxxx
XX DT
XX DE
Sequence 27, Application US/08148058A
CC CC Sequence 27, Application US/08148058A
CC Patent No. 5804407
CC GENERAL INFORMATION:
CC APPLICANT: TAMAOKI, TAIKI
CC APPLICANT: NAKABAYASHI, HIDEKAZU
CC TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
CC TITLE OF INVENTION: MAMMALIAN CELLS
CC NUMBER OF SEQUENCES: 46
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 PRINCE STREET
CC CITY: ALEXANDRIA
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/148,058A
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CC FILING DATE: 04-NOV-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: MOOI, LESLIE A.
CC REGISTRATION NUMBER: 37,047
CC REFERENCE/DOCKET NUMBER: 028722-074
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-854-7400
CC TELEFAX: 415-854-8275
CC INFORMATION FOR SEQ ID NO: 27:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 194 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 194 AA; 21235 MW; 187002 CN;

Query Match 76.3%; Score 45; DB 2; Length 194;
Best Local Similarity 62.5%; Pred. No. 1.02e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 60 KYDAAGS 67
11::11
QY 2 KYNSAAYS 9

RESULT 7
ID US-08-724-394A-7 STANDARD: PRT; 487 AA.
AC xxxxxx
XX
DT
DE Sequence 7, Application US/08724394A
XX Sequence 7, Application US/08724394A
CC Patent No. 5872237
CC GENERAL INFORMATION:
CC APPLICANT: Feder, John N.
CC APPLICANT: Krommal, Gregory S.
CC APPLICANT: Lauer, Peter H.
CC APPLICANT: Ruddy, David A.
CC APPLICANT: Thomas, Winston
CC APPLICANT: Tsuchinashi, Zenta
CC APPLICANT: Wolff, Roger K.
CC TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
CC TITLE OF INVENTION: Sequences and Antibodies Thereof
CC NUMBER OF SEQUENCES: 31
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/724,394A
CC FILING DATE: 01-OCT-1996
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitts, Renee A.
CC REGISTRATION NUMBER: 35,136
CC REFERENCE/DOCKET NUMBER: 017957-000100
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-576-0200
CC TELEFAX: 415-576-0300
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 487 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC FEATURE:
CC NAME/KEY: Region
CC LOCATION: 1..487
CC OTHER INFORMATION: /note="52 kD Ro"
SQ SEQUENCE 487 AA; 55491 MW; 1241027 CN;

Query Match 76.3%; Score 45; DB 2; Length 487;
Best Local Similarity 44.4%; Pred. No. 1.02e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 398 OKYAGTYP 406
11::11
QY 1 OKYNSAAYS 9

RESULT 8
ID US-08-564-972-1 STANDARD: PRT; 535 AA.
AC xxxxxx
XX
DT
DE Sequence 1, Application US/08564972
XX Sequence 1, Application US/08564972
CC Patent No. 5843462
CC GENERAL INFORMATION:
CC APPLICANT: Conti-Fine, B. M.
CC TITLE OF INVENTION: DIPHTHERIA TOXIN EPTOPES
CC NUMBER OF SEQUENCES: 79
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Schwegman, Lundberg, Woessner & Riuth, P.A.
CC STREET: P.O. Box 2938
CC CITY: Minneapolis
CC STATE: MN
CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,972
CC FILING DATE: 30-NOV-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Woessner, Warren D
CC REGISTRATION NUMBER: 30,440
CC REFERENCE/DOCKET NUMBER: 600.344US1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 612-339-0331
CC TELEFAX: 612-339-3061
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 535 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: Internal
CC ORIGINAL SOURCE:

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 107 AA: 11654 MW: 62438 CN;

Query Match 71.2%; Score 42; DB 3; Length 107;
Best Local Similarity 44.4%; Pred. No. 2.07e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 88 OOHSSPYT 96
| | | | |
QY 1 OKYNSAAYS 9

RESULT 12
ID US-08-899-575-87 STANDARD; PRT; 107 AA.
XX xxxxxx
DE Sequence 87, Application US/08899575
CC Sequence 87, Application US/08899575
CC Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 107 AA: 11654 MW: 62438 CN;

Query Match 71.2%; Score 42; DB 2; Length 107;
Best Local Similarity 44.4%; Pred. No. 2.07e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 88 OOHSSPYT 96
| | | | |
QY 1 OKYNSAAYS 9

RESULT 13
ID US-08-276-852-87 STANDARD; PRT; 107 AA.
XX xxxxxx
DE Sequence 87, Application US/08276852
CC Sequence 87, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ

Query Match 71.2%; Score 42; DB 1; Length 107;
Best Local Similarity 44.4%; Pred. No. 2.07e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 88 OQYHSPYT 96
| : : : :
OY 1 OKYNSAAYS 9

RESULT 14
US-08-899-575-87 STANDARD: PRT; 107 AA.
xxxxxx

Sequence 87, Application US/08899575
Sequence 87, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbos, Carlos F
APPLICANT: Ierner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRL452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid

CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ

Query Match 71.2%; Score 42; DB 2; Length 107;
Best Local Similarity 44.4%; Pred. No. 2.07e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 88 OQYHSPYT 96
| : : : :
OY 1 OKYNSAAYS 9

RESULT 15
US-08-688-342-4 STANDARD: PRT; 292 AA.
xxxxxx

Sequence 4, Application US/08688342
Sequence 4, Application US/08688342
Patent No. 5871964
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1235724
SEQUENCE 292 AA; 32937 MW; 431088 CN;
SQ

Query Match 71.2%; Score 42; DB 2; Length 292;
Best Local Similarity 55.6%; Pred. No. 2.07e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 205 OKYLSAAYT 213
| : : : :
OY 1 OKYNSAAYS 9

Fri Sep 3 09:53:02 1999

US-08-599-226-21.ra1

Page 8

Search completed: Thu Sep 2 12:03:56 1999
Job time : 7 secs.

MUSE (TM)

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Muscle protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 12:01:07 1999; MasPar time 3.09 Seconds
116.718 Million cell updates/sec
Tabular output not generated.

Title: >US-08-599-226-21
Description: (1-9) from US08593226.pep
Perfect Score: 59
Sequence: 1 OKNSAAYS 9

Scoring table: PAM 150
Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr60
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 21.906; Variance 27.106; scale 0.808

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	48	81.4	1573	2	I50806	complement component 6.73e+00
2	47	79.7	397	2	E70317	hypothetical protein 1.08e+01
3	47	79.7	846	2	S13795	neurotactin - fruit f 1.08e+01
4	47	79.7	846	2	S12005	neurotactin - fruit f 1.08e+01
5	47	79.7	1139	2	S61918	protein kinase C (EC 1.08e+01
6	46	78.0	480	2	S74228	fatty acid hydroperox 1.71e+01
7	46	78.0	530	2	S12320	PRP protein - yeast 1.71e+01
8	46	78.0	1203	2	S27545	pullulanase - Thermo 1.71e+01
9	45	76.3	475	1	A37241	52K autoantigen Ro/SS 2.71e+01
10	45	76.3	560	1	DOCGA	NAD+-diphthamide ADP 2.71e+01
11	45	76.3	560	1	DOCGPO	NAD+-diphthamide ADP 2.71e+01
12	45	76.3	863	2	B64138	uridylyltransferase h 2.71e+01
13	44	74.6	138	2	PC1206	envelope protein - me 4.24e+01
14	44	74.6	295	2	A23750	30K actin-binding pr 4.24e+01
15	44	74.6	521	2	I39956	neutral protease (E 4.24e+01
16	44	74.6	544	2	A42464	microbial metalloprot 4.24e+01
17	44	74.6	546	2	JC4113	neutral proteinase (E 4.24e+01
18	44	74.6	546	2	S72176	thermolysin (EC 3.4.2 4.24e+01
19	44	74.6	546	2	S72175	thermolysin (EC 3.4.2 4.24e+01
20	44	74.6	548	1	HYBS5	thermolysin (EC 3.4.2 4.24e+01
21	44	74.6	582	1	S42614	membrane protein P60 4.24e+01
22	44	74.6	585	1	JC1486	neopullulanase (EC 3. 4.24e+01
23	44	74.6	588	1	A37008	neopullulanase (EC 3. 4.24e+01

24	44	74.6	591	2	S48130	cyclomaltoextrinase 4.24e+01
25	44	74.6	1240	2	T03097	CDO protein - human 4.24e+01
26	44	74.6	1256	2	T03096	alpha-amylase - rat 4.24e+01
27	44	74.6	1301	2	S18118	alpha-amylase - Allis 4.24e+01
28	44	74.6	1391	2	S47862	rec12 protein - f1ss1 6.60e+01
29	43	72.9	189	2	S61210	probable GTP binding 6.60e+01
30	43	72.9	217	1	D64411	flagellin B2 precursor 6.60e+01
31	43	72.9	270	2	A26480	knob protein - Plasm 6.60e+01
32	43	72.9	473	2	A54494	knob-associated hist1 6.60e+01
33	43	72.9	624	2	S67382	hypothetical protein 6.60e+01
34	43	72.9	634	2	A28412	histidine-rich protei 6.60e+01
35	43	72.9	634	2	A54495	knob protein precursor 6.60e+01
36	43	72.9	654	2	B71623	knob-associated His-r 6.60e+01
37	43	72.9	657	2	A29454	knob-associated hist1 6.60e+01
38	43	72.9	757	2	C70034	conserved hypothetical 6.60e+01
39	43	72.9	887	2	S43196	uridylyltransferase (6.60e+01
40	43	72.9	890	2	G64740	uridylyltransferase (6.60e+01
41	43	72.9	1388	2	A57655	tim (timeless) protei 1.02e+02
42	42	71.2	364	2	A70474	conserved hypothetical 1.02e+02
43	42	71.2	867	2	T00118	hrSH2 protein - sea s 1.02e+02
44	42	71.2	1087	1	S41797	cellulose 1,4-beta-ce 1.02e+02
45	42	71.2	1231	1	A46490	endo-1,4-beta-xylanas 1.02e+02

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE 150806 #type fragment
ORGANISM complement component C3 - Japanese lamprey (fragment)
DATE 13-Sep-1996 #sequence #revision 13-Sep-1996 #text_change 21-Aug-1998

ACCESSIONS 150806
#authors Nonaka, M.; Takahashi, M.
#journal J. Immunol. (1992) 148:3290-3295
#title Complete complementary DNA sequence of the third component of complement of lamprey; implication for the evolution of thioester containing protein.
#cross-references MUID:92251197
#accession 150806
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues 1-1673 ##label NON
#cross-references GB:DI0087; NID:q222887; PID:q222888
CLASSIFICATION #superfamily alpha-2-macroglobulin
SUMMARY #length 1673 #checksum 8983

Query Match 81.4%; Score 48; DB 2; Length 1673;
Best Local Similarity 75.0%; Pred. No. 6.73e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 443 OKNSASY 450
||| |||
QY 1 OKNSAAY 8

RESULT 2
ENTRY E70317 #type complete
TITLE hypothetical protein sq.183 - Aquifex aeolicus
ORGANISM #formal_name Aquifex aeolicus
DATE 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998

ACCESSIONS E70317
#authors Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Ienox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.; Keller, M.; Aufay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
#cross-references MUID:98196666

```

#accession      E70317
#status
#preliminary: nucleic acid sequence not shown;
#translation not shown
##molecule_type DNA
##residues      1-397 #label AOF
##cross-references GB:AE000677; NID:g2982900; PID:g2982913; GB:AE000657
##experimental_source strain vF5

GENETICS
#gene            ag_183
SUMMARY          #length 397 #molecular_weight 46821 #checksum 9057

Query Match      79.7%: Score 47; DB 2; Length 397;
Best Local Similarity 66.7%: Pred. No. 1.08e+01;
Matches          6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db              362 QKYSRDIYS 370
OY              1 OKYNSAAYS 9

RESULT           3
ENTRY            #type complete
TITLE            neurotactin - fruit fly (Drosophila melanogaster)
ORGANISM         #formal_name Drosophila melanogaster
DATE             21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                24-Sep-1998

ACCESSIONS
REFERENCE
#authors         Hortsch, M.; Patel, N.H.; Bleber, A.J.; Traquina, Z.R.;
                Goodman, C.S.
#journal         Development (1990) 110:1327-1340
#title           Drosophila neurotactin, a surface glycoprotein with homology
                to serine esterases, is dynamically expressed during
                embryogenesis.
#cross-references EMBL:X54999; NID:g8289; PID:g8290
#accession      S13795
#status          preliminary
##molecule_type mRNA
##residues      1-846 #label HOR
##cross-references EMBL:X54999; NID:g8289; PID:g8290
GENETICS
#gene            FlyBase:Nr1
#keywords        phosphoprotein; transmembrane protein
SUMMARY          #length 846 #molecular_weight 92745 #checksum 4655

Query Match      79.7%: Score 47; DB 2; Length 846;
Best Local Similarity 44.4%: Pred. No. 1.08e+01;
Matches          4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db              717 EKNASSYA 725
OY              1 OKYNSAAYS 9

RESULT           4
ENTRY            #type complete
TITLE            neurotactin - fruit fly (Drosophila sp.)
ORGANISM         #formal_name Drosophila sp.
DATE             13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                24-Sep-1998

ACCESSIONS
REFERENCE
#authors         de la Escalera, S.; Bockamp, E.O.; Moya, F.; Plovant, M.;
                Jimenez, F.
#journal         EMBO J. (1990) 9:3593-3601
#title           Characterization and gene cloning of neurotactin, a
                Drosophila transmembrane protein related to
                cholinesterases.
#cross-references MUID:91006059
#accession      S12005
#status          preliminary
##molecule_type mRNA

```

```

##residues      1-846 ##label ESC
GENETICS      ##cross-references EMBL:X53837; NID:96287; PID:98288
#gene
#FlyBase:Nrt
#cross-references FlyBase:FBgn0004108
KEYWORDS      phosphoprotein; transmembrane protein
SUMMARY       #length 846 #molecular-weight 92805 #checksum 5987

Query Match      79.7%; Score 47; DB 2; Length 846;
Best Local Similarity 44.4%; Pred. No. 1.08e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 717 EKNASSTA 725
:||||:|
OY 1 OKYNSAAYS 9

RESULT 5
ENTRY
TITLE      S61918 #type complete
ORGANISM    protein kinase C (EC 2.7.1.-) PKC1 - fungus (Trichoderma reesei)
DATE        #formal_name Trichoderma reesei
ACCESSIONS  23-Jul-1996 #sequence_revision 13-Mar-1997 #text_change
REFERENCE    17-Mar-1999
#authors     S61918
#journal      Morawetz, R.; Lendenfeld, T.; Mischak, H.; Muehlbauer, M.;
#title        Gruber, F.; Goodnight, J.; de Graaff, L.H.; Vliesser, J.;
              Mushinski, J.F.; Kubicek, C.P.
              Mol. Gen. Genet. (1996) 250:17-28
              Cloning and characterisation of genes (pkc1 and pkca)
              encoding protein kinase C homologues from Trichoderma
              reesei and Aspergillus niger.
#cross-references MUID:96158841
#accession    S61918
#status        preliminary; nucleic acid sequence not shown
#molecule_type DNA
#residues      1-1139 ##label MOR
#cross-references EMBL:U10016; NID:g501074; PID:g501075
GENETICS
#gene
#introns      pkc1
CLASSIFICATION 139/1; 228/1; 555/1; 917/2; 984/3; 1120/1
#superfamily yeast protein kinase C; protein kinase C
#zinc-binding repeat homology; protein kinase homology
KEYWORDS      ATP; duplication; phospholipid binding; phosphotransferase;
              serine/threonine-specific protein kinase; zinc
FEATURE
455-502      #domain protein kinase C zinc-binding repeat homology
              #label K21\
533-572      #domain protein kinase C zinc-binding repeat homology
              #label K22\
812-1073      #domain protein kinase homology #label K1V\
820-828      #region protein kinase ATP-binding motif
SUMMARY       #length 1139 #molecular-weight 126055 #checksum 3417

Query Match      79.7%; Score 47; DB 2; Length 1139;
Best Local Similarity 55.6%; Pred. No. 1.08e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 707 EKNPADYA 715
:||||:|
OY 1 OKYNSAAYS 9

RESULT 6
ENTRY
TITLE      S74228 #type complete
ORGANISM    fatty acid hydroperoxide lyase - pepper
DATE        #formal_name Capsicum annuum #common_name pepper
ACCESSIONS  29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change
REFERENCE    04-Sep-1998
              S74228; S78210
#authors     Matsui, K.; Shibutani, M.; Hase, T.; Kajiwara, T.

```

#journal FEBS Lett. (1996) 394:21-24
#title Bell pepper fruit fatty acid hydroperoxide lyase is a
#cross-references EMBL:U01674
#accession S74228
#molecule_type mRNA
#residues 1-480 #label MAT
#cross-references EMBL:U01674
#experimental_source fruits
#accession S78210
#molecule_type protein
#residues 89-98;149-166 #label MAY
#classification #superfamily fatty acid hydroperoxide lyase
#keywords heme
#feature 279-311
433-464 #domain oxygen binding #status predicted #label OBG
#length 480 #molecular-weight 54125 #checksum 3272
SUMMARY
Query Match 78.0%; Score 46; DB 2; Length 480;
Best Local Similarity 55.6%; Pred. No. 1.71e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 461 OKYDSVFS 469
OY 1 OKYNSMAY 9
RESULT 7
ENTRY S12320 #type complete
TITLE PRP9 protein - yeast (Saccharomyces cerevisiae) (strain
S288C)
ALTERNATE_NAMES protein D2773; protein YD030W
ORGANISM #formal_name Saccharomyces cerevisiae
#strain S288C
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
06-Feb-1998
ACCESSIONS S12320; S67563
REFERENCE S12319
#authors Legrain, P.; Choulika, A.
#journal EMBL J. (1990) 9:2775-2781
#title The molecular characterization of PRP6 and PRP9 yeast genes
reveals a new cysteine/histidine motif common to several
splicing factors.
#cross-references MVID:90360988
#accession S12320
#molecule_type DNA
#residues 1-530 #label LBG
#cross-references EMBL:X53466; NID:94240; PID:94241
#experimental_source strain S288C
REFERENCE S67560
#authors Paulin, L.; Saren, A.M.; Laamanen, P.
#submission submitted to the Protein Sequence Database, July 1996
#accession S67563
#molecule_type DNA
#residues 1-530 #label PAU
#cross-references EMBL:Z74078; NID:91431007; PID:e253198; PID:91431008;
MIPS:YD030W
#experimental_source strain S288C
GENETICS
#gene SGD:PRP9
#cross-references SGD:S0002188; MIPS:YD030W
#map_position 4L
KEYWORDS nucleus; RNA binding; zinc finger
SUMMARY #length 530 #molecular-weight 63029 #checksum 402
Query Match 78.0%; Score 46; DB 2; Length 530;
Best Local Similarity 62.5%; Pred. No. 1.71e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 359 OKYEAPAY 366
OY 1 OKYNSMAY 8

RESULT 8
ENTRY S27545 #type complete
TITLE pullulanase - Thermoaerobacterium thermosulfurigenes
ORGANISM #formal_name Thermoaerobacterium thermosulfurigenes
DATE 09-Jun-1994 #sequence_revision 26-May-1995 #text_change
26-May-1995
ACCESSIONS S27545
REFERENCE S27544
#authors Burchardt, G.; Haackel, K.; Spreinat, A.; Antanikhan, G.;
Ball, H.
#submission submitted to the EMBL Data Library, March 1992
#description Nucleotide sequence of the pullulanase gene from Clostridium
thermosulfurigenes EMI and processing of the enzyme.
#accession S27545
#status preliminary
#molecule_type DNA
#residues 1-1203 #label BUR
#cross-references EMBL:M57692
#note the source is given as Clostridium thermosulfurigenes
SUMMARY #length 1203 #molecular-weight 134472 #checksum 2163
Query Match 78.0%; Score 46; DB 2; Length 1203;
Best Local Similarity 44.4%; Pred. No. 1.71e+01;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Db 484 HKYDADYT 492
OY 1 OKYNSMAY 9
RESULT 9
ENTRY A37241 #type complete
TITLE 52K autoantigen Ro/SS-A - human
ALTERNATE_NAMES Sjogren syndrome antigen A
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Feb-1992 #sequence_revision 26-May-1995 #text_change
18-Sep-1998
ACCESSIONS A55642; A37241; A37240
REFERENCE A55642
#authors Tsugu, H.; Horowitz, R.; Gidson, N.; Frank, M.B.
#journal Genomics (1994) 24:541-548
#title The location of a disease-associated polymorphism and genomic
structure of the human 52-kDa Ro/SSA locus (SSA1).
#cross-references MVID:95229155
#accession A55642
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-475 #label TSU
#cross-references GB:U13657
REFERENCE A37241
#authors Itoh, K.; Itoh, Y.; Frank, M.B.
#journal J. Clin. Invest. (1991) 87:177-186
#title Protein heterogeneity in the human Ro/SSA ribonucleoproteins.
The 52- and 60-kD Ro/SSA autoantigens are encoded by
separate genes.
#cross-references MVID:91086445
#accession A37241
#molecule_type mRNA
#residues 1-475 #label ITO
#cross-references GB:M34551; NID:9337484; PID:9337485
REFERENCE A37240
#authors Chan, E.K.T.; Hamel, J.C.; Buyn, J.P.; Tan, E.M.
#journal J. Clin. Invest. (1991) 87:68-76
#title Molecular definition and sequence motifs of the 52-kD
component of human SS-A/Ro autoantigen.
#cross-references MVID:91086480
#accession A37240
#molecule_type mRNA
#residues 1-51, 'A', 53-475 #label CHA
#cross-references GB:M62800; NID:9338489; PID:9338490; GB:M35041
GENETICS

```

#gene          GDB:SSA1
#cross-references GDB:133758; OMIM:109092
#map_position 11p15.5-11p15.5
#altions      136/3; 168/3; 245/3; 253/2; 287/1
CLASSIFICATION #superfamily rfp transforming protein; RING finger homology
KEYWORDS       DNA binding; nucleus; zinc finger
FEATURE
  12-60
SUMMARY        #domain RING finger homology #label RING
               #length 475 #molecular-weight 54169 #checksum 7482

Query Match      76.3%; Score 45; DB 1; Length 475;
Best Local Similarity 44.4%; Pred. No. 2.71e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db      386 OKYAGTYP 394
OY      1 OKYNSAAYS 9

RESULT 10
ENTRY  DOGGA      #type complete
TITLE  MDA+-diphthamide ADP-ribosyltransferase (EC 2.4.2.36)
CONTAINS precursor - corynebacteriophage beta
ORGANISM #formal_name corynebacteriophage beta
DATE      24-Apr-1984 #sequence_revision 10-Feb-1995 #text_change
         05-Sep-1997
ACCESSION A05128; A00729; A00730
REFERENCE A05128
#authors      Greenfield, L.; Bjorn, M.J.; Horn, G.; Fong, D.; Buck, G.A.;
#journal      Collier, R.J.; Kaplan, D.A.
#title        Proc. Natl. Acad. Sci. U.S.A. (1983) 80:6853-6857
               Nucleotide sequence of the structural gene for diphtheria
               toxin carried by corynebacteriophage beta.
#cross-references M01D:84070728
#accession      A05128
               ##molecule_type DNA
               ##residues      1-560 ##label GRE
               ##cross-references GB:K01722; NID:g166118; PID:g166119
REFERENCE      A92256
#authors      Delange, R.J.; Williams, L.C.; Drazin, R.E.; Collier, R.J.
#journal      J. Biol. Chem. (1979) 254:5838-5842
#title        The amino acid sequence of fragment A, an enzymically active
               fragment of diphtheria toxin. III. The chymotryptic
               peptides, the peptides derived by cleavage at tryptophan
               residues, and the complete sequence of the protein.
#cross-references M01D:79194138
#accession      A00729
               ##molecule_type protein
               ##residues      26-170, 'VES', 174-218 ##label DEL
               ##note          this is the final paper in a series of three
               this protein is found in three forms, terminating with
               residue 215-Arg, 217-Arg, or 218-Arg; all three forms
               have approximately equal enzymatic activity
#cross-references M01D:83275723
#accession      A00730
               ##molecule_type DNA
               ##residues      1-103, 'D', 105-186, 'K', 188-221, 'G', 223-402, 'S', 404-455,
               'S', 457-560 ##label KAC
               ##cross-references GB:K01723
               ##note          a nontoxic diphtheria toxin homolog, produced by
               corynebacteriophage beta after
               N-methyl-N'-nitro-N-nitrosoguanidine mutagenesis
               either of the first two mutations completely abolishes
               ADP-ribosylating activity of fragment A; the last two
               may reduce receptor binding
REFERENCE      A90616

```

```

#authors      Michel, A.; Dirckx, J.
#journal      Biochim. Biophys. Acta (1977) 491:286-295
#title        Occurrence of tryptophan in the enzymically active site of
               diphtheria toxin fragment A.
#cross-references M01D:77134304
#contents      annotation: active site
#note          modification of Trp-153 inactivates the enzyme; this residue
               may be concerned with catalysis or with substrate binding
REFERENCE      A44679
#authors      Choe, S.; Bennett, M.J.; Fujii, G.; Cumml, P.M.G.;
               Kantardjiev, K.A.; Collier, R.J.; Eisenberg, D.
#journal      Nature (1992) 357:216-222
#title        The crystal structure of diphtheria toxin.
#contents      annotation: X-ray crystallography, 2.0 angstroms
               Diphtheria toxin, produced by a bacteriophage infecting
               Corynebacterium diphtheriae, catalyzes the covalent attachment of
               ADP-ribose from NAD to the diphthamide residue of eukaryotic
               translation elongation factor 2, blocking protein synthesis. One
               molecule is sufficient to cause cell death.
               Fragment B binds to the receptor protein and is responsible for the
               movement of fragment A across the cell membrane. After a
               trypsin-like cleavage and reduction, intracellular fragment A
               becomes catalytically active.
COMMENT
GENETICS      #start_codon      GTG
               #superfamily diphtheria toxin
               #glycosyltransferase; NAD; pentosyltransferase; toxin
CLASSIFICATION KEYWORDS
FEATURES      1-25
               26-560
               26-218
               26-218
               219-560
               230-403
               411-560
               46,90
               173
               211-226,486-496
SUMMARY      #length 560 #molecular-weight 60814 #checksum 485

Query Match      76.3%; Score 45; DB 1; Length 560;
Best Local Similarity 62.5%; Pred. No. 2.71e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db      84 KYNAAGYS 91
OY      2 KYNSAAYS 9

RESULT 11
ENTRY  DOGGO      #type complete
TITLE  MDA+-diphthamide ADP-ribosyltransferase (EC 2.4.2.36)
CONTAINS precursor - corynebacteriophage omega
ORGANISM #formal_name corynebacteriophage omega
DATE      19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change
         05-Sep-1997
ACCESSION A00728; A00137; A31356; A33131; A33880
REFERENCE A00728
#authors      Ratti, G.; Rappuoli, R.; Giannini, G.
#journal      Nucleic Acids Res. (1983) 11:6589-6595
#title        The complete nucleotide sequence of the gene coding for
               diphtheria toxin in the corynebacteriophage omega (tox+) genome.
#cross-references M01D:84041471
#accession      A00728
               ##molecule_type DNA
               ##residues      1-560 ##label RAT
               ##cross-references GB:M9546; NID:g166116; PID:g166117; EMBL:V01536;
               NID:g15475; PID:g579179
REFERENCE      A60137

```

```

#authors      Falmagne, P.; Capiau C.; Lambotte, P.; Zanen, J.; Cabiiaux,
#journal      V.; Ruysschaert, J.M.C. Blochim. Biophys. Acta (1985) 827:45-50
#title        Blochim. Biophys. Acta (1985) 827:45-50
#accession    The complete amino acid sequence of diphtheria toxin fragment
#molecule-   B. Correlation with its lipid-binding properties.
#type protein A60137
#residues     219-325, 'V', 327-413, 'N', 415-560 #label FAL
REFERENCE     A11356
#authors      Clepiak, W.; Hasemann, C.; Eldels, L.
#journal      Biochem. Biophys. Res. Commun. (1988) 157:747-754
#title        Specific cleavage of diphtheria toxin by human urokinase.
#cross-references MUID:89076312
#accession    A11356
#molecule-   #molecule-type protein
#residues     219-225, 'X', 227, 'M', 229-230 #label CIE
REFERENCE     A31131
#authors      Palmer, R.D.; Behringer, R.R.; Qualife, C.J.; Maxwell, F.;
#journal      Maxwell, I.H.; Brinster, R.L. Cell (1987) 50:435-443
#title        Cell lineage ablation in transgenic mice by cell-specific
#cross-references MUID:87273505
#note          annotation
#contents      the authors demonstrate a technique of ablating select
#note          lineages of cells by transgenic expression of a construct
#note          containing fragment A under control of an enhancer and
#note          promoter specific for that cell lineage
#note          the sequence shown for this construct has been revised
#comment       Diphtheria toxin, produced by a bacteriophage infecting
#comment       Corynebacterium diphtheriae, catalyzes the covalent attachment of
#comment       ADP-ribose from NAD to the diphthamide residue of eukaryotic
#comment       translation elongation factor 2, blocking protein synthesis. One
#comment       molecule is sufficient to cause cell death.
#comment       Fragment B binds to the receptor protein and is responsible for the
#comment       movement of fragment A across the cell membrane. After a
#comment       trypsin-like cleavage and reduction, intracellular fragment A
#comment       becomes catalytically active.

GENETICS
#start-codon  GTG
CLASSIFICATION #superfamily diphtheria toxin
KEYWORDS       glycosyltransferase; NAD; pentosyltransferase; toxin
FEATURE
1-25
26-560
#domain signal sequence #status predicted #label SIG\
#product diphtheria toxin #status experimental #label
#MAY\
26-218
#product NAD+--diphthamide ADP-ribosyltransferase
#(diphtheria toxin fragment A) #status experimental
#label FRA\
26-218
#domain catalytic #status experimental #label CAT\
#product diphtheria toxin fragment B #status
#experimental #label FRB\
230-403
#domain membrane insertion #status predicted #label MIN\
#domain receptor binding #status predicted #label RBD\
#binding-site NAD (His, Tyr) #status predicted\
#active-site glu #status predicted\
#disulfide_bonds #status predicted
211-226, 486-496
#length 560 #molecular-weight 60814 #checksum 485
SUMMARY

Query Match 76.3%: Score 45; DB 1; Length 560;
Best Local Similarity 62.5%: Pred. No. 2, 71e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 84 KYDAGYS 91
||:|:|:|
OY 2 KYNSAYS 9

RESULT 12
ENTRY B64138 #type complete
TITLE uridylyltransferase homolog - Haemophilus influenzae (strain
ORGANISM Rd KW20)
#formal_name Haemophilus influenzae

```

```

DATE 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
18-Sep-1998
ACCESSIONS B64138
REFERENCE B64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shriver, R.; Liu, L.I.; Glodet, A.; Kelley, J.M.; Weldman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Frichman, J.L.; Fuhrmann,
J.L.; Geisbrenner, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal Science (1995) 269:496-512
#title Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.
#cross-references MUID:95350630
#accession B64138
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-663 #label TIGR
#cross-references GB:U32844; GB:U42023; NID:g1574563; PID:g1574572;
TIGR:HI1719
CLASSIFICATION #superfamily uridylyltransferase
SUMMARY #length 863 #molecular-weight 100172 #checksum 231
Query Match 76.3%; Score 45; DB 2; Length 863;
Best Local Similarity 44.4%; Pred. No. 2,71e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
DB 185 ORYNTAYN 193
OY 1 OKNSAAYS 9
RESULT 13
ENTRY PC1206 #type fragment
TITLE envelope protein - hepatitis C virus (strain RS3-3)
#(fragment)
ORGANISM #formal_name hepatitis C virus
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
29-May-1998
ACCESSIONS PC1206
REFERENCE PC1182
#authors Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Sekiya,
H.; Hijikata, M.; Shimotohno, K.
#journal Biochem. Biophys. Res. Commun. (1992) 189:119-127
#title Characterization of hypervariable regions in the putative
envelope protein of hepatitis C virus.
#cross-references MUID:93080545
#accession PC1206
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-138 #label KAT
#cross-references DDBJ:D12942; DDBJ:D12972
CLASSIFICATION #superfamily hepatitis C virus genome polyprotein; DEAD/H box
helicase homology
KEYWORDS envelope protein
SUMMARY #length 138 #checksum 8283
Query Match 74.6%; Score 44; DB 2; Length 138;
Best Local Similarity 44.4%; Pred. No. 4,24e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
DB 77 HKNSGGT 85
OY 1 OKNSAAYS 9
RESULT 14
ENTRY A23750 #type complete
TITLE 30K actin-bundling protein - slime mold (Dictyostelium

```

```

ORGANISM          discoidium)
DATE              #formal_name Dictyostelium discoidium
                  #sequence_revision 31-Mar-1992 #text_change
                  09-Sep-1997
ACCESSIONS       A23750
REFERENCE        A23750
#authors         Fecheimer, M.; Murdock, D.; Carney, M.; Glover, C.V.C.
#journal         J. Biol. Chem. (1991) 266:2883-2889
#title           Isolation and sequencing of cDNA clones encoding the
                  Dictyostelium discoidium 30,000-dalton actin-bundling
                  protein.
#cross-references MIMD:91131582
#accession       A23750
#molecule_type mRNA
#residues        1-295 #label FEC
#cross-references GB:M58022; NID:g167577; PID:g167578
KEYWORDS         actin binding
SUMMARY          #length 295 #molecular-weight 33353 #checksum 2408

Query Match      74.6%; Score 44; DB 2; Length 295;
Best Local Similarity 75.0%; Pred. No. 4.24e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 254 KYGSAVS 261
11:11111
QY 2 KYNSAAYS 9

RESULT 15
ENTRY          139956 #type complete
TITLE          neutral proteinase (EC 3.4.24.-) - Bacillus amyloliquefaciens
ORGANISM       #formal_name Bacillus amyloliquefaciens
DATE           19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
              18-Mar-1997
ACCESSIONS     139956
REFERENCE      139956
#authors       Shimada, H.; Honjo, M.; Mita, I.; Nakayama, A.; Akaoka, A.;
              Manabe, K.; Furutani, Y.
#journal       J. Biotechnol. (1985) 2:75-85
#title         The nucleotide sequence and some properties of the neutral
              139956 proteinase gene of Bacillus amyloliquefaciens.
#accession     139956
#status        preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues      1-521 #label RES
#cross-references GB:M36723; NID:g143352; PID:g143353
GENETICS       #start_codon GTG
CLASSIFICATION #superfamily thermolysin
KEYWORDS       hydrolase; metalloproteinase
SUMMARY        #length 521 #molecular-weight 56725 #checksum 6816

Query Match      74.6%; Score 44; DB 2; Length 521;
Best Local Similarity 62.5%; Pred. No. 4.24e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 308 OKYNSY 315
1111:1
QY 1 OKYNSAY 8

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Search completed: Thu Sep 2 12:01:17 1999
 Job time : 10 secs.

FT	CHAIN	14	1673	COMPLEMENT C3.
FT	CHAIN	14	653	BETA CHAIN (BY SIMILARITY).
FT	CHAIN	657	1375	ALPHA CHAIN (BY SIMILARITY).
FT	CHAIN	1379	1673	GAMMA CHAIN (BY SIMILARITY).
FT	PEPTIDE	657	732	C3A ANAPHYLATOXIN (BY SIMILARITY).
FT	DOMAIN	678	713	ANAPHYLATOXIN-LIKE.
FT	DISULFID	678	705	BY SIMILARITY.
FT	DISULFID	679	712	BY SIMILARITY.
FT	DISULFID	692	713	BY SIMILARITY.
FT	THIOLEST	986	990	BY SIMILARITY.
SO	SEQUENCE	1673 AA;	187767 MM;	D837446F CRC32;
Query Match				
Best Local Similarity		81.4%;	Score 48;	DB 1; Length 1673;
Matches		6; Conservative	1;	Mismatches 1; Indels 0; Gaps 0;
Db	443 OKYASAY	450		
	1 OKYNSAAY	8		
RESULT				
ID	NRT DROME	STANDARD:	PRT:	846 AA.
AC	P23654;			
DT	01-NOV-1991 (REL. 20, CREATED)			
DT	01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	NEUROTACTIN.			
GN	NRT.			
OS	DROSOPHILA MELANGASTER (FRUIT FLY).			
OC	EUKARYOTA, METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;			
OC	PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;			
OC	DROSOPHILIDAE; DROSOPHILA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 91301057.			
RA	HOTSCH M., PATEL N.P., BIBBER A.J., TRAGUINA Z.R., GOODMAN C.S.;			
RT	"Drosophila neurotactin, a surface glycoprotein with homology to			
RT	serine esterases, is dynamically expressed during embryogenesis.";			
RL	DEVELOPMENT 110:1327-1340(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN-OREGON-R; TISSUE-EMBRYO;			
RC	MEDLINE: 91006059.			
RA	DE LA ESCALERA S., BOCKAMP E.O., MOYA F., PIOVANT M., JIMENEZ F.;			
RT	"Characterization and gene cloning of neurotactin, a Drosophila			
-RT	transmembrane protein related to cholinesterases.";			
RL	EMBO J. 9:3593-3601(1990).			
RN	[3]			
RP	FUNCTION.			
RX	MEDLINE: 91006060.			
RA	BARTHALAY T., HIDEAU-JACQUOTTE R., DE LA ESCALERA S., JIMENEZ F.,			
RT	PIOVANT M.;			
RT	"Drosophila neurotactin mediates heterophilic cell adhesion.";			
RL	EMBO J. 9:3603-3609(1990).			
CC	-1- FUNCTION: MAY MEDIATE OR MODULATE CELL ADHESION BETWEEN EMBRYONIC			
CC	CELLS DURING DEVELOPMENT.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED IN MEMBRANES DURING EMBRYOGENESIS			
CC	AND THEN ACCUMULATES IN CNS AND PNS.			
CC	-1- PTM: PHOSPHORYLATED.			
CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY			
CC	IN THE EXTRACELLULAR DOMAIN.			
CC	-----			
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RESULT 6
ID APU_THESA STANDARD: PRT: 1279 AA.

AC P36505: 01-JUN-1994 (REL. 29, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE AMYLOPULULANASE PRECURSOR (ALPHA-AMYLASE/PULULANASE) (EC 3.2.1.1) /
DE (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (ALPHA-DEXTRIN
DE ENDO-1,6-ALPHA-GLUCOSIDASE).
GN APU.
OS THERMOANEROBACTER SACCHAROLYTICUM.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
OC THERMOANEROBACTER GROUP; THERMOANEROBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B6A-RI.
RX MEDLINE: 94161525.
RA RAMSHE M.V., PODKOVOYOV S.M., LOWE S.E., ZEIKUS J.G.;
RT "Cloning and sequencing of the Thermoanaerobacterium saccharolyticum
RT B6A-RI apu gene and purification and characterization of the
RT amylopululanase from Escherichia coli";
RT APPL. ENVIRON. MICROBIOL. 60:94-101(1994).
RL [2]
RM IDENTIFICATION OF PROBABLE VECTOR CONTAMINATION.
RN ROBISON K.;
RA UNPUBLISHED OBSERVATIONS (NOV-1994).
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES
CC (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULULAN AND STARCH TO
CC FORM MALTOSE.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN BY THE PRESENCE OF
CC AN EXTRA C-TERMINAL SEGMENT OF 9 RESIDUES THAT SEEMS TO ORIGINATE
CC FROM A PDC-TYPE VECTOR.
CC
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CC EMBL: L07762; G154620; ALT_SEQ.
CC PFAM: PF00041; fn3; 2.
CC PFM: PF00128; alpha-amyase; 1.
CC KW HYDROLASE; GLYCOSIDASE; CARBOHYDRATE METABOLISM; SIGNAL; REPEAT;
CC KM MULTIFUNCTIONAL ENZYME.
CC FT SIGNAL 1 35
CC FT CHAIN 36 1279
CC FT ACT_SITE 629 629
CC FT ACT_SITE 658 658
CC FT ACT_SITE 735 735
CC FT DOMAIN 929 1017
CC FT DOMAIN 1156 1248
CC FT SEQUENCE 1279 AA; 142430 MW; D4982E83 CRC32;
CC
CC Query Match 78.0%; Score 46; DB 1; Length 1279;
CC Best Local Similarity 44.4%; Pred. No. 6,37e+00;
CC Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

AC P38536; 01-OCT-1994 (REL. 30, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE AMYLOPULULANASE PRECURSOR (ALPHA-AMYLASE/PULULANASE) (EC 3.2.1.1) /
DE (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (ALPHA-DEXTRIN
DE ENDO-1,6-ALPHA-GLUCOSIDASE) (PULULANASE TYPE II).
GN APU.
OS THERMOANEROBACTER THERMOSULFURIGENES (CLOSTRIDIUM
OS THERMOSULFURIGENES).
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
OC THERMOANEROBACTER GROUP; THERMOANEROBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DSM 3896 / EML;
RX MEDLINE: 94252998.
RA MATSCHER M., BURCHARDT G., SAHM K., BAHL H.;
RT "Pululanase of Thermoanaerobacterium thermosulfurigenes EML
RT (Clostridium thermosulfurigenes): molecular analysis of the gene,
RT composite structure of the enzyme, and a common model for its
RT attachment to the cell surface";
RT J. BACTERIOL. 176:3295-3302(1994).
RL [2]
RM CATALYTIC ACTIVITY: ENDOLYOLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES
CC (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULULAN AND STARCH TO
CC FORM MALTOSE.
CC -1- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN
CC S-LAYER ANCHOR.
CC -1- PIN: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
CC
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CC
CC EMBL: M57692; G1235795; -
CC PROSITE: PS01072; SLH_DOMAIN; 3.
CC PFAM: PF00041; fn3; 2.
CC PFM: PF00128; alpha-amyase; 1.
CC KW MULTIFUNCTIONAL ENZYME; GLYCOPROTEIN.
CC FT SIGNAL 1 35
CC FT CHAIN 36 1861
CC FT ACT_SITE 628 628
CC FT ACT_SITE 657 657
CC FT ACT_SITE 734 734
CC FT DOMAIN 928 1018
CC FT DOMAIN 1157 1248
CC FT DOMAIN 1681 1739
CC FT DOMAIN 1740 1803
CC FT DOMAIN 1804 1861
CC FT CONFLICT 1734 1734
CC FT SEQUENCE 1861 AA; 206104 MW; AEC2A80B CRC32;
CC
CC Query Match 78.0%; Score 46; DB 1; Length 1861;
CC Best Local Similarity 44.4%; Pred. No. 6,37e+00;
CC Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

ID R052.HUMAN STANDARD: PRT: 475 AA.
AC P19474:
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE 52-KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).
GN SSAL OR R052.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-THYMOCYTES;
RX MEDLINE: 91086445.
RA ITOH K., ITOH Y., FRANK M.B.;
RT "Protein heterogeneity in the human Ro/SSA ribonucleoproteins. The
RT 52- and 60-kD Ro/SSA autoantigens are encoded by separate genes.";
RL J. CLIN. INVEST. 87:177-186(1991).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE: 91086480.
RA CHAN E.K., HAMEL J.C., BOYON J.P., TAN E.M.;
RT "Molecular definition and sequence motifs of the 52-kD component of
RT human SS-A/Ro autoantigen.";
RL J. CLIN. INVEST. 87:68-76(1991).
RN (3)
RN SEQUENCE FROM N.A.
RX MEDLINE: 95229135.
RA TSUO H., HOROWITZ R., GIBSON N., FRANK M.B.;
RT "The location of a disease-associated polymorphism and genomic
RT structure of the human 52-kDa Ro/SSA locus (SSAL).";
RL GENOMICS 24:541-548(1994).
RN (4)
RN SEQUENCE FROM N.A.
RX MEDLINE: 96215393.
RA KEECH C.L., GORDON T.P., MCCUSKEY J.;
RT "Structural differences between the human and mouse 52-kD Ro
RT autoantigens associated with poorly conserved autoantibody activity
RT across species.";
RL CLIN. EXP. IMMUNOL. 104:255-263(1996).
CC -1- FUNCTION: RO/SSA IS A RIBONUCLEOPROTEIN PARTICLE COMPOSED OF A
CC SINGLE POLYPEPTIDE AND ONE OF FOUR SMALL RNA MOLECULES. IT IS
CC PRESENT IN ALL MAMMALIAN CELLS STUDIED BUT HAS NO KNOWN FUNCTION.
CC AT LEAST TWO ISOPROFORMS ARE PRESENT IN NUCLEATED & RED BLOOD CELLS,
CC AND TISSUE SPECIFIC DIFFERENCES IN RO/SSA PROTEINS HAVE BEEN
CC IDENTIFIED. THE COMMON FEATURE OF THESE PROTEINS IS THEIR
CC ABILITY TO BIND HY RNAs.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR.
CC -1- DISEASE: SERA FROM PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS OR
CC PRIMARY SJOGREN'S SYNDROME OFTEN CONTAIN ANTIBODIES THAT REACT
CC WITH NORMAL CELLULAR A C3HC4-CLASS ZINC FINGER.
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC -----
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CC -----
DR EMBL: U01882; G665918; -
DR EMBL: M34551; G337485; -
DR EMBL: M62800; G338490; -
DR EMBL: U13658; G747927; -
DR EMBL: U13657; G747927; JOINED.
DR PIR: A37241; A37241.
DR MIM: 109092; -
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFAM: PF00097; zf-C3HC4; 1.
DR PFAM: PF00622; SPRY; 1.
DR PFAM: PF00643; zf-B_Box; 1.
KW SYSTEMIC LUPUS ERYTHEMATOSUS; ZINC-FINGER; ANTIGEN; RNA-BINDING;

KW RIBONUCLEOPROTEIN; DNA-BINDING.
FT ZN FING 16 54 C3HC4-TYPE.
FT DOMAIN 92 123 B BOX (CYS/HIS-RICH).
FT DOMAIN 211 232 LEUCINE-ZIPPER.
FT CONFLICT 52 52 P -> A (IN REF. 2).
SQ SEQUENCE 475 AA; 54169 MW; 9094248F CRC32;
Query Match 76.3%; Score 45; DB 1; Length 475;
Best Local Similarity 44.4%; Pred. No. 1.06e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Db 386 ORXENATYP 394
Query 1 ORXENATYP 9
RESULT 9
ID CP74.LINUS STANDARD: PRT: 536 AA.
AC P48417:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE ALLENE OXIDE SYNTHASE PRECURSOR (EC 4.2.1.92) (HYDROPEROXIDE
DE DEHYDRASE) (CYTOCHROME P450 74A).
GN CYP74A OR CYP74.
OS LINUM STRYPTISIMUM (FLAX) (LINSEED).
OC EUKARYOTA; VIRIDIPHYTES; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC LINALES; LINACEAE; LINUM.
RN (1)
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-EMBRYO.
RX MEDLINE: 93391385.
RA SONG W.-C., FUNK C.D., BRASH A.R.;
RT "Molecular cloning of an allelic oxide synthase: a cytochrome P450
RT specialized for the metabolism of fatty acid hydroperoxides.";
RL PROC. NATL. ACAD. SCI. U.S.A. 90:8519-8523(1993).
CC -1- FUNCTION: IS INVOLVED IN THE BIOSYNTHESIS OF JASMONIC ACID, A
CC GROWTH REGULATOR THAT IS IMPLICATED ALSO AS A SIGNALING MOLECULE
CC IN PLANT DEFENSE. ACTS ON A NUMBER OF UNSATURATED FATTY-ACID
CC HYDROPEROXIDES, FORMING THE CORRESPONDING ALLENE OXIDES.
CC -1- CATALYTIC ACTIVITY: (9Z,11E,14Z)-(13S)-HYDROPEROXYOCTADEC-
CC (9,11,14)-TRIENONE - (9Z)-(13S)-12,13-EPOXYOCTADEC-9,11-
CC DIENONE + H(2)O.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
DR EMBL: U00428; G404866; -
DR PROSITE: PS00086; CYTOCHROME_P450; FALSE_NEG.
DR PFAM: PF00067; P450; 1.
KW LYASE; HEME; CHLOROPLAST; TRANSIT PEPTIDE; POLYMORPHISM.
FT TRANSIT 1 58 CHLOROPLAST.
FT CHAIN 59 536 ALLENE OXIDE SYNTHASE.
FT BINDING 489 489 HEME (BY SIMILARITY).
FT VARIANT 525 525 S -> T.
SQ SEQUENCE 536 AA; 59669 MW; 25031B69 CRC32;
Query Match 76.3%; Score 45; DB 1; Length 536;
Best Local Similarity 62.5%; Pred. No. 1.06e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 108 ORXKSTYV 115
Query 1 ORXENATYP 8

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RESULT 10
ID DTX COROM STANDARD; PRT: 560 AA.
AC P00587;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DIPHTHERIA TOXIN PRECURSOR (DT) (NAD(+)--DIPHTHAMIDE ADP-
DE RIBOSYLTRANSFERASE) (EC 2.4.2.36).
OS CORNEPHAGE BETA.
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; SIPHOVIRIDAE;
OC LAMBDA PHAGE GROUP.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 84041471.
RA RATTI G., RAPPOLOI R., GIANNINI G.;
RT "The complete nucleotide sequence of the gene coding for diphtheria
RT toxin in the cornephage omega (tox+) genome."
RL NUCLEIC ACIDS RES. 11:6589-6595(1983).
CC -1- FUNCTION: DIPHTHERIA TOXIN, PRODUCED BY A PHAGE INFECTING
CC CORNEBACTERIUM DIPHTHERIAE, IS A PROENZYME THAT, AFTER
CC ACTIVATION, CATALYZES THE COVALENT ATTACHMENT OF THE ADP RIBOSE
CC MOIETY OF NAD TO ELONGATION FACTOR 2.
CC -1- CATALYTIC ACTIVITY: NAD(+) + PEPTIDE DIPHTHAMIDE - NICOTINAMIDE +
CC PEPTIDE N-(ADP-D-RIBOSYL)DIPHTHAMIDE.
CC -1- SUBUNIT: HOMODIMER.
CC -----
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CC -----
DR EMBL: V01536; G579179; -
DR EMBL: M19546; G166117; -
DR PIR: A00728; DOCGPO.
DR PFAM: PF01324; Diphtheria_tox; 1.
DR HSSP: P00588; 1XDT.
KW TOXIN; TRANSFERASE; GLYCOSYLTRANSFERASE; NAD; SIGNAL.
FT SIGNAL 1 25
FT CHAIN 26 218
FT FT
FT CHAIN 219 560
FT FT
FT CHAIN
FT ACT_SITE 46 46 FRAGMENT A (RESPONSIBLE FOR ENZYMATIC
FT ACT_SITE 90 90 ADP-RIBOSYLATION OF ELONGATION FACTOR 2).
FT ACT_SITE 173 173 FRAGMENT B (RESPONSIBLE FOR BINDING OF
FT DISULFID 211 226 TOXIN TO CELL RECEPTORS & ENTRY OF
FT DISULFID 486 496 FRAGMENT A).
FT SEQUENCE 560 AA; 60814 MW; 2170B928 CRC32; BY SIMILARITY.
BY SIMILARITY.
Query Match 76.3%; Score 45; DB 1; Length 560;
Best Local Similarity 62.5%; Pred. No. 1.06e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 84 KYDAGS 91
OY 2 KYNSAAYS 9

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RESULT 11
ID DTX CORBE STANDARD; PRT: 560 AA.
AC P00589;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DIPHTHERIA TOXIN HOMOLOG CRM228 PRECURSOR.
OS CORNEPHAGE BETA.
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; SIPHOVIRIDAE;
OC LAMBDA PHAGE GROUP.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 84070728.
RA GREENFIELD L., BJORN M.J., HORN G., FONG D., BUCK G.A., COLLIER R.J.,
RA KAPLAN D.A.;
RT "Nucleotide sequence of the structural gene for diphtheria toxin
RT carried by corneobacteriophage beta."
RL PROC. NATL. ACAD. SCI. U.S.A. 80:6853-6857(1983).
RN SEQUENCE OF 33-225.

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RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 83275723.
RA KACZOREK M., DELPEYROUX F., CHENCINER N., STRECK R.E., MURPHY J.R.,
RA BOUQUET P., TIOLLAIS P.;
RT "Nucleotide sequence and expression of the diphtheria tox228 gene in
RT Escherichia coli."
RL SCIENCE 221:855-858(1983).
CC -1- THIS DIPHTHERIA TOXIN HOMOLOG IS A NONTOXIC CROSS-REACTING
CC MATERIAL (CRM) PRODUCED BY A STRAIN OF CORNEPHAGE BETA THAT HAD
CC UNDERGONE N-METHYL-N'-NITRO-N-NITROGUANIDINE MUTAGENESIS. THIS
CC TREATMENT INDUCES GUANINE-ADENINE TRANSITIONS IN THE DNA: THE
CC DIFFERENCES FROM THE WILD-TYPE SEQUENCE AT POSITIONS 104, 187,
CC 222, 456, & 532 CAN BE EXPLAINED BY SUCH MUTATIONS. EITHER OF THE
CC FIRST 2 MUTATIONS WILL COMPLETELY ABOLISH ALL ADP-RIBOSYLATING
CC ACTIVITY OF FRAGMENT A. THE LAST 2 MUTATIONS MAY BE RESPONSIBLE
CC FOR THE REDUCED RECEPTOR-BINDING CAPACITY OF THIS PROTEIN.
CC -1- IN WILD-TYPE ACTIVE DIPHTHERIA TOXIN, FRAGMENT A CATALYZES THE
CC ADP-RIBOSYLATION OF ELONGATION FACTOR 2 AND BLOCKS PROTEIN
CC SYNTHESIS IN EUKARYOTIC CELLS; FRAGMENT B BINDS TO THE RECEPTOR
CC PROTEIN AND IS NECESSARY FOR THE MOVEMENT OF FRAGMENT A INTO THE
CC CELL.
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CC -----
DR EMBL: K01723; G166121; -
DR PIR: A00730; DOCGH8.
DR PFAM: PF01324; Diphtheria_tox; 1.
DR HSSP: P00588; 1XDT.
KW SIGNAL.
FT SIGNAL 1 25
FT CHAIN 26 218 FRAGMENT A.
FT FT
FT CHAIN 219 560 FRAGMENT B.
FT DISULFID 211 226 BY SIMILARITY.
FT DISULFID 486 496 BY SIMILARITY.
FT SEQUENCE 560 AA; 60920 MW; 480921D8 CRC32; BY SIMILARITY.
Query Match 76.3%; Score 45; DB 1; Length 560;
Best Local Similarity 62.5%; Pred. No. 1.06e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 84 KYDAGS 91
OY 2 KYNSAAYS 9

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RA MEDLINE: 79194138.
 RA DELANGE R.J., WILLIAMS L.C., DRAZIN R.E., COLLIER R.J.;
 RT "The amino acid sequence of fragment A, an enzymically active
 RT fragment of diphtheria toxin. III. The chymotryptic peptides, the
 RT peptides derived by cleavage at tryptophan residues, and the complete
 RT sequence of the protein.";
 RT J. BIOL. CHEM. 254:5838-5842(1979).
 RN [3]
 RP ACTIVE SITE TRP-185.
 RA MEDLINE: 77134904.
 RA MICHEL A., DIRKX J.;
 RT "Occurrence of tryptophan in the enzymically active site of
 RT diphtheria toxin fragment A.";
 RT J. BIOCHEM. BIOPHYS. ACTA 491:286-295(1977).
 RN [4]
 RP ACTIVE SITE TYR-97.
 RA MEDLINE: 9111874.
 RA PAPINI E., SANTUCCI A., SCHIAVO G., DOMENIGHINI M., NERI P.,
 RA RAPUOLU R., MONTECUCO C.;
 RT "Tyrosine 65 is photolabeled by 8-azidoadenine and 8-azidoadenosine
 RT at the NAD binding site of diphtheria toxin.";
 RT J. BIOL. CHEM. 266:2494-2498(1991).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RA MEDLINE: 92269934.
 RA CHOE S., BENNETT M.J., FUJII G., CURMI P.M.G., KANTARDJIEFF K.A.,
 RA COLLIER R.J., EISENBERG D.;
 RT "The crystal structure of diphtheria toxin.";
 RT NATURE 357:216-222(1992).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA MEDLINE: 96155972.
 RA BELL C.E., EISENBERG D.;
 RT "Crystal structure of diphtheria toxin bound to nicotinamide adenine
 RT dinucleotide.";
 RT BIOCHEMISTRY 35:1137-1149(1996).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA MEDLINE: 97164901.
 RA BELL C.E., EISENBERG D.;
 RT "Crystal structure of nucleotide-free diphtheria toxin.";
 RT BIOCHEMISTRY 36:481-488(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF COMPLEX WITH RECEPTOR.
 RA MEDLINE: 98324089.
 RA LOUIE G.V., YANG W., BOWMAN M.E., CHOE S.;
 RT "Crystal structure of the complex of diphtheria toxin with an
 RT extracellular fragment of its receptor.";
 RT MOL. CELL. 1:67-78(1997).
 CC -1- FUNCTION: DIPHTHERIA TOXIN, PRODUCED BY A PHAGE INJECTING
 CC CORNENBACTERIUM DIPHTHERIAE, IS A PROENZYME THAT, AFTER
 CC ACTIVATION, CATALYZES THE COVALENT ATTACHMENT OF THE ADP RIBOSE
 CC MOLETYL OF NAD TO ELONGATION FACTOR 2.
 CC -1- CATALYTIC ACTIVITY: NAD(+) + PEPTIDE DIPHTHAMIDE - NICOTINAMIDE +
 CC PEPTIDE N-(ADP-D-RIBOSYL)DIPHTHAMIDE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -----
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 CC -----
 DR EMBL: X00703; G758186; -;
 DR EMBL: K01722; G166119; ALT_INTF.
 DR PIR: A00729; DOGGA
 DR PIR: A05128; A05128.
 DR PDB: 1DDT; 31-JUL-94.
 DR PDB: 1DDT; 31-JUL-94.
 DR PDB: 1DTP; 01-NOV-94.
 DR PDB: 1TOX; 10-JUN-96.

DR PDB: 1SGK; 23-DEC-96.
 DR PDB: 1XDT; 25-FEB-98.
 DR PFAM: PF01324; Diphtheria_tox_1.
 KM TOXIN; TRANSFERASE; GLYCOSYLTRANSFERASE; NAD; SIGNAL; 3D-STRUCTURE.
 FT SIGNAL 1 32
 FT CHAIN 33 225
 FT CHAIN 226 567
 FT FT
 FT ACT_SITE 53 53
 FT ACT_SITE 97 97
 FT ACT_SITE 180 180
 FT ACT_SITE 185 185
 FT FT
 FT DISULFID 218 233
 FT DISULFID 493 503
 FT CONFLICT 178 180
 SQ SEQUENCE 567 AA; 61601 MW; 18976DFD CRC32;
 Query Match 76.3%; Score 45; DB 1; Length 567;
 Best Local Similarity 62.5%; Pred. No. 1.06e+01;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 DB 91 KYDAGYS 98
 QY 2 KYNSAYS 9
 RESULT 13
 ID GIND HAEIN STANDARD; PRT; 863 AA.
 AC P43819;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE [PROTEIN-PII] URIDYLTRANSFERASE (EC 2.7.7.59) (PII URIDYL-
 DE TRANSFERASE) (URIDYLIC REMOVING ENZYME) (UTASE).
 GN GIND OR H11719.
 OS HAEMOPHILUS INFLUENZAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURILLACEAE;
 OC HAEMOPHILUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE: 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BULL C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZGHG W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIO L.-I., GLADER A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOW E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDER D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEEM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RT SCIENCE 269:496-512(1995).
 CC -1- FUNCTION: MODIFIES, BY URIDYLATION OR DEURIDYLATION THE PII
 CC (GNB) REGULATORY PROTEIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: UTP + [PROTEIN-PII] - PYROPHOSPHATE +
 CC URIDYLIC-[PROTEIN-PII].
 CC -1- SIMILARITY: TO OTHER BACTERIAL GIND.
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 CC -----
 DR EMBL: U32844; G1574572; -;

DR TIGR; H11719; -
 KW TRANSFERASE; NUCLEOTIDYLTRANSFERASE.
 SQ SEQUENCE 863 AA; 100173 MW; AFBF5FD CRC32;

Query Match 76.38; Score 45; DB 1; Length 863;
 Best Local Similarity 44.48; Pred. No. 1.06e+01;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 ORYNTAYN 193
 1:1:1:1:1:1:
 OY 1 OKYNSAAYS 9

RESULT 14
 ID ACTB.DICDI STANDARD: PRT: 295 AA.
 AC P24005:
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE CALCIUM-REGULATED ACTIN BUNDLING PROTEIN (34 KD ACTIN BINDING PROTEIN).
 OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 OC EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 7-22 AND 225-237.
 RA MEDLINE; 91131582.
 RX FECHHEIMER M., MURDOCK D., CARNEY M., GLOVER C.V.C.;
 RT "Isolation and sequencing of cDNA clones encoding the Dictyostelium discoidium 30,000-dalton actin-bundling protein.";
 RL J. BIOL. CHEM. 266:2883-2889(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AX3;
 RX MEDLINE; 97081098.
 RA RIVERO F., FURUKAWA R., NOGEL A.A., FECHHEIMER M.;
 RT "Dictyostelium discoidium cells lacking the 34,000-dalton actin-binding protein can grow, locomote, and develop, but exhibit defects in regulation of cell structure and movement: a case of partial redundancy.";
 RT J. CELL BIOL. 135:965-980(1996).
 RL -1- FUNCTION: MAY CONTRIBUTE TO THE STRUCTURE AND REORGANIZATION OF FILOPODIA AND PSEUDOPODIA ACCOMPANYING CELL MOVEMENTS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.

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 CC
 CC EMBL; M58022; G167578; -
 DR EMBL; Z50156; E190032; -
 DR EMBL; U32112; G1794190; -
 DR PIR; A23750; A23750.
 DR DICTYDB; DD01032; -
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 KW CALCIUM-BINDING; ACTIN-BINDING.
 FT CA_BIND 93 104 POTENTIAL.
 FT CA_BIND 144 155 POTENTIAL.
 FT SIMILAR 196 210 TO CHICKEN GIZZARD CALDESMON REPEATS AND TO HUMAN CYTOVILLIN (AA 360-374).
 FT DOMAIN 256 275 ARG/LYS-RICH (BASIS).
 FT DOMAIN 286 295 ARG/LYS-RICH (BASIS).
 FT SEQUENCE 295 AA; 33353 MW; C7A/DID6 CRC32;

Query Match 74.68; Score 44; DB 1; Length 295;
 Best Local Similarity 75.08; Pred. No. 1.73e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 254 KIGGAAYS 261

OY 2 KYNSAAYS 9
 1:1:1:1:1:1:

RESULT 15
 ID NPRE_BACCL STANDARD: PRT: 544 AA.
 AC P23384;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DT 01-NOV-1991 (REL. 32, LAST ANNOTATION UPDATE)
 DE BACILLOLYSIN PRECURSOR (EC 3.4.24.28) (THERMOSTABLE NEUTRAL PROTEASE).
 GN NPRE.
 OS BACILLUS CALDOLYTICUS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91286196.
 RA VAN DEN BERG B., ENEQUIST H.G., VAN DE HAAR M.E., EUSINK V.G.H., STUPE B.K., VENEMA G.;
 RT "A highly thermostable neutral protease from *Bacillus caldolyticus*: cloning and expression of the gene in *Bacillus subtilis* and characterization of the gene product.";
 RL J. BACTERIOL. 173:4107-4115(1991).
 CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.
 CC -1- CATALYTIC ACTIVITY: SIMILAR, BUT NOT IDENTICAL, TO THAT OF THERMOLYSIN.
 CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.

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 CC
 CC EMBL; M63575; G143251; -
 DR PIR; A42464; A42464.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR HSSP; P00800; TLTP.
 KW HYDROLASE; METALLOPROTEASE; ZINC; CALCIUM; ZINC; ZINC; SIGNAL.
 FT SIGNAL 1 25
 FT PROPEP 26 225
 FT CHAIN 226 544
 FT METAL 370 370
 FT ACT_SITE 371 371
 FT METAL 374 374
 FT METAL 394 394
 FT ACT_SITE 459 459
 FT SEQUENCE 544 AA; 59413 MW; 2079A17D CRC32;

Query Match 74.68; Score 44; DB 1; Length 544;
 Best Local Similarity 55.68; Pred. No. 1.73e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 242 OKYNTTYS 250
 1:1:1:1:1:1:
 OY 1 OKYNSAAYS 9

Search completed: Thu Sep 2 12:01:42 1999
 Job time : 8 secs.

RT 0139 are closely related to those of Vibrio cholerae 022.*;
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567; -
 SQ SEQUENCE 337 AA; 40147 MW; 1768466B CRC32;

Query Match 83.1%; Score 49; DB 2; Length 337;
 Best Local Similarity 75.0%; Pred. No. 3.14e+00;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 147 OKYNSAPY 154
 |||:|:|
 QY 1 OKYNSAPY 8

RESULT 3
 ID 065569 PRELIMINARY; PRT; 397 AA.
 AC 065569;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 46.8 KD PROTEIN.
 GN A0183.
 OS AQUIFEX AEOLICUS.
 OC BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VF5;
 RX MEDLINE; 98196666.
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., ADJAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RT NATURE 392:353-358(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VF5;
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., ADJAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: A800677; G3982913; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 397 AA; 46821 MW; 29F9AF24 CRC32;

Query Match 79.7%; Score 47; DB 2; Length 397;
 Best Local Similarity 66.7%; Pred. No. 8.59e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 362 OKYRSDTYS 370
 |||:|:|
 QY 1 OKYNSAPY 9

RESULT 4
 ID 039443 PRELIMINARY; PRT; 480 AA.
 AC 039443;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE FATTY ACID HYDROPEROXIDE LIASE.
 OS CAPSICUM ANNUUM (BELL PEPPER).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; CAPSICUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FRUIT;
 RA MATSUI K., SHIBUTANI M., KAJIWARA T., HASE T.;
 RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U51674; G1272340; -
 DR PFM: P00067; P450; 1.5e5; 1.
 DR MENDEL; 7585; CAPAN; 1095; 1.

KW LYASE.
 SQ SEQUENCE 480 AA; 54056 MW; 5962F3CD CRC32;

Query Match 78.0%; Score 46; DB 10; Length 480;
 Best Local Similarity 55.6%; Pred. No. 1.41e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 461 OKYDSVSFS 469
 |||:|:|
 QY 1 OKYNSAPY 9

RESULT 5
 ID 001481 PRELIMINARY; PRT; 283 AA.
 AC 001481;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO C3HC4-TYPE ZINC FINGERS AND HSP90.
 GN C06A5.8.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERRS M.,
 RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA CRATON M., DEAR S., DU Z., DUBREIN R., FAVELLO A., FULTON L.,
 RA GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATEILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SANDERS D., SHOMKNEEN R.,
 RA SMALDON N., SMITH A., SONNHAUSER E., STADEN R., STOUTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMANN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RT NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA DAVIDSON S., WOHLDMANN P.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 DR EMBL: U97193; G1943784; -
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR PFM: P00097; ZF-C3HC4; 1.
 KW ZINC-FINGER.
 SQ SEQUENCE 283 AA; 31648 MW; 8D388767 CRC32;

Query Match 76.3%; Score 45; DB 5; Length 283;
 Best Local Similarity 62.5%; Pred. No. 2.28e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 70 OKYNSAPY 77
 |||:|:|
 QY 1 OKYNSAPY 8

RESULT 6
 ID 056863 PRELIMINARY; PRT; 292 AA.
 AC 056863;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE WBCB PROTEIN (ORF.5).

GN WBCB.
 OS YERSINIA ENTEROCOLITICA.
 OC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE;
 OC YERSINIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-8081C / SEROTYPE O:8;
 RX MEDLINE: 97157942.
 RA ZHANG L., RADZIELEWSKA-LEBERECHT J., KRAJEWSKA-PIETRASIK D.,
 RA TOIVANEN P., SKRNIK M.;
 RT "Molecular and chemical characterization of the lipopolysaccharide
 O-antigen and its role in the virulence of yersinia enterocolitica
 serotype O:8.";
 RL MOL. MICROBIOL. 23:63-76(1997).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE PRODUCTION OF
 CC CDP-6-DEOXY-D-GLUCOSE.
 CC -1- PATHWAY: O ANTIGEN SYNTHESIS IN LIPOLYSACCHARIDE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -1- SIMILARITY: TO CDP-ABEODOSE SYNTHASES.
 EMBL: U46859; G1197643; -
 LIPOPOLYSACCHARIDE BIOSYNTHESIS.
 SEQUENCE 292 AA; 32922 MW; C4056269 CRC32;

Query Match 76.3%; Score 45; DB 2; Length 292;
 Best Local Similarity 75.0%; Pred. No. 2.28e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 119 QKYN5ADY 126
 1:|||||1
 1 QKYN5AAY 8

RESULT 7 PRELIMINARY; PRT; 138 AA.
 ID Q81372;
 AC Q81372;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE POLYPROTEIN (FRAGMENT).
 OS HEPATITIS C VIRUS (HCV).
 OC VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE: FLAVIVIRIDAE;
 OC HEPATITIS C-LIKE VIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RS3-3;
 RX MEDLINE: 93080545.
 RA KATO N., OOSUYAMA Y., OHKOSHI S., NAKAZAWA T., SEKIYA H.,
 RA HUIKATA M., SHIMOTOHNO K.;
 RT "Characterization of hypervariable regions in the putative envelope
 protein of hepatitis C virus.";
 BIOCHEM. BIOPHYS. RES. COMMUN. 189:119-127(1992).
 EMBL: D12966; D1002840; -
 POLYPROTEIN: ENVELOPE PROTEIN.
 KW METAL-BINDING.
 FT NON_TER 1
 FT TER 138
 SQ SEQUENCE 138 AA; 14904 MW; 57CA7F1F CRC32;

Query Match 74.6%; Score 44; DB 14; Length 138;
 Best Local Similarity 44.4%; Pred. No. 3.68e+01;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 77 HKNSGDT 85
 1:|||||1
 1 QKYN5AAY 9

RESULT 8 PRELIMINARY; PRT; 521 AA.
 ID Q44677;
 AC Q44677;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE NEUTRAL PROTEASE.

OS BACILLUS AMYLILIQUEFACIENS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SHIMADA H., HONJO M., MITA I., NAKAYAMA A., AKAKURA A., MANABE K.,
 RA FURUTANI Y.;
 RT J. BIOTECHNOL. 2:75-85(1985).
 DR EMBL: M36723; G143353; -
 DR PFM: PF00099; zn-Protease; 1.
 KW PROTEASE.
 SQ SEQUENCE 521 AA; 56725 MW; 64AFE5F CRC32;

Query Match 74.6%; Score 44; DB 2; Length 521;
 Best Local Similarity 62.5%; Pred. No. 3.68e+01;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 308 QKYN5AY 315
 1:|||||1
 1 QKYN5AAY 8

RESULT 9 PRELIMINARY; PRT; 546 AA.
 ID Q59223;
 AC Q59223;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE THERMOLYSIN PRECURSOR (EC 3.4.24.27)
 DE (THERMOSTABLE NEUTRAL PROTEINASE).
 GN NPR.
 OS BACILLUS SP. (STRAIN EAL).
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96328267.
 RA SAUT D.J., WILLIAMS L.C., TOOGOOD H.S., DANIEL R.M., BERGQUIST P.L.;
 RT "Sequence of the gene encoding a highly thermostable neutral
 proteinase from Bacillus sp. strain EAL: expression in Escherichia
 coli and characterization.";
 RT BIOCHIM. BIOPHYS. ACTA 1308:74-80(1996).
 RL CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.
 CC -1- HAS COLLAGENASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: XAA-|-LEU > XAA-|-PHE.
 CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
 CC PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4
 CC (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.
 DR EMBL: U25630; G995784; -
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR HYDROLASE: METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL;
 KW METAL-BINDING.
 FT SIGNAL 1
 FT PROPEP 25
 FT CHAIN 229
 FT METAL 372
 FT METAL 372
 FT ACT_SITE 373
 FT METAL 376
 FT METAL 396
 FT ACT_SITE 461
 FT ACT_SITE 461
 SQ SEQUENCE 546 AA; 59812 MW; 1DD9D39E CRC32;

Query Match 74.6%; Score 44; DB 2; Length 546;
 Best Local Similarity 55.6%; Pred. No. 3.68e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 244 QKYN5AY 252
 1:|||||1
 1 QKYN5AAY 9

RESULT 10

ID 04380 PRELIMINARY; PRT: 546 AA.
AC 04380;
DT 01-NOV-1998 (TREMREL. 08, CREATED)
DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE THERMOLYSIN PRECURSOR (EC 3.4.24.27)
DE THERMOLYSIN PRECURSOR (EC 3.4.24.27)
OS ALICYCLOBACILLUS ACIDOCALARIUS (BACILLUS ACIDOCALARIUS).
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC ALICYCLOBACILLUS GROUP; ALICYCLOBACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BT1;
RA MEDLINE: 95309716.
RT "Cloning and sequencing of the neutral protease-encoding gene from a thermophilic strain of Bacillus sp.";
RL GENE 158,147-148(1995).
CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: XAA-I-LEU > XAA-I-PHE.
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4
(ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.
DR EMBL: U07824; G563121; PROTEASE; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL;
KW METAL-BINDING.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 228 ACTIVATION PEPTIDE.
FT CHAIN 229 546 THERMOLYSIN.
FT METAL 372 372 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 373 373 BY SIMILARITY.
FT METAL 376 376 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 396 396 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 461 461 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 546 AA; 59769 MW; 3EE6EBBA CRC32;
Query Match 74.6%; Score 44; DB 2; Length 546;
Best Local Similarity 55.6%; Pred. No. 3.68e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DB 244 OKYINTTYS 252
OY 1 OKYNSAAYS 9
RESULT 11
AC 059193 PRELIMINARY; PRT: 546 AA.
DT 01-NOV-1998 (TREMREL. 08, CREATED)
DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE THERMOLYSIN PRECURSOR (EC 3.4.24.27)
DE (THERMOSTABLE NEUTRAL PROTEINASE).
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Y-T;
RA MEDLINE: 96328267.
RT "SAUD D.J., WILLIAMS L.C., TOOGOOD H.S., DANIEL R.M., BERGQUIST P.L.; Sequence of the gene encoding a highly thermostable neutral protease from Bacillus sp. strain EAL: expression in Escherichia coli and characterization.";
RL BIOCHIM. BIOPHYS. ACTA 1308:74-80(1996).
CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: XAA-I-LEU > XAA-I-PHE.
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4

CC (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.
DR EMBL: U25629; G995782; -
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW HYDROLASE; METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL;
RN METAL-BINDING.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 228 ACTIVATION PEPTIDE.
FT CHAIN 229 546 THERMOLYSIN.
FT METAL 372 372 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 373 373 BY SIMILARITY.
FT METAL 376 376 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 396 396 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 461 461 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 546 AA; 59770 MW; 924389F1 CRC32;
Query Match 74.6%; Score 44; DB 2; Length 546;
Best Local Similarity 55.6%; Pred. No. 3.68e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DB 244 OKYINTTYS 252
OY 1 OKYNSAAYS 9
RESULT 12
AC 049558 PRELIMINARY; PRT: 582 AA.
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE MEMBRANE PROTEIN P60.
OS MYCOPLASMA HOMINIS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
OC MYCOPLASMACTACEAE; MYCOPLASMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PG21;
RA BERNIS G.;
RL THESIS (1994), INST. F. MED. MICROBIOLOGY AND VIROLOGY,
RL HEINRICH-HEINE-UNIVERSITY.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PG21;
RA MEDLINE: 93293315.
RA HENRICH B., FELDAMANN R., HADDING U.;
RT "Cytoadhesins of Mycoplasma hominis";
RL INFECT. IMMUN. 61:2945-2951(1993).
DR EMBL: Z29069; G435305; -
KW MEMBRANE.
SQ SEQUENCE 582 AA; 66630 MW; 3CF62652 CRC32;
Query Match 74.6%; Score 44; DB 2; Length 582;
Best Local Similarity 75.0%; Pred. No. 3.68e+01;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 133 KYNPAFS 140
OY 2 KYNPAAYS 9
RESULT 13
AC 069007 PRELIMINARY; PRT: 588 AA.
DT 01-AUG-1998 (TREMREL. 07, CREATED)
DT 01-AUG-1998 (TREMREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMREL. 07, LAST ANNOTATION UPDATE)
DE MALTOGENIC AMYLASE.
OS THERMUS SP.
OC BACTERIA; THERMUS/DEINOCOCCUS GROUP; THERMUS GROUP; THERMUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IM6501;
RA KIM T.J., KIM J.W., PARK K.H.;

RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF060204; G3089607; -
 SQ SEQUENCE 588 AA; 68210 NM; BC219F4F CRC32;

Query Match 74.6%; Score 44; DB 2; Length 588;
 Best Local Similarity 50.0%; Pred. No. 3.68e+01;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 205 HKD7ADY 212
 OY 1 OKYNSAAY 8

RESULT 14 PRELIMINARY: PRT: 779 AA.
 AC 035269;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DT PUTATIVE PHEROMONE RECEPTOR.
 GO-VN5

RATTUS NORVEGICUS (RAT)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE: 97433086.
 RA HERADA G., DULAC C.;
 RT "A novel family of putative pheromone receptors in mammals with a
 RT topographically organized and sexually dimorphic distribution."
 RL CELL 90:763-773(1997).
 DR EMBL: AF016182; G2367613; -
 DR PRAM: PF00003; 7cml_3; 1
 SQ SEQUENCE 779 AA; 88096 NM; B89CE4D5 CRC32;

Query Match 74.6%; Score 44; DB 11; Length 779;
 Best Local Similarity 55.6%; Pred. No. 3.68e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 258 OKYNSKYP 266
 OY 1 OKYNSAAYS 9

RESULT 15 PRELIMINARY: PRT: 1129 AA.
 ID 002144
 AC 002144;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO HUMAN ATRAXIN-1 X79204.
 GN C46G7.4A.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIDA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONTFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STILSON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHIDMAN P.;
 RT "2.2 kb of contiguous nucleotide sequence from chromosome III of C.
 RL NATURE 368:32-38(1994).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MURRAY J., HAWKINS J.;
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U97593; G1946974; -
 SQ SEQUENCE 1129 AA; 126714 NM; 91E9C80E CRC32;

Query Match 74.6%; Score 44; DB 5; Length 1129;
 Best Local Similarity 55.6%; Pred. No. 3.68e+01;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 692 ONYSSAAY 700
 OY 1 OKYNSAAYS 9

Search completed: Thu Sep 2 12:02:26 1999
 Job time : 27 secs.

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(JMI)

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generated:

QOYNSAPDT 9

PAM 150

122810 seqs, 40068593 residues

Listing first 45 summaries

1:plr1 2:plr2 3:plr3 4:plr4

mean 20.730; variance 21.808; scale 0.951

ved by analysis of the total score distribution

SUMMARIES

0.7 109 2 D30601

45 40 69.0

ALIGNMENTS

DATE 19-May-1994 # 20-May-1998

00012
066T-TPW-02
20 Mar 1998

REFERENCE 540312

#journal Eur. J. Immunol.

hypermutat1

```
##status preliminary
```

#residues 1-108 #

CLASSIFICATION #superfamily

STIMMARY #1 and 4 108

Quorum Watch 02 09

Best vocal similarity 00.58

15

11/11/11

12-11-19

RESULT 2

TITLE Ig kappa chain

DATE 06-JUL-1982 #

ACCESSIONS A01892

#authors Andrews, D.W.

Amino acid se

and 1 - Gamma =

[illegible]

1-100 44
molecular_weight protein

COMMENT This chain was isolated from an IGM with anti-gamma globulin activity.

GENETICS

#gene GDB:IGKV3

#cross-references GDB:136266

#map_position 2p12-2p11

COMPLEX An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into larger oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer

KEYWORDS

FEATURE #domain immunoglobulin homology #label IMM\

16-91 #disulfide_bonds #status predicted

23-89 #length 109 #molecular_weight 11775 #checksum 5885

SUMMARY

Query Match 79.3%; Score 46; DB 1; Length 114;

Best Local Similarity 66.7%; Pred. No. 2.06e+00;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 94 OQYSSPST 102

OY 1 OQYNSAPDT 9

RESULT 3

ENTRY S49532 #type complete

TITLE anti-5m antibody VL chain (V kappa 3/J kappa 2) - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 08-Sep-1997

ACCESSIONS S49532

REFERENCE S48797

#authors Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

#description Submitted to the EMBL Data Library, October 1994

#molecular_weight 14093 #checksum 6407

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY

Query Match 79.3%; Score 46; DB 2; Length 129;

Best Local Similarity 66.7%; Pred. No. 2.06e+00;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 110 OQYSSPST 118

OY 1 OQYNSAPDT 9

RESULT 4

ENTRY K3HUT1 #type complete

TITLE Ig kappa chain V-II region (Ti) - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 15-Aug-1997

ACCESSIONS A01895

REFERENCE A01651

#authors Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.

#journal Hoppe-Seyler's Z. Physiol. Chem. (1972) 353:189-208

#title Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom kappa-Typ, Subgruppe III (Bence-Jones-Protein Ti).

#cross-references MUID:72188439

#accession A01895

#molecule_type Protein

#residues 1-109 #label SUR

#note the sequence of the C region, which has the Inv (3) marker, is also given

COMMENT This is a Bence Jones protein.

GENETICS

#gene GDB:IGKV3

#cross-references GDB:136266

#map_position 2p12-2p11

COMPLEX An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into larger oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer

KEYWORDS

FEATURE #disulfide_bonds #status predicted

23-89 #length 109 #molecular_weight 11788 #checksum 6324

SUMMARY

Query Match 77.6%; Score 45; DB 1; Length 109;

Best Local Similarity 66.7%; Pred. No. 3.59e+00;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 90 OQYSSPST 98

OY 1 OQYNSAPDT 9

RESULT 5

ENTRY F44151 #type fragment

TITLE Ig kappa chain V region (JM-01) - human (fragment)

ORGANISM #formal_name Homo sapiens #common_name man

DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 16-Aug-1996

ACCESSIONS F44151

REFERENCE A44151

#authors Zebede, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotchen, R.H.; Graff, R.; Degraw, J.; Pyteli, J.; Lapolla, R.; Burton, D.R.; Lerner, R.A.; Thornton, G.B.

#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179

#title Human combinatorial antibody libraries to hepatitis B surface antigen.

#accession F44151

#status Preliminary; not compared with conceptual translation

#molecule_type mRNA

#residues 1-109 #label ZEB

CLASSIFICATION #note nucleotide translation not given

#superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin

SUMMARY

Query Match 77.6%; Score 45; DB 2; Length 109;

Best Local Similarity 66.7%; Pred. No. 3.59e+00;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 89 OQYSSPST 97

OY 1 OQYNSAPDT 9

RESULT 6

ENTRY S37532 #type fragment

TITLE Ig kappa chain V region (V-kappa 4) - human (fragment)

ORGANISM #formal_name Homo sapiens #common_name man

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

ACCESSIONS S37532

REFERENCE S37501

#authors Klein, U.; Kuipers, R.; Rajewsky, K.

#journal Submitted to the EMBL Data Library, September 1993

#title Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood, expresses V(kappa) genes with no or little somatic mutation throughout life.

#accession S37532
#status preliminary
#molecule_type mRNA
#residues 1-92 #label KLE
#cross-references EMBL:226628; NID:g405706; PID:g405707
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 92 #checksum 7895

Query Match 74.1%; Score 43; DB 2; Length 92;
Best Local Similarity 66.7%; Pred. No. 1.06e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 73 OQYNSPST 81
1 OQYNSAPDT 9

RESULT 7
ENTRY F30607 #type fragment
TITLE Ig kappa chain V-JII region (Bor) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS F30607
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGlinis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.

#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession F30607
#status preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6514

Query Match 74.1%; Score 43; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 1.06e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 90 OQYNSPOT 98
1 OQYNSAPDT 9

RESULT 8
ENTRY A42008 #type complete
TITLE homeotic protein HOX4E - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997

ACCESSIONS A42008
REFERENCE A42008
#authors Redline, R.W.; Williams, A.J.; Patterson, P.; Collins, T.
#journal Genomics (1992) 13:425-430
#title Human HOX4E: a gene strongly expressed in the adult male and female urogenital tracts.
#cross-references MUID:92307679
#accession A42008
#status not compared with conceptual translation
#molecule_type DNA; mRNA
#residues 1-340 #label RED

GENETICS
#map_position 2
#introns 249/1
CLASSIFICATION #superfamily unassigned homeobox proteins; homeobox homology
KEYWORDS DNA binding; homeobox; nucleus; transcription regulation
FEATURE

267-323
SUMMARY #domain homeobox homology #label HOX
#length 340 #molecular_weight 38411 #checksum 7745

Query Match 74.1%; Score 43; DB 2; Length 340;
Best Local Similarity 50.0%; Pred. No. 1.06e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 164 OEYNSPE 171
1 OQYNSAPD 8

RESULT 9
ENTRY S18650 #type complete
TITLE homeotic protein HOXD-4D
ALTERNATE_NAMES homeotic protein Hox 4D
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Dec-1997

ACCESSIONS S18650; S14936
REFERENCE S18649
#authors Zappavigna, V.; Renucci, A.; Izpisua-Belmonte, J.C.; Urier, G.; Peschle, C.; Duboule, D.
#journal EMBO J. (1991) 10:4177-4187
#title HOX4 genes encode transcription factors with potential auto- and cross-regulatory capacities.
#cross-references MUID:92097538
#accession S18650
#status preliminary
#molecule_type mRNA
#residues 1-340 #label ZAP
#cross-references EMBL:X59373; NID:g32392; PID:g32393

REFERENCE S07541
#authors Acampora, D.; d'Esposito, M.; Patel, A.; Pannese, M.; Migliaccio, E.; Morelli, F.; Stornaiolo, A.; Nigro, V.; Simeone, A.; Boncinelli, E.
#journal Nucleic Acids Res. (1989) 17:10385-10402
#title The human HOX gene family.
#cross-references MUID:90098876
#accession S14936
#status not compared with conceptual translation
#molecule_type DNA
#residues 266-331 #label ACA
#note the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 301-Arg

GENETICS
#gene GDB:HOXD10
#cross-references GDB:120679; OMIM:142984
#map_position 2q31-2q31
CLASSIFICATION #superfamily unassigned homeobox proteins; homeobox homology
KEYWORDS DNA binding; homeobox; nucleus; transcription regulation
FEATURE

SUMMARY 267-323
#domain homeobox homology #label HOX
#length 340 #molecular_weight 38509 #checksum 8357

Query Match 74.1%; Score 43; DB 2; Length 340;
Best Local Similarity 50.0%; Pred. No. 1.06e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 164 OEYNSPE 171
1 OQYNSAPD 8

RESULT 10
ENTRY S20879 #type complete
TITLE homeotic protein Hox 4.4 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Dec-1997

ACCESSIONS S20879
REFERENCE S20879
#authors Renucci, A.; Zappavigna, V.; Zakany, J.; Izpisua-Belmonte,

J.C.; Buerki, K.; Duboule, D.
EMBO J. (1992) 11:1459-1468
#journal Comparison of mouse and human HOX-4 complexes defines
#title conserved sequences involved in the regulation of Hox-4.4.
#cross-references MUID:9222484
#accession S20879
#molecule_type DNA
#residues 1-340 #label REN
#cross-references EMBL:X62669; NID:951414; PID:951415
GENETICS
#gene Hox-4.4
#introns 249/1
CLASSIFICATION #superfamily unassigned homeobox proteins; homeobox homology
KEYWORDS DNA binding; homeobox; nucleus; transcription regulation
FEATURE
SUMMARY #domain homeobox homology #label HOX
#length 340 #molecular-weight 38358 #checksum 5627
Query Match 74.1%; Score 43; DB 2; Length 340;
Best Local Similarity 50.0%; Pred. No. 1.06e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 164 QCYNSAP 171
OY 1 QCYNSAP 8
RESULT 11
ENTRY W2VZG1 #type complete
TITLE GIL protein - Amsacta moorei poxvirus
ORGANISM #formal_name Amsacta moorei poxvirus
DATE 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 05-Sep-1997
ACCESSIONS A41561
REFERENCE A41561
#authors Hall, R.L.; Moyer, R.W.
#journal J. Virol. (1991) 65:6516-6527
#title Identification, cloning, and sequencing of a fragment of Amsacta moorei entomopoxvirus DNA containing the spheroidin gene and three vaccinia virus-related open reading frames.
#cross-references MUID:92046310
#accession A41561
#molecule_type DNA
#residues 1-464 #label HAL
CLASSIFICATION #cross-references GB:M77182; NID:9209631; PID:9209632
KEYWORDS #superfamily vaccinia virus I7 protein late protein
SUMMARY #length 464 #molecular-weight 55541 #checksum 9465
Query Match 74.1%; Score 43; DB 1; Length 464;
Best Local Similarity 62.5%; Pred. No. 1.06e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 308 HYNSTPNT 315
OY 2 QYNSAPD 9
RESULT 12
ENTRY RNBV2L #type complete
TITLE DNA-directed RNA polymerase (EC 2.7.7.6) II 215K chain - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein D2150; protein YDL140C; RNA polymerase II largest chain
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 04-Dec-1986 #sequence_revision 23-Aug-1996 #text_change 12-Dec-1997
ACCESSIONS S67686; A00692; S64647; S20985
REFERENCE S67677
#authors Saluz, H.P.; Moelfl, S.; Hanemann, V.
#submission submitted to the Protein Sequence Database, July 1996
#accession S67686
#molecule_type DNA

##residues 1-1733 #label SAL
#cross-references EMBL:Z74188; NID:g1431216; PID:e253056; PID:g1431217;
#accession MIRS:YDL140C
#experimental_source strain S288C
REFERENCE A90870
#authors Allison, L.A.; Moyle, M.; Shales, M.; Ingles, C.J.
#journal Cell (1985) 42:599-610
#title Extensive homology among the largest subunits of eukaryotic and prokaryotic RNA polymerases.
#cross-references MUID:85282617
#accession A00692
#molecule_type DNA
#residues 1-1513, 'V', 1515-1523, 'A', 1525-1555, 1563-1607, 'W', 1609-1733 #label ALL
#cross-references EMBL:X03128; NID:g4397; PID:g4398
REFERENCE S64646
#authors Cronan Jr., J.E.; Wallace, J.C.
#journal FEMS Microbiol. Lett. (1995) 130:221-230
#title The gene encoding the biotin-apoprotein ligase of Saccharomyces cerevisiae.
#accession S64647
#status translation not shown
#molecule_type DNA
#residues 1669-1733 #label CRO
#cross-references EMBL:U27182; NID:g886080; PID:g886082
GENETICS
#gene SGD:RPO21
#cross-references SGD:S0002299; MIRS:YDL140C
#map_position 4L
CLASSIFICATION #superfamily human DNA-directed RNA polymerase II largest chain
KEYWORDS DNA binding; nucleotidyltransferase; tandem repeat; transcription; zinc finger
FEATURE 1567-1733
SUMMARY #region 7-residue repeats
#length 1733 #molecular-weight 191610 #checksum 5698
Query Match 74.1%; Score 43; DB 1; Length 1733;
Best Local Similarity 85.7%; Pred. No. 1.06e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 4 QCYSSAP 10
OY 1 QCYNSAP 7
RESULT 13
ENTRY A34153 #type complete
TITLE Ig kappa chain V-IV region (Dep) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 16-Aug-1996
ACCESSIONS A34153
REFERENCE A34153
#authors Mihaesco, E.; Ayadi, H.; Congy, N.; Gendron, M.C.; Roy, J.P.; Heyermann, H.; Frangione, B.; Brouet, J.C.
#journal J. Biol. Chem. (1989) 264:21481-21485
#title Multiple mutations in the variable region of the kappa light chains of three monoclonal human IgM with anti-myelin-associated glycoprotein activity.
#cross-references MUID:90094313
#accession A34153
#status preliminary
#molecule_type protein
#residues 1-102 #label MTH
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin
KEYWORDS #length 102 #molecular-weight 11477 #checksum 2909
SUMMARY
Query Match 72.4%; Score 42; DB 2; Length 102;
Best Local Similarity 71.4%; Pred. No. 1.80e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Db      95 QOYHSSP 101
      |||:|:|
OY      1 QOYNSAP 7

RESULT 14
ENTRY   S28085 #type complete
TITLE   nef protein - simian immunodeficiency virus
ORGANISM #formal name simian immunodeficiency virus, SIV
DATE     17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
        17-Mar-1999
ACCESSIONS
REFERENCE S28085
AUTHORS   Tsujimoto, H.; Hasegawa, A.; Maki, N.; Fukasawa, M.; Miura,
          T.; Speidel, S.; Cooper, R.W.; Moriyama, E.N.; Gojohort,
          T.; Hayami, M.
#journal Nature (1989) 341:539-541
#title     Sequence of a novel simian immunodeficiency virus from a
          wild-caught African mandrill.
#cross-references MUID:90015168
#accession S28085
#status     nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues   1-214 #label TSU
#cross-references GB:M27470; EMBL:X15781; NID:g334683; PID:g334691
#note       the nucleotide sequence was submitted to the EMBL Data
          Library, July 1989

GENETICS
#gene       nef
SUMMARY     #length 214 #molecular-weight 24259 #checksum 5341

Query Match      72.4% Score 42; DB 2; Length 214;
Best Local Similarity 55.6%; Pred. No. 1.80e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db      146 QOYTGPGT 154
      |||:|:|
OY      1 QOYNSAPDT 9

RESULT 15
ENTRY   TVHUF #type complete
TITLE   protein-tyrosine kinase (EC 2.7.1.112) fes/fps - human
ORGANISM #formal name Homo sapiens #common name man
DATE     28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
        03-Feb-1999
ACCESSIONS
REFERENCE A24673; A60188
AUTHORS   Roebroek, A.J.M.; Schalken, J.A.; Verbeek, J.S.; Van den
          Ouweland, A.M.W.; Onnekink, C.; Bloemers, H.P.J.; Van den
          Ven, W.J.M.
#journal EMBO J. (1985) 4:2897-2903
#title     The structure of the human c-fes/fps proto-oncogene.
#cross-references MUID:86055727
#accession A24673
#molecule_type DNA
#residues   1-822 #label ROE
#cross-references GB:X06292; GB:M14209; GB:M14589; NID:g31348;
          PID:g31349

REFERENCE
A60188
Alcalay, M.; Antolinf, F.; Van de Ven, W.J.; Lanfrancone, L.;
Gignani, F.; Pelicci, P.G.
#journal Oncogene (1990) 5:267-275
#title     Characterization of human and mouse c-fes cDNA clones and
          identification of the 5' end of the gene.
#cross-references MUID:90191711
#accession A60188
#molecule_type mRNA
#residues   1-718, 'S', 720-822 #label ALC
#cross-references GB:X32192; NID:g29890; PID:g29891
#note       the authors translated the codon TCC for residue 719 as
          Leu

GENETICS

```

```

#gene      GDB:FES
#cross-references GDB:119906; OMIM:190030
#map position 15q26.1-15q26.1
#introns   71/3; 129/3; 162/1; 223/2; 269/2; 309/2; 350/2; 412/3; 440/3;
          510/3; 51/3; 569/3; 609/2; 641/1; 682/2; 735/1; 776/1

FUNCTION
#description catalyzes the phosphorylation of a peptidyl tyrosine residue
          by ATP
CLASSIFICATION #superfamily protein-tyrosine kinase fps; protein kinase
          homology; SH2 homology
KEYWORDS       ATP; autophosphorylation; blocked amino end; lipoprotein;
          myristylation; phosphoprotein; phosphotransferase;
          proto-oncogene; transforming protein; tyrosine-specific
          protein kinase

FEATURE
2-822
460-545 #product protein-tyrosine kinase fes/fps #status
559-821 #predicted #label MAT\
567-575 #domain SH2 homology #label SH2\
2        #domain protein kinase homology #label KIN\
          #region protein kinase ATP-binding motif\
          #modified_site myristylated amino end (Gly) (in mature
          form) #status predicted\
          #active_site Lys #status predicted
SUMMARY     #length 822 #molecular-weight 93496 #checksum 7719

Query Match      72.4% Score 42; DB 1; Length 822;
Best Local Similarity 75.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db      266 ROYGSAPD 273
      |||:|:|
OY      1 QOYNSAPD 8

Search completed: Thu Sep 2 12:03:32 1999
Job time : 11 secs.

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MIRIS (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPSrch.p protein - protein database search, using Smith-Waterman algorithm
on on: Thu Sep 2 12:06:50 1999; Maspar time 1.37 Seconds
66.926 Million cell updates/sec
Tabular output not generated.

Title: >US-08-599-226-22
Description: (1-9) from US08599226.pep
Perfect Score: 58
Sequence: 1 QOYNAPDR 9

Scoring table:
PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A.COMB 2:5B.COMB 3:PCT9.COMB 4:backfilea1

Statistics: Mean 14.240; Variance 38.096; scale 0.374

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	45	77.6	107	2	US-08-477-Sequence 14, Applicat	3.44e+01
2	45	77.6	107	2	US-08-472-Sequence 14, Applicat	3.44e+01
3	45	77.6	107	2	US-08-082-Sequence 14, Applicat	3.44e+01
4	45	77.6	107	2	US-08-107-Sequence 14, Applicat	3.44e+01
5	45	77.6	108	1	US-08-488-Sequence 150, Applicat	3.44e+01
6	45	77.6	108	2	US-08-477-Sequence 150, Applicat	3.44e+01
7	45	77.6	108	2	US-08-646-Sequence 150, Applicat	3.44e+01
8	45	77.6	114	2	US-08-561-Sequence 43, Applicat	3.44e+01
9	45	77.6	114	3	PCT-US95-0Sequence 43, Applicat	3.44e+01
10	45	77.6	114	2	US-08-202-Sequence 25, Applicat	6.05e+01
11	45	74.1	107	2	US-08-107-Sequence 20, Applicat	6.05e+01
12	45	74.1	107	1	US-08-488-Sequence 156, Applicat	6.05e+01
13	45	74.1	107	2	US-08-477-Sequence 156, Applicat	6.05e+01
14	45	74.1	107	2	US-08-646-Sequence 156, Applicat	6.05e+01
15	45	74.1	107	2	US-08-477-Sequence 20, Applicat	6.05e+01
16	45	74.1	107	2	US-08-082-Sequence 20, Applicat	6.05e+01
17	45	74.1	107	2	US-08-472-Sequence 20, Applicat	6.05e+01
18	45	74.1	464	1	US-08-107-Sequence 2, Applicatio	6.05e+01
19	45	74.1	464	1	US-07-891-Sequence 2, Applicatio	6.05e+01
20	45	72.4	107	3	PCT-US95-0Sequence 87, Applicat	8.00e+01
21	45	72.4	107	2	US-08-899-Sequence 87, Applicat	8.00e+01
22	45	72.4	107	1	US-08-276-Sequence 87, Applicat	8.00e+01
23	45	72.4	107	2	US-08-899-Sequence 87, Applicat	8.00e+01

24	41	70.7	106	3	PCT-US95-0	Sequence 85, Applicat	1.06e+02
25	41	70.7 <th>106</th> <th>2</th> <th>US-08-899-</th> <th>Sequence 85, Applicat</th> <th>1.06e+02</th>	106	2	US-08-899-	Sequence 85, Applicat	1.06e+02
26	41	70.7 <th>106</th> <th>2</th> <th>US-08-276-</th> <th>Sequence 85, Applicat</th> <th>1.06e+02</th>	106	2	US-08-276-	Sequence 85, Applicat	1.06e+02
27	41	70.7 <th>106</th> <th>2</th> <th>US-08-899-</th> <th>Sequence 85, Applicat</th> <th>1.06e+02</th>	106	2	US-08-899-	Sequence 85, Applicat	1.06e+02
28	41	70.7 <th>107</th> <th>3</th> <th>PCT-US95-0</th> <th>Sequence 84, Applicat</th> <th>1.06e+02</th>	107	3	PCT-US95-0	Sequence 84, Applicat	1.06e+02
29	41	70.7 <th>107</th> <th>3</th> <th>PCT-US95-0</th> <th>Sequence 84, Applicat</th> <th>1.06e+02</th>	107	3	PCT-US95-0	Sequence 84, Applicat	1.06e+02
30	41	70.7 <th>107</th> <th>2</th> <th>US-08-276-</th> <th>Sequence 84, Applicat</th> <th>1.06e+02</th>	107	2	US-08-276-	Sequence 84, Applicat	1.06e+02
31	41	70.7 <th>107</th> <th>1</th> <th>US-08-899-</th> <th>Sequence 82, Applicat</th> <th>1.06e+02</th>	107	1	US-08-899-	Sequence 82, Applicat	1.06e+02
32	41	70.7 <th>107</th> <th>1</th> <th>US-08-276-</th> <th>Sequence 82, Applicat</th> <th>1.06e+02</th>	107	1	US-08-276-	Sequence 82, Applicat	1.06e+02
33	41	70.7 <th>107</th> <th>2</th> <th>US-08-899-</th> <th>Sequence 84, Applicat</th> <th>1.06e+02</th>	107	2	US-08-899-	Sequence 84, Applicat	1.06e+02
34	41	70.7 <th>107</th> <th>2</th> <th>US-08-899-</th> <th>Sequence 82, Applicat</th> <th>1.06e+02</th>	107	2	US-08-899-	Sequence 82, Applicat	1.06e+02
35	41	70.7 <th>107</th> <th>2</th> <th>US-08-899-</th> <th>Sequence 84, Applicat</th> <th>1.06e+02</th>	107	2	US-08-899-	Sequence 84, Applicat	1.06e+02
36	41	70.7 <th>112</th> <th>2</th> <th>US-08-276-</th> <th>Sequence 151, Applicat</th> <th>1.06e+02</th>	112	2	US-08-276-	Sequence 151, Applicat	1.06e+02
37	41	70.7 <th>112</th> <th>2</th> <th>PCT-US95-0</th> <th>Sequence 151, Applicat</th> <th>1.06e+02</th>	112	2	PCT-US95-0	Sequence 151, Applicat	1.06e+02
38	41	70.7 <th>112</th> <th>2</th> <th>US-08-899-</th> <th>Sequence 151, Applicat</th> <th>1.06e+02</th>	112	2	US-08-899-	Sequence 151, Applicat	1.06e+02
39	41	70.7 <th>112</th> <th>2</th> <th>US-08-899-</th> <th>Sequence 151, Applicat</th> <th>1.06e+02</th>	112	2	US-08-899-	Sequence 151, Applicat	1.06e+02
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42	40	69.0 <th>116</th> <th>2</th> <th>US-08-096-</th> <th>Sequence 183, Applicat</th> <th>1.39e+02</th>	116	2	US-08-096-	Sequence 183, Applicat	1.39e+02
43	40	69.0 <th>116</th> <th>1</th> <th>US-08-053-</th> <th>Sequence 183, Applicat</th> <th>1.39e+02</th>	116	1	US-08-053-	Sequence 183, Applicat	1.39e+02
44	40	69.0 <th>435</th> <th>1</th> <th>US-08-111-</th> <th>Sequence 16, Applicat</th> <th>1.39e+02</th>	435	1	US-08-111-	Sequence 16, Applicat	1.39e+02
45	40	69.0 <th>435</th> <th>1</th> <th>US-08-734-</th> <th>Sequence 2, Applicatio</th> <th>1.39e+02</th>	435	1	US-08-734-	Sequence 2, Applicatio	1.39e+02

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	107 AA.
ID	US-08-477-531B-14			
XX	xxxxxx			
AC				
XX				
DT				
XX				
DE	Sequence 14, Application US/08477531B			
XX				
CC	Sequence 14, Application US/08477531B			
CC	Patent No. 5821123			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Studnicka, Gary M.			
CC	TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)			
CC	NUMBER OF SEQUENCES: 67			
CC	CORRESPONDENCE ADDRESSES:			
CC	ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.			
CC	STREET: 1100 New York Ave., N.W., Suite 600			
CC	CITY: Washington			
CC	STATE: D.C.			
CC	COUNTRY: United States of America			
CC	ZIP: 20005-3934			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Patentin Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/477,531B			
CC	FILING DATE: 07-JUN-1995			
CC	CLASSIFICATION: 436			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: 08/107,669			
CC	FILING DATE: 13-AUG-1993			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: PCT/US92/10906			
CC	FILING DATE: 14-DEC-1992			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US 07/808,464			
CC	FILING DATE: 13-DEC-1991			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Michele A. Cimbalia			
CC	REGISTRATION NUMBER: 33,851			
CC	REFERENCE/DOCKET NUMBER: 0610.1000004/MAC			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: 202/371-2600			
CC	TELEFAX: 202/371-2540			

CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11430 MW: 65173 CN;

Query Match 77.6%; Score 45; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYSSPXT 97
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||| |:
OY 1 QOYNSAPDT 9

RESULT 2
ID US-08-472-788A-14 STANDARD: PRT: 107 AA.

XX xxxxxx

DE Sequence 14, Application US/08472788A

CC Sequence 14, Application US/08472788A

CC Patent No. 5770196

CC GENERAL INFORMATION:

CC APPLICANT: Studnicka, Gary M.

CC TITLE OF INVENTION: Modified Antibody Variable Domains

CC NUMBER OF SEQUENCES: 89

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

CC STREET: 1100 New York Ave., N.W., Suite 600

CC CITY: Washington

CC STATE: D.C.

CC COUNTRY: USA

CC ZIP: 20005-3934

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/472,788A

CC FILING DATE: 07-JUN-1995

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/082,842

CC FILING DATE: 23-JUN-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US92/10906

CC FILING DATE: 14-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/808,464

CC FILING DATE: 13-DEC-1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Cimbal, Michele A.

CC REGISTRATION NUMBER: 33,851

CC REFERENCE/DOCKET NUMBER: 0610.1000003

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 202/371-2600

CC TELEFAX: 202/371-2540

CC TELEX:

CC INFORMATION FOR SEQ ID NO: 14:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 107 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 107 AA: 11430 MW: 65173 CN;

Query Match 77.6%; Score 45; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYSSPXT 97
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||| |:
OY 1 QOYNSAPDT 9

RESULT 3
ID US-08-082-842A-14 STANDARD: PRT: 107 AA.

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DE Sequence 14, Application US/08082842A

CC Sequence 14, Application US/08082842A

CC Patent No. 5869619

CC GENERAL INFORMATION:

CC APPLICANT: Studnicka, Gary M.

CC TITLE OF INVENTION: Modified Antibody Variable Domains

CC NUMBER OF SEQUENCES: 89

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

CC STREET: 1100 New York Ave., N.W., Suite 600

CC CITY: Washington

CC STATE: D.C.

CC COUNTRY: USA

CC ZIP: 20005-3934

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/082,842A

CC FILING DATE: 23-JUN-1993

CC CLASSIFICATION: 530

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US92/10906

CC FILING DATE: 14-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/808,464

CC FILING DATE: 13-DEC-1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Cimbal, Michele A.

CC REGISTRATION NUMBER: 33,851

CC REFERENCE/DOCKET NUMBER: 0610.1000002

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 202/371-2600

CC TELEFAX: 202/371-2540

CC TELEX:

CC INFORMATION FOR SEQ ID NO: 14:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 107 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 107 AA: 11430 MW: 65173 CN;

Query Match 77.6%; Score 45; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYSSPXT 97
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||| |:
OY 1 QOYNSAPDT 9

RESULT 4
ID US-08-107-669D-14 STANDARD: PRT: 107 AA.

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AC xxxxxx
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DT
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DE Sequence 14, Application US/08107669D
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CC Sequence 14, Application US/08107669D
CC Patent No. 5766886
CC GENERAL INFORMATION:
CC APPLICANT: Studnicka, Gary M.
CC TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
CC NUMBER OF SEQUENCES: 67
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
CC STREET: 1100 New York Ave., N.W., Suite 600
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: United States of America
CC ZIP: 20005-3934
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/107,669D
CC FILING DATE: 13-AUG-1993
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10906
CC FILING DATE: 14-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/808,464
CC FILING DATE: 13-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Michele A. Cimbala
CC REGISTRATION NUMBER: 33,851
CC REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202/371-2600
CC TELEFAX: 202/371-2540
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11430 MW; 65173 CN;
Query Match 77.6%; Score 45; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYGSSEPT 97
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QY 1 QOYNSAPDT 9

RESULT 5
ID US-08-488-113B-150 STANDARD; PRT; 108 AA.
XX xxxxxx
AC
DT
XX
DE Sequence 150, Application US/08488113B
XX
CC Sequence 150, Application US/08488113B
CC Patent No. 5744580
CC GENERAL INFORMATION:
CC APPLICANT: Better, Marc D.
CC APPLICANT: Carroll, Stephen F.

CC APPLICANT: Studnicka, Gary M.
CC TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
CC NUMBER OF SEQUENCES: 169
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: McAndrews, Held & Malloy, Ltd.
CC STREET: 500 West Madison Street, 34th floor
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60661
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/488,113B
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/425,336
CC FILING DATE: 18-APR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/064,691
CC FILING DATE: 12-MAY-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/988,430
CC FILING DATE: 09-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/901,707
CC FILING DATE: 19-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/787,567
CC FILING DATE: 04-NOV-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: McNicholas, Janet M.
CC REGISTRATION NUMBER: 32,918
CC REFERENCE/DOCKET NUMBER: 110220507/200-70.P3.C2A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/707-8889
CC TELEFAX: 312/707-9155
CC TELEX: 650 388-1248
CC INFORMATION FOR SEQ ID NO: 150:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11530 MW; 67356 CN;
Query Match 77.6%; Score 45; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 90 QOYGSSEPT 98
||| |||
QY 1 QOYNSAPDT 9

RESULT 6
ID US-08-477-484B-150 STANDARD; PRT; 108 AA.
XX xxxxxx
AC
DT
XX
DE Sequence 150, Application US/08477484B
XX
CC Sequence 150, Application US/08477484B
CC Patent No. 5756699
CC GENERAL INFORMATION:

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CC APPLICANT: Better, Marc D.
CC APPLICANT: Carroll, Stephen F.
CC APPLICANT: Studnka, Gary M.
CC TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
CC TITLE OF INVENTION: Proteins
CC NUMBER OF SEQUENCES: 169
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: McAndrews, Held & Malloy, Ltd.
CC STREET: 500 West Madison Street, 34th floor
CC City: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60661
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,484B
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/425,336
CC FILING DATE: 18-APR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/064,691
CC FILING DATE: 12-MAY-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/988,430
CC FILING DATE: 09-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/901,707
CC FILING DATE: 19-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/787,567
CC FILING DATE: 04-NOV-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: McNicholas, Janet M.
CC REGISTRATION NUMBER: 32,918
CC REFERENCE/DOCKET NUMBER: 110220507/200-70.P3.C2A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/707-8889
CC TELEFAX: 312/707-9155
CC TELEX: 650 388-1248
CC INFORMATION FOR SEQ ID NO: 150:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11530 MW; 67356 CN;
CC
DB 90 Q0YGS5PXT 98
    ||| | | |
QY 1 Q0YNSAPDT 9

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CC Patent No. 5837491
CC GENERAL INFORMATION:
CC APPLICANT: Better, Marc D.
CC APPLICANT: Carroll, Stephen F.
CC APPLICANT: Studinka, Gary M.
CC TITLE OF INVENTION: Immunotoxins Complicing Ribosome-Inactivating
CC CC TITLE OF INVENTION: Proteins
CC NUMBER OF SEQUENCES: 173
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: McAndrews, Held & Malloy, Ltd.
CC STREET: 500 West Madison Street, 34th floor
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60661
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/646,360
CC FILING DATE: 13-MAY-1996
CC CLASSIFICATION:
CC CLASSIFICATION: 330
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/05348
CC FILING DATE: 12-MAY-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/064,691
CC FILING DATE: 12-MAY-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/988,430
CC FILING DATE: 09-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/901,707
CC FILING DATE: 19-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/787,567
CC FILING DATE: 04-NOV-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: McNicholas, Janet M.
CC REGISTRATION NUMBER: 32,918
CC REFERENCE/DOCKET NUMBER: 200-70.P4
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/707-8889
CC TELEFAX: 312/707-9155
CC TELEX: 650 388-1248
CC INFORMATION FOR SEO ID NO: 150:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC CC
CC SEQUENCE 108 AA; 11530 MM; 67356 CN;
SQ
Query Match 77.6%; Score 45; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 90 QOYGSSPXT 98
QY 1 QOYNSAPDT 9
RESULT 8
ID US-08-561-521-43 STANDARD; PRT; 114 AA.
AC xxxxxx
XX
XX
DE Sequence 43, Application US/08561521

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XX Sequence 43, Application US/08561521
CC Patent No. 5840299
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
CC TITLE OF INVENTION: Adhesion Molecule VIA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/561,521
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/186,269A
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 43:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 114 AA; 12436 MW; 76800 CN;
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Query Match 77.6%; Score 45; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 95 QOYNSLPE 102
OY 1 QOYNSAPD 8
RESULT 9
ID PCT-US95-01219-43 STANDARD; PRT: 114 AA.
XX PC-9501219
AC xxxxxx
XX
XX
XX
XX
XX Sequence 43, Application PC/TUS9501219
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
CC TITLE OF INVENTION: Adhesion Molecule VIA-4
CC NUMBER OF SEQUENCES: 45

CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/186,269
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 43:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 114 AA; 12436 MW; 76800 CN;
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Query Match 77.6%; Score 45; DB 3; Length 114;
Best Local Similarity 75.0%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 95 QOYNSLPE 102
OY 1 QOYNSAPD 8
RESULT 10
ID US-08-202-047-25 STANDARD; PRT: 114 AA.
XX US-08-202-047-25
AC xxxxxx
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XX
XX Sequence 25, Application US/08202047
CC Patent No. 5800815
CC GENERAL INFORMATION:
CC APPLICANT: CHESNOT, Robert W.
CC APPLICANT: POLLEY, Margaret J.
CC APPLICANT: PAULSON, James C.
CC APPLICANT: JONES, S. Tarran
CC APPLICANT: SALDANHA, Jose W.
CC APPLICANT: BENDIG, Mary M.
CC TITLE OF INVENTION: Antibodies to P-selectin and Their Uses
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/202,047
CC FILING DATE: 25-FEB-1994
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smlich, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14137-77
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 25:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..114
CC OTHER INFORMATION: /label= human_kappa_1
SQ SEQUENCE 114 AA; 12391 MW; 76746 CN;

Query Match 77.6%; Score 45; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 3.44e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 94 QOYNSLPE 101
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1
QOYNSAPD 8

RESULT 11
ID US-08-107-669D-20 STANDARD: PRT; 107 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 20, Application US/08107669D
CC
CC Sequence 20, Application US/08107669D
CC Patent No. 5766886
CC GENERAL INFORMATION:
CC APPLICANT: Studnicka, Gary M.
CC TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
CC NUMBER OF SEQUENCES: 67
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
CC STREET: 1100 New York Ave., N.W., Suite 600
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: United States of America
CC ZIP: 20005-3934
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/107,669D
CC FILING DATE: 13-AUG-1993
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10906
CC FILING DATE: 14-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/808,464
CC FILING DATE: 13-DEC-1991

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Michele A. Cimbala
CC REGISTRATION NUMBER: 33,851
CC REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202/371-2600
CC TELEFAX: 202/371-2540
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11658 MW; 69708 CN;

Query Match 74.1%; Score 43; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 6.05e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYSTPYT 97
111111
1
QOYNSAPDT 9

RESULT 12
ID US-08-488-113B-156 STANDARD: PRT; 107 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 156, Application US/08488113B
CC
CC Sequence 156, Application US/08488113B
CC Patent No. 5744580
CC GENERAL INFORMATION:
CC APPLICANT: Better, Marc D.
CC APPLICANT: Carroll, Stephen F.
CC APPLICANT: Studnicka, Gary M.
CC TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
CC NUMBER OF SEQUENCES: 169
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: McAndrews, Held & Malloy, Ltd.
CC STREET: 500 West Madison Street, 34th floor
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60661
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/488,113B
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/425,336
CC FILING DATE: 18-APR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/064,691
CC FILING DATE: 12-MAY-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/988,430
CC FILING DATE: 09-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/901,707
CC FILING DATE: 19-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/787,567
CC FILING DATE: 04-NOV-1991

CC ATTORNEY/AGENT INFORMATION:
CC NAME: McNicholas, Janet M.
CC REGISTRATION NUMBER: 32,918
CC REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/707-9155
CC TELEFAX: 312/707-8889
CC TELE: 650 388-1248
CC INFORMATION FOR SEQ ID NO: 156:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11729 MW; 69508 CN;
SQ

Query Match 74.1%; Score 43; DB 1; Length 107;
Best Local Similarity 66.7%; Pred. No. 6.05e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 89 QOYSTPXT 97
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QY 1 QOYNSAPDT 9

RESULT 13
ID US-08-477-484B-156 STANDARD; PRT: 107 AA.
XX xxxxxx
XX

Sequence 156, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
CC APPLICANT: Better, Marc D.
CC APPLICANT: Carroll, Stephen F.
CC APPLICANT: Studlika, Gary M.
CC TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
CC TITLE OF INVENTION: Proteins
CC NUMBER OF SEQUENCES: 169
CC CORRESPONDENCE ADDRESSES:
CC ADDRESS: McAndrews, Held & Malloy, Ltd.
CC STREET: 500 West Madison Street, 34th floor
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60661
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,484B
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/425,336
CC FILING DATE: 18-APR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/064,691
CC FILING DATE: 12-MAY-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/988,430
CC FILING DATE: 09-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/901,707
CC FILING DATE: 19-JUN-1992
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/787,567
CC FILING DATE: 04-NOV-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: McNicholas, Janet M.
CC REGISTRATION NUMBER: 32,918
CC REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/707-9155
CC TELEFAX: 312/707-9155
CC TELE: 650 388-1248
CC INFORMATION FOR SEQ ID NO: 156:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11729 MW; 69508 CN;
SQ

Query Match 74.1%; Score 43; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 6.05e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 89 QOYSTPXT 97
|||:|:|
QY 1 QOYNSAPDT 9

RESULT 14
ID US-08-646-360-156 STANDARD; PRT: 107 AA.
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Sequence 156, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
CC APPLICANT: Better, Marc D.
CC APPLICANT: Carroll, Stephen F.
CC APPLICANT: Studlika, Gary M.
CC TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
CC TITLE OF INVENTION: Proteins
CC NUMBER OF SEQUENCES: 173
CC CORRESPONDENCE ADDRESSES:
CC ADDRESS: McAndrews, Held & Malloy, Ltd.
CC STREET: 500 West Madison Street, 34th floor
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60661
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/646,360
CC FILING DATE: 13-MAY-1996
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/05348
CC FILING DATE: 12-MAY-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/064,691
CC FILING DATE: 12-MAY-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/988,430
CC FILING DATE: 09-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/901,707

 M P E R E H
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MParch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Sep 2 12:05:31 1999; Maspar time 2.15 Seconds
 Tabular output not generated. 118.412 Million cell updates/sec

Title: >US-08-599-226-22
 Description: (1-9) from US0859226.pep
 Perfect Score: 58
 Sequence: 1 QOYNSAPDT 9

Scoring table: PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 trawisprot

Statistics: Mean 21.288; Variance 19.808; scale 1.075

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description	Pred. No.
1	46	79.3	109	1 KY3B_HUMAN IG KAPPA CHAIN V-III R	6.94e+01
2	45	77.6	109	1 KY3D_HUMAN IG KAPPA CHAIN V-III R	1.28e+00
3	43	74.1	340	1 HXDA_HUMAN HOMEOBOX PROTEIN HOX-D	4.19e+00
4	43	74.1	340	1 HXDA_MOUSE HOMEOBOX PROTEIN HOX-D	4.19e+00
5	43	74.1	464	1 VGIL_MOUSE GIL PROTEIN	4.19e+00
6	43	74.1	715	1 ERF2_CANAL EUKARYOTIC PEPTIDE CHA	4.19e+00
7	43	74.1	1733	1 RPBI_YEAST DNA-DIRECTED RNA POLIM	4.19e+00
8	42	72.4	214	1 NEF_SIVGB NEGATIVE FACTOR (F-PRO	7.48e+00
9	42	72.4	822	1 FES_HUMAN PROTO-ONCOGENE TYROSIN	1.32e+01
10	41	70.7	56	1 Y6K_TNVA HYPOTHEICAL 6.2 KD PR	1.32e+01
11	41	70.7	112	1 KY1U_HUMAN IG KAPPA CHAIN V-I REG	1.32e+01
12	41	70.7	183	1 VRBD_ECOLI HYPOTHEICAL 19.6 KD P	1.32e+01
13	41	70.7	266	1 PIR5_MOUSE URIDINE 5'-MONOPHOSPHA	1.32e+01
14	41	70.7	335	1 YMT1_YEAST HYPOTHEICAL 38.2 KD P	1.32e+01
15	41	70.7	409	1 Y4DM_RHISN HYPOTHEICAL 45.3 KD P	1.32e+01
16	41	70.7	467	1 INVO_MOUSE INVOLUCRIN	1.32e+01
17	41	70.7	480	1 PYR5_HUMAN URIDINE 5'-MONOPHOSPHA	1.32e+01
18	40	69.0	108	1 KY3A_HUMAN IG KAPPA CHAIN V-III R	2.30e+01
19	40	69.0	109	1 KY3G_HUMAN IG KAPPA CHAIN V-III R	2.30e+01
20	40	69.0	129	1 KY3M_HUMAN IG KAPPA CHAIN PRECURS	2.30e+01
21	40	69.0	233	1 SOML_ONCKE SOMATOLACTIN PRECURSOR	2.30e+01
22	40	69.0	295	1 CFYQ_CYAME CFYQ PROTEIN HOMOLOG	2.30e+01
23	40	69.0	359	1 MKK2_DROME MAP KINASE-ACTIVATED P	2.30e+01

24	40	69.0	382	1 GBS2_DROME GUANINE NUCLEOTIDE-BIN	2.30e+01
25	40	69.0	385	1 GBS1_DROME GUANINE NUCLEOTIDE-BIN	2.30e+01
26	40	69.0	470	1 GLG1_SOLTU GLUCOSE-1-PHOSPHATE AD	2.30e+01
27	40	69.0	476	1 CBPH_HUMAN CARBOXYPEPTIDASE H PRE	2.30e+01
28	40	69.0	497	1 VE2_HPVAZ REGULATOR PROTEIN E2	2.30e+01
29	40	69.0	553	1 YMB8_YEAST HYPOTHEICAL 64.4 KD P	2.30e+01
30	40	69.0	628	1 V7OK_TYMWV 69 KD PROTEIN	2.30e+01
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35	40	69.0	1641	1 RA54_HUMAN X-LINKED HELICASE II (2.30e+01
36	39	67.2	109	1 YCCK_HAEIN HYPOTHEICAL PROTEIN H	3.96e+01
37	39	67.2	194	1 VP30_ASPE7 PHOSPHOPROTEIN P30	3.96e+01
38	39	67.2	196	1 VP32_ASPE7 PHOSPHOPROTEIN P32	3.96e+01
39	39	67.2	271	1 YSM4_CABEL HYPOTHEICAL 30.6 KD P	3.96e+01
40	39	67.2	287	1 YAHF_ECOLI HYPOTHEICAL 32.3 KD P	3.96e+01
41	39	67.2	315	1 SOX2_CHICK TRANSCRIPTION FACTOR S	3.96e+01
42	39	67.2	321	1 YX11_CABEL HYPOTHEICAL 29.9 KD P	3.96e+01
43	39	67.2	560	1 YECO_YEAST HYPOTHEICAL 61.3 KD P	3.96e+01
44	39	67.2	1077	1 XINY_CLOTM ENDO-1,4-BETA-XYLANASE	3.96e+01
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ALIGNMENTS

RESULT 1	ID	KY3B_HUMAN	STANDARD;	PRT;	109 AA.
AC	P01620;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)				
DE	IG KAPPA CHAIN V-III REGION (SIE).				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE; 82046598.				
RA	ANDREWS D.W., CAPRA J.D.:				
RT	"Amino acid sequence of the variable regions of light chains from two				
RT	Idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa				
RT	group."				
RL	BIOCHEMISTRY 20:5816-5823(1981).				
CC	-I- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN				
CC	ACTIVITY.				
DR	PIR; A01892; K3HUSI.				
DR	PEAM; PF00047; 1q; 1.				
DR	HSSP; P01789; 2MCP.				
KM	IMMUNOGLOBULIN V REGION.				
FT	DISULFID 23 89				
FT	NON_TER 109 109				
SO	SEQUENCE 109 AA; 11775 MW; 0085DSD CRC32;				
Query Match					
Best Local Similarity	79.3%;				
Matches	6; Conservative				
	2; Mismatches				
	1; Indels				
	0; Gaps				
	0;				
Db	90 QOYNSAPDT 98				
QY	1 QOYNSAPDT 9				
RESULT 2	ID	KY3D_HUMAN	STANDARD;	PRT;	109 AA.
AC	P01622;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)				
DE	IG KAPPA CHAIN V-III REGION (TI).				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				

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RN [1]
RP SEQUENCE.
RX MEDLINE: 72188439.
RA SUTER L., BARNIKOL H.U., MATANABE S., HILSCHMANN N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT 11). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HUT1.
DR PFAM: PF00047; 19; 1.
DR HSSP: P01789; 2MCP.
KM IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; D03795B1 CRC32;

Query Match 77.6%; Score 45; DB 1; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.28e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 90 QOYGSSEPT 98
OY 1 QOYNSAPDT 9

RESULT 3
ID HXDA.HUMAN STANDARD; PRT; 340 AA.
AC P28358;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE HOMEOBOX PROTEIN HOX-D10 (HOX-4D) (HOX-4E).
GN HOXD10 OR HOXD.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPINAL CORD.
RX MEDLINE: 92097538.
RA ZAPPAVIGNA V., RENUCCI A., IZPISUA-BELMONTE J.-C., URIER G.,
RA PESCHLE C., DOUBOULE D.;
RT "HOX4 genes encode transcription factors with potential auto- and
RT cross-regulatory capacities."
RL EMBO J. 10:4177-4187(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92307679.
RA REDLINE R.W., WILLIAMS A.J., PATTERSON P., COLLINS T.;
RT "Human HOXA4: a gene strongly expressed in the adult male and female
RT urogenital tracts."
RL GENOMICS 13:425-430(1992).
RN [3]
RP SEQUENCE OF 266-331 FROM N.A.
RX MEDLINE: 90098876.
RA ACAMORA D., DESPOSITO M., FAIELLA A., PANNESSE M., MIGLIACCIO E.,
RA MORELLI F., STORNALUONO A., NIGRO V., SIMEONE A., BONCINELLI E.;
RT "The human HOX gene family."
RL NUCLEIC ACIDS RES. 17:10385-10402(1989).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE ADULT MALE AND
CC FEMALE UROGENITAL TRACTS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LIMB BUDS.
CC -1- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
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CC -----
DR EMBL: X59373; G32393; -.
DR PIR: S18650; S18650.
DR PIR: S14930; S14936.
DR PIR: A42008; A42008.
DR MIM: 142984; -.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS50071; HOMEOBOX_2; 1.
DR PFAM: PF00046; homeobox; 1.
DR HSSP: P02833; ISAN.
DR TRANSFAC: T01425; -.
KM HOMEOBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
KW TRANSCRIPTION REGULATION.
FT DNA_BIND 266 325 HOMEOBOX.
FT CONFLICT 150 150 R -> G (IN REF. 2).
FT CONFLICT 189 189 Q -> E (IN REF. 2).
SQ SEQUENCE 340 AA; 38509 MW; D69D5F4C CRC32;

Query Match 74.1%; Score 43; DB 1; Length 340;
Best Local Similarity 50.0%; Pred. No. 4.19e+00;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 164 QOYNSPE 171
OY 1 QOYNSAPD 8

RESULT 4
ID HXDA.MOUSE STANDARD; PRT; 340 AA.
AC P28359;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HOMEOBOX PROTEIN HOX-D10 (HOX-4.5) (HOX-5.3).
GN HOXD10 OR HOXD-10 OR HOX-4.5.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92224884.
RA RENUCCI A.G.P., ZAPPAVIGNA V., ZAKANY J., IZPISUA-BELMONTE J.-C.,
RA BUENRI K., DOUBOULE D.;
RT "Comparison of mouse and human HOX-4 complexes defines conserved
RT sequences involved in the regulation of Hox-4.4."
RL EMBO J. 11:1459-1468(1992).
RN [2]
RP SEQUENCE OF 266-325 FROM N.A.
RX MEDLINE: 89356622.
RA DOLE P., DOUBOULE D.;
RT "Two gene members of the murine HOX-5 complex show regional and cell-
RT type specific expression in developing limbs and gonads."
RL EMBO J. 8:1507-1515(1989).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LIMB BUDS.
CC -1- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
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DR EMBL: X62669; G51415; -
 DR EMBL: X14715; -; NOT_ANNOTATED_CDS.
 DR EMBL: M21046; -; NOT_ANNOTATED_CDS.
 DR PIR: S09399; S09399.
 DR PIR: S09370; S09370.
 DR PIR: S20879; S20879.
 DR MGD: M61:96202; HOXD10.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 DR PRAM: PF00046; homeobox; 1.
 DR HSP: P02833; ISAN.
 DR TRANSFAC: T01157; -
 KM HOMEOBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
 KM TRANSCRIPTION REGULATION.
 FT DNA_BIND 266 HOMEBOX
 FT SEQUENCE 340 AA; 38358 MW; 17AACCF6 CRC32;

Query Match 74.1%; Score 43; DB 1; Length 340;
 Best Local Similarity 50.0%; Pred. No. 4.19e+00;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

164 QYNSPQ 171

1 QYNSAPD 8

RESULT 5

ID VG1L_AMEPV STANDARD; PRT; 464 AA.

AC P29817;

DT 01-APR-1993 (REL. 25, CREATED)

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DE G1L PROTEIN.

OS AMSACTA MOOREI ENTOMOPOXVIRUS (AMEPV).

OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; ENTOMOPOXVIRINAE;

CC ENTOMOPOXVIRUS B.

CC [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 92046310.

RA HALL R.L.; MOYER R.W.;

RT "Identification, cloning, and sequencing of a fragment of Amsacta

RT moorei entomopoxvirus dna containing the spheroidin gene and three

RT vaccinia virus-related open reading frames.";

RL J. VIROL. 65:6516-6527(1991).

CC -1- SIMILARITY: TO VACCINIA VIRUS PROTEIN 17.

CC -----

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CC EMBL: M7182; G209632; -

DR PIR: A41561; W2VZG1.

DR LATE PROTEIN.

SK SEQUENCE 464 AA; 55541 MW; DD876FB5 CRC32;

Query Match 74.1%; Score 43; DB 1; Length 464;
 Best Local Similarity 62.5%; Pred. No. 4.19e+00;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

308 HYNSTPNT 315

2 QYNSAPD 9

RESULT 6

ID ERF2_CANAL STANDARD; PRT; 715 AA.

AC 013354;

DT 15-JUL-1998 (REL. 36, CREATED)

DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE EURARYOTIC PEPTIDE CHAIN RELEASE FACTOR GTP-BINDING SUBUNIT (ERF2)
 DE (TRANSLATION RELEASE FACTOR 3) (ERF3) (ERF-3).
 GN SUP35.
 OS CANDIDA ALBICANS (YEAST).
 CC EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
 CC CANDIDACEAE; CANDIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-2005E;
 RA RESENDE C.G.; FERREIRA P.C.; TUTTE M.F.; DUARTE J.B.;
 RA SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: INVOLVED IN TRANSLATION TERMINATION. STIMULATES THE
 ACTIVITY OF ERF1. BINDS GUANINE NUCLEOTIDES.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC ERF3 SUBFAMILY.
 CC -----

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CC EMBL: AF020554; G2582369; -

DR PROSITE: PS00301; EFACOR_GTP; 1.

DR PRAM: PF00009; GTP_EFTU; 1.

DR HSSP: P02990; 1FTU.

KW PROTEIN BIOSYNTHESIS; REPEAT; PHOSPHORYLATION; GTP-BINDING.

FT DOMAIN 5 128 SEVERAL SORT OF REPEATS.

FT DOMAIN 129 285 CHARGED.

FT SIMILAR 286 715 TO ELONGATION FACTORS EF-1.

FT NP_BIND 299 306 GTP (BY SIMILARITY).

FT NP_BIND 376 380 GTP (BY SIMILARITY).

FT NP_BIND 438 441 GTP (BY SIMILARITY).

FT MOD_RES 373 373 PHOSPHORYLATION (BY SIMILARITY).

FT SEQUENCE 715 AA; 79074 MW; BC4A2398 CRC32;

Query Match 74.1%; Score 43; DB 1; Length 715;
 Best Local Similarity 75.0%; Pred. No. 4.19e+00;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

113 QYNSPQ 120

1 QYNSAPD 8

RESULT 7

ID RPB1_YEAST STANDARD; PRT; 1733 AA.

AC P04050; Q12364;

DT 01-NOV-1986 (REL. 03, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (B220).

GN RPB1 OR RPO21 OR RPB220 OR SUA8 OR YDL140C OR D2150.

OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).

CC EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
 CC SACCCHAROMYCETACEAE; SACCCHAROMYCES.

CC [1]

RP SEQUENCE FROM N.A.

RX STRAIN-A364A;

RA MEDLINE: 85282617.

RA ALITSON L.A.; MOYLE M.; SHALES M.; INGLES C.J.;

RT "Extensive homology among the largest subunits of eukaryotic and

RT prokaryotic RNA polymerases.";

RL CELL 42:599-610(1985).

CC [2]

RP SEQUENCE FROM N.A.

RC STRAIN-S288C / FY1679;

RX MEDLINE: 97127826.

RA WOELFEL S., HANEMAN V., SALUZ H.P.;
 RT "Analysis of a 26,756 bp segment from the left arm of yeast
 chromosome IV."
 RL YEAST 12:1549-1554(1996).
 RN [3]
 RP SEQUENCE OF 1669-1733 FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE: 95377607.
 RA CROMAN J.E. JR., WALLACE J.C.;
 RT "The gene encoding the biotin-apolipoprotein ligase of *Saccharomyces cerevisiae*."
 RL FEBS MICROBIOL. LETT. 130:221-230(1995).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE + RNA(N).
 CC -1- SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE II.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED. THE PHOSPHORYLATION ACTIVATES POL2.
 CC -1- THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S AND 5.8S RRNA GENES.
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X03128; G4388; -;
 DR EMBL: X96876; E239065; -;
 DR EMBL: 274188; E253056; -;
 DR EMBL: U27182; G886082; -;
 DR PIR: A00692; RNBYZL;
 DR SGD: L0001744; RPO21.
 DR PROSITE: P500115; RNA_POL_II_REPEAT; 22.
 DR PFAM: PF00623; RNA_POL_A; 1.
 KW TRANSFERRING: DNA-DIRECTED RNA POLYMERASE; TRANSCRIPTION; ZINC; REPEAT;
 KM DNA-BINDING; NUCLEAR PROTEIN; PHOSPHORYLATION; ZINC-FINGER.
 FT 2N-FING 67 83 C2H2-TYPE (POTENTIAL).
 FT DOMAIN 1544 1719 CARBOXYL-TERMINAL 7-RESIDUE REPEATS.
 FT VARIANT 1653 1659 MISSING (IN STRAIN A364A).
 FT CONFLICT 1514 1514 A -> V (IN REF. 1).
 FT CONFLICT 1524 1524 G -> A (IN REF. 1).
 FT CONFLICT 1601 1601 T -> M (IN REF. 1).
 SQ SEQUENCE 1733 AA; 191610 MW; BB65D7EE CRC32;
 Query Match 74.18; Score 43; DB 1; Length 1733;
 Best Local Similarity 85.78; Pred. No. 4.19e+00;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 4 OQYSSAP 10
 1111111
 QY 1 OQYNSAP 7
 RESULT 8
 ID NEF-SIVGB STANDARD; PRT; 214 AA.
 AC P22378;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KD PROTEIN) (3'ORF).
 NEF.
 OS SIMIAN IMMUNODEFICIENCY VIRUS (ISOLATE GB1).
 GN
 OS VIROSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90015168.
 RA TSUTSUMOTO H., HASEGAWA A., MAKI N., FUKASAWA M., MIURA T., SPEIDEL S., COOPER R.W., MORIYAMA E.N., GOTOHORI T., HAYAMI M.;
 RT "Sequence of a novel simian immunodeficiency virus from a wild-caught African mandrill."
 RL NATURE 341:539-541(1989).
 CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES. IT SEEM TO DOWN REGULATE THE CD4(T4) ANTIGEN.
 CC -1- THIS IS AN AFRICAN MANDRILL ISOLATE.
 CC -----
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 CC -----
 DR EMBL: M27470; G334691; -;
 DR PIR: S28085; S28085.
 DR PFAM: PF00469; F-protein; 1.
 DR HSP: P03406; IEFN.
 KW AIDS; MYRISTYLATION; GTP-BINDING.
 FT LIPID 2 MYRISTATE (BY SIMILARITY).
 SQ SEQUENCE 214 AA; 24259 MW; 3FD6B666 CRC32;
 Query Match 72.48; Score 42; DB 1; Length 214;
 Best Local Similarity 53.68; Pred. No. 7.48e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Db 146 OQYTGPGT 154
 1111111
 QY 1 OQYNSAPDT 9
 RESULT 9
 ID FES-HUMAN STANDARD; PRT; 822 AA.
 AC P07332;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT 01-NOV-1993 (REL. 32, LAST ANNOTATION UPDATE)
 DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES).
 GN FES OR FPS.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90191711.
 RA ALCALAY M., ANTOLINI F., VAN DE VEN W.J., LANFRANCONE L., GRIGNANI F., PELICCI P.G.;
 RT "Characterization of human and mouse c-fes cDNA clones and RT identification of the 5' end of the gene."
 RL ONCOGENE 5:267-275(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86055727.
 RA ROEBROEK A.J.M., SCHALKEN J.A., VERBEEK J.S., VAN DEN Ouweland A.M.W., ONNERINK C., BLOEMERS H.P.J., VAN DE VEN W.J.M.;
 RT "The structure of the human c-fes/fps proto-oncogene."
 RL EMBO J. 4:2897-2903(1985).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE FES/FPS SUBFAMILY.
 CC -----
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DR ECGENE; EG12799; YRBD.
 KW HYPOTHETICAL PROTEIN; SIGNAL.
 FT SIGNAL 1 28
 FT CHAIN 29 183
 SQ SEQUENCE 183 AA: 19576 MW: 8525888 CRC32;

Query Match 70.7%; Score 41; DB 1; Length 183;
 Best Local Similarity 66.7%; Pred. No. 1.32e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYNHPT 96
 1 11111
 QY 1 QOYNAPDT 9

RESULT 13
 ID PYR5 MOUSE STANDARD: PRT: 266 AA.
 AC P13439
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
 PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10) AND OROTIDINE 5'-PHOSPHATE
 DECARBOXYLASE (EC 4.1.1.23)) (FRAGMENT).
 GN UMP.
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC ROSENTIA; SCUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 86140253.
 RA OHNSTEDE C.A., LANGDON S.D., CHAE C.B., JONES M.E.;
 RT "Expression and sequence analysis of a cDNA encoding the
 RT orotidine-5'-monophosphate decarboxylase domain from Ehrlich ascites
 RT uridylylate synthase.";
 RL J. BIOL. CHEM. 261:4276-4282(1986).

CC -1- CATALYTIC ACTIVITY: OROTIDINE-5'-PHOSPHATE + PYROPHOSPHATE -
 CC -1- CATALYTIC ACTIVITY: OROTIDINE-5'-PHOSPHATE - UMP + CO(2).
 CC -1- PATHWAY: FIFTH AND SIXTH STEP IN PYRIMIDINE BIOSYNTHESIS.
 CC -----
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EMBL; M29395; G387502; -.
 DR PIR; A25323; DCM5OP.
 DR PROSITE; PS00103; PUR_PYR_PR.TRANSFER; PARTIAL.
 DR PROSITE; PS00156; OMPDECASE; 1.
 DR PFAM; PF00215; OMPdecase; 1.
 KW PYRIMIDINE BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME; TRANSFERASE;
 KW GLYCOSYLTRANSFERASE; LYASE; DECARBOXYLASE.
 FT DOMAIN 1 5
 FT NON_TER 1 1
 FT DOMAIN <1 5
 FT ACT_SITE 6 266
 FT ACT_SITE 99 99
 FT ACT_SITE 99 99
 SO SEQUENCE 266 AA: 28866 MW: 6063052 CRC32;

Query Match 70.7%; Score 41; DB 1; Length 266;
 Best Local Similarity 62.5%; Pred. No. 1.32e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 215 QOYNAPDT 222
 1 11111
 QY 1 QOYNAPDT 8

RESULT 14
 ID YML1_YEAST STANDARD: PRT: 335 AA.

AC Q04212;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 38.2 KD PROTEIN IN SUB1-ANGRI INTERGENIC REGION.
 GN YMR041C OR YMR532.06C.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCAROMYCETALES;
 CC SACCAROMYCETACEAE; SACCAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA ODELL C., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.;
 RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
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DR EMBL; Z48502; G695721; -.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 335 AA: 38220 MW: 4475049A CRC32;

Query Match 70.7%; Score 41; DB 1; Length 335;
 Best Local Similarity 44.4%; Pred. No. 1.32e+01;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 26 QOYDEPES 34
 1 11111
 QY 1 QOYNAPDT 9

RESULT 15
 ID Y4DM_RHISN STANDARD: PRT: 409 AA.
 AC P55412;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 45.3 KD PROTEIN Y4DM.
 GN Y4DM.
 OS RHIZOBIUM SP. (STRAIN NGR234).
 CC PLASMID SWM PNGR234A.
 CC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
 CC RHIZOBIACEAE; RHIZOBIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 97305956.
 RA FRIERBERG C.A., FELLAY R., BAIRROCH A., BROUGHTON W.J., ROSENTHAL A.,
 RA PERRIER X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes.";
 RL NATURE 387:394-401(1997).
 CC -1- SIMILARITY: TO E.COLI HIPA AND H.INFLUENZAE HI0665.
 CC -1- SIMILARITY: TO Y4ME.

CC -----
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DR EMBL; AEO00069; G2182356; -.
 KW HYPOTHETICAL PROTEIN; PLASMID.
 SQ SEQUENCE 409 AA: 45310 MW: ADF1F05D CRC32;

Query Match 70.7%; Score 41; DB 1; Length 409;
 Best Local Similarity 50.0%; Pred. No. 1.32e+01;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 176 QOYSGVPE 183
|||:|:
QY 1 QOYNSAPD 8

Search completed: Thu Sep 2 12:05:39 1999
Job time : 8 secs.

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 W27581
 (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:02:43 1999; MasPar time 3.39 Seconds
 Tabular output not generated. 56.476 Million cell updates/sec

Title: >US-08-599-226-22
 Description: (1-9) from US08599226.pep
 Perfect Score: 58
 Sequence: 1 QQYNSAPDR 9

Scoring table:
 PAM 150
 Gap 15

Searched: 170751 seqs, 21266608 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq35
 1:part1 2:part3 3:part4 4:part5 5:part6 6:part7 7:part8
 8:part9 9:part10 10:part11 11:part12 12:part13 13:part14
 14:part15 15:part16 16:part17 17:part18 18:part19
 19:part20 20:part21 21:part22 22:part23 23:part24
 24:part25 25:part26 26:part27 27:part28 28:part29
 29:part30 30:part31 31:part32 32:part33 33:part34
 34:part35 35:part36 36:part37 37:part38 38:part39
 39:part39

Statistics: Mean 15.023; Variance 39.392; scale 0.381
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	58	100.0	9	27	W27581	Anti-TNF-alpha antibo
2	46	79.3	12	3	R15366	Ig idiotype determin
3	46	79.3	150	29	W40069	Human monoclonal anti
4	46	79.3	287	29	W40071	Human H11-scFv const
5	46	79.3	304	29	W40070	Human H11-scFv const
6	45	77.6	107	31	W58493	Human kappa light cha
7	45	77.6	107	7	R38593	Human lambda light ch
8	43	74.1	107	31	W58499	Human kappa light cha
9	43	74.1	107	7	R38599	Human heavy chain sub
10	43	74.1	464	5	R29651	Human heavy chain sub
11	43	74.1	464	10	R55572	AMEPY Spheroidin asso
12	43	74.1	464	28	W41297	AMEPY Spheroidin asso
13	42	72.4	107	10	R54308	Anti-HIV gp120 immuno
14	42	72.4	107	19	W01266	VL region of HIV neut
15	42	72.4	214	2	R10281	Simian immunodeficien
16	41	70.7	106	28	W31724	Alpha light chain eml

Result ID	Score	Query Match	Length	ID	Description	Pred. No.
17	41	70.7	106	10	R54306	Anti-HIV gp120 immuno
18	41	70.7	107	19	W01264	VL region of HIV neut
19	41	70.7	107	19	W01261	VL region of HIV neut
20	41	70.7	107	10	R54305	Anti-HIV gp120 immuno
21	41	70.7	107	19	W01263	VL region of HIV neut
22	41	70.7	107	10	R54303	Anti-HIV gp120 immuno
23	41	70.7	112	10	R54279	Anti-HIV gp41 immunog
24	41	70.7	112	19	W01324	VL of Fab' SS 41 8, b
25	41	70.7	120	11	R61240	Monoclonal antibody L
26	40	69.0	9	27	W27577	Anti-TNF-alpha antibo
27	40	69.0	9	27	W27576	Anti-TNF-alpha antibo
28	40	69.0	9	27	W27570	Anti-TNF-alpha antibo
29	40	69.0	9	27	W27574	Anti-TNF-alpha antibo
30	40	69.0	100	5	W80140	Light chain CDR3 pep
31	40	69.0	100	5	R25324	Consensus human rh
32	40	69.0	107	6	R30770	Consensus human rh
33	40	69.0	109	39	W84096	Human V kappa subgrou
34	40	69.0	109	9	R47041	Sequence of the conse
35	40	69.0	116	31	W54010	Human Anti-CD4 antibo
36	40	69.0	116	20	W03948	DNA fragment vk65.8
37	40	69.0	116	7	R38650	Human V-kappa fragmen
38	40	69.0	116	28	W41146	Human V-kappa fragmen
39	40	69.0	116	36	W62184	Human V-kappa fragmen
40	40	69.0	116	12	R62930	Human DNA vkappa65.8
41	40	69.0	129	7	R38672	Human V-kappa vk65.8
42	40	69.0	234	27	W17478	Hormone-like protein.
43	40	69.0	470	13	R66240	ADPpP large subunit.
44	40	69.0	470	4	R20255	Sequence encoded by t
45	40	69.0	470	13	R77847	ADP-glucose-pyrophosp

ALIGNMENTS

RESULT 1
 ID W27581 standard; peptide; 9 AA.

AC W27581:
 DE 19-MAR-1998 (first entry)
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW Light chain; complementarily determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; Obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226. mti
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labrowsky B,
 PI Manxovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI; 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20, Page 71, 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L939 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC scleriosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.59e+00;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gqygsapdt 9
 |||||
 QY 1 QOYNSAPDT 9

RESULT 2
 R15366 standard; Protein: 12 AA.
 AC R15366:

DE 05-MAR-1992 (first entry)
 DE Ig idiotype determinant PS13.
 KW Rheumatoid factor; RF; S1e; antigen; light chain; CDR; IGH.
 OS Synthetic.

FT Key Location/Qualifiers
 FT region 1 /note="residue belonging to adjacent framework
 FT region"

PN US5068177-A.
 PD 26-NOV-1991.
 PE 05-AUG-1985: 762698.
 PR 28-DEC-1983: US-566172.
 PR 05-AUG-1985: US-762698.
 PA (SCRI-) SCRIPPS CLINIC RES.
 PI Carson DA, Fong S, Chen PP;
 PI WPI: 91-368612/50.
 PT Synthetic polypeptide(s) for inducing anti-idiotypic antibodies -
 PT useful for treating autoimmune, endocrine- and
 PT rheumatic-diseases and myasthenia gravis
 PS Claim 23: Page 43; 44pp: English.
 CC The sequence is as reported by Capra et al. [(Proc. Natl. Acad.
 CC Sci. USA, 71:4032 (1974); and Proc. Natl. Acad. Sci. USA, 78:
 CC 3699 (1981)].
 CC PSL3 means as follows:
 CC 'P' designates that the code named material is a synthetic peptide;
 CC the second letter designates the corresp. parent protein (S1e 88-99);
 CC the third letter designates the light (L) chain;
 CC the numeral designates the CDR, the idiotype antigenic determinant
 CC of the IGM-rheumatoid factor.
 CC See also R15365-74 and R15375.
 SQ Sequence 12 AA;

Query Match 79.3%; Score 46; DB 3; Length 12;
 Best Local Similarity 66.7%; Pred. No. 5.51e+01;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2 gqygsapdt 10
 |||||
 QY 1 QOYNSAPDT 9

RESULT 3
 W40069 standard; Protein: 150 AA.

DE 29-MAY-1998 (first entry)
 DE Human monoclonal antibody H11 protein variable region H chain.
 KW H11: monoclonal antibody; Mab; C-antigen; variable region heavy chain;
 KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
 KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
 KW malignant melanoma; adenocarcinoma; small cell lung carcinoma.

OS Homo sapiens.
 PN WO9744461-A2.
 PD 27-NOV-1997.
 PE 22-MAY-1997: 008962.
 PR 22-MAY-1996: US-657449.
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 PI Dan MD, Kaplan HA, Malti PK;
 PI WPI: 98-018515/02.
 DR N-PSDB: V10111.
 PT Antigen binding fragment from monoclonal antibody, H11 - allows
 PT tumour specific detection and treatment of neoplasia

PS Claim 1: Page 87-88; 126pp: English.
 CC This sequence represents the human H11 monoclonal antibody variable (V)
 CC region heavy (H) chain which specifically recognises the C-antigen. Such
 CC an antigen binding fragment may be used for treating a patient with
 CC neoplasia. It is especially useful in the detection of lymphomas and
 CC leukaemias where the tumour cells bearing the C antigen are circulating
 CC in the patients bloodstream. The polynucleotide sequence may be used as a
 CC primer or a probe and the encoded protein may be used in a vaccine or
 CC for gene therapy. The human monoclonal antibody (Mab), designated H11,
 CC specifically recognises cancerous cells. H11 is specific for
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
 CC prostate adenocarcinoma. The antigen binding fragment may also be used
 CC to detect C-antigen in a sample.
 SQ Sequence 150 AA;

Query Match 79.3%; Score 46; DB 29; Length 150;
 Best Local Similarity 66.7%; Pred. No. 5.51e+01;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 114 gqygsapdt 122
 |||||
 QY 1 QOYNSAPDT 9

RESULT 4
 W40071 standard; Protein: 287 AA.

DE 29-MAY-1998 (first entry)
 DE Human H11-scFv construct dimer forming protein.
 KW H11: monoclonal antibody; Mab; C-antigen; variable region heavy chain;
 KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
 KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
 KW malignant melanoma; adenocarcinoma; small cell lung carcinoma;
 KW single chain variable region; scFv.

OS Synthetic.
 OS Homo sapiens.
 PN WO9744461-A2.
 PD 27-NOV-1997.
 PE 22-MAY-1997: 008962.
 PR 22-MAY-1996: US-657449.
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 PI Dan MD, Kaplan HA, Malti PK;
 PI WPI: 98-018515/02.
 DR N-PSDB: V10119.
 PT Antigen binding fragment from monoclonal antibody, H11 - allows
 PT tumour specific detection and treatment of neoplasia

PS Claim 5: Page 95-96; 126pp: English.
 CC This sequence represents a human H11 monoclonal antibody single chain V
 CC region fragment (H11-scFv) construct which is capable of forming
 CC dimers. This construct is used to determine the ability of H11-scFv
 CC antibody fragments to bind specifically to the C-antigen on cancer cells.
 CC Such antigen binding fragments may be used for treating a patient with
 CC neoplasia. It is especially useful in the detection of lymphomas and
 CC leukaemias where the tumour cells bearing the C antigen are circulating
 CC in the patients bloodstream. The polynucleotide sequence may be used as a
 CC primer or a probe and the encoded protein may be used in a vaccine or for
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,
 CC specifically recognises cancerous cells. H11 is specific for
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
 CC prostate adenocarcinoma.

SQ Sequence 287 AA;
 Query Match 79.3%; Score 46; DB 29; Length 287;
 Best Local Similarity 66.7%; Pred. NO. 5.51e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 113 qgyssspct 121
 |||1:1:1
 QY 1 QOYNSAPDT 9
 RESULT 5
 ID W40070 standard; Protein: 304 AA.
 AC W40070;
 DT 29-MAY-1998 (first entry)
 DE Human H11-scfv construct monomer forming protein.
 KW H11 monoclonal antibody; Mb; C-antigen; variable region heavy chain;
 V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
 KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
 malignant melanoma; adenocarcinoma; small cell lung carcinoma;
 single chain variable region; scfv.
 Synthetic.
 OS Homo sapiens.
 PN WO9744461-A2.
 PD 27-NOV-1997.
 PR 22-MAY-1997; U08962.
 PF 22-MAY-1996; US-657449.
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 PI Dan MD, Kaplan HA, Mafti PK;
 DR N-PADB: V10118.
 PT Antigen binding fragment from monoclonal antibody, H11 - allows
 tumour specific detection and treatment of neoplasia
 PS Claim 5; Page 92-93; 126pp; English.
 CC This sequence represents a human H11 monoclonal antibody single chain V
 region fragment (H11-scfv) construct which is capable of forming
 monomers. This construct is used to determine the ability of H11-scfv
 antibody fragments to bind specifically to the C-antigen on cancer cells.
 CC Such antigen binding fragments may be used for treating a patient with
 neoplasia. It is especially useful in the detection of lymphomas and
 leukemias where the tumour cells bearing the C antigen are circulating
 in the patients bloodstream. The polynucleotide sequence may be used as a
 primer or a probe and the encoded protein may be used in a vaccine or for
 gene therapy. The human monoclonal antibody (Mb), designated H11,
 specifically recognises cancerous cells. H11 is specific for
 glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
 lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
 prostate adenocarcinoma.
 Sequence 304 AA;
 Query Match 79.3%; Score 46; DB 29; Length 304;
 Best Local Similarity 66.7%; Pred. NO. 5.51e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 113 qgyssspct 121
 |||1:1:1
 QY 1 QOYNSAPDT 9
 RESULT 6
 ID W58493 standard; protein: 107 AA.
 AC W58493;
 DT 18-AUG-1998 (first entry)
 DE Human kappa light chain subgroup 3 consensus sequence hK3.
 KW humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
 depletion; cytotoxic; immunocongulate; fusion protein; psoriasis;
 autoimmune disease; rheumatoid arthritis; type I diabetes.
 Synthetic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 96 /note= "not specified"
 PN US5770196-A.

PD 23-JUN-1998. 472788.
 PF 07-JUN-1995; US-082842.
 PR 23-JUN-1993; US-082842.
 PR 13-DEC-1991; US-808464.
 PR 14-DEC-1992; WO-010906.
 PR 07-JUN-1995; US-472788.
 PA (XOMA) XOMA CORP.
 PI Studnicka GM;
 DR WPI: 98-376744/32.
 PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
 with humanised variable regions
 PS Disclosure; Column 51-54; 77pp; English.
 CC A method has been developed of depleting CD5+ cells in an animal. The
 method comprises administering a cytotoxic protein containing a modified
 immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
 molecule or an immunocongulate or fusion protein containing an anti-CD5
 Ig molecule, and where the modified Ig variable domain comprises at
 least one of (a) a modified light chain variable region (see W58478 or
 W58480), and (b) a modified heavy chain variable region (see W58479 or
 W58481), where W58478 and W58479 are humanised forms of the H65 light
 and heavy chain variable domains with low risk amino acid substitutions
 [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
 W58481 are humanised forms of the H65 light and heavy chain variable
 domains with moderate risk amino acid substitutions and are present in
 humanised H65 antibody h63 (ATCC HB 11206). The method is useful for
 treating autoimmune diseases, especially systemic lupus erythematosus,
 rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
 represents a consensus amino acid sequence for light chain subgroups of
 human antibody variable domains, from the present invention.
 Sequence 107 AA;
 Query Match 77.6%; Score 45; DB 31; Length 107;
 Best Local Similarity 66.7%; Pred. NO. 7.32e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 89 qgyssspct 97
 |||1:1:1
 QY 1 QOYNSAPDT 9
 RESULT 7
 ID R38593 standard; peptide: 107 AA.
 AC R38593;
 DT 28-OCT-1993 (first entry)
 DE Human lambda light chain subgroup 3 (hL3).
 KW Antibody; variable domain; light; L; heavy; H; consensus;
 affinity; antigen; immunogenicity; humanisation; framework.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 96 /note= "residue conserved in less than 50% of the
 known sequences of hL3"
 PN WO9311794-A.
 PD 24-JUN-1993.
 PR 14-DEC-1992; U10906.
 PR 13-DEC-1991; US-808464.
 PA (XOMA) XOMA CORP.
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 DR WPI: 93-213827/26.
 PT Antibodies prep. used for treatment of auto-immune diseases - by
 replacement of critical residues to reduce immunogenicity but
 retain binding affinity, etc.
 PS Claim 2; Page 93-94; 160pp; English.
 CC The consensus amino acid sequences for the subgroups of light
 chains (hK1 - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 -
 R38592, hL3 - R38593, hL6 - R38594, hK4 - R38595, hL4 - R38596,
 and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
 hH2 - R38600) of human variable domains may be used to prepare, for
 example, a modified mouse antibody variable domain that retains the
 affinity of the natural domain for antigen while exhibiting reduced
 immunogenicity in humans.
 CC Unlike other methods of humanisation, which advocate the
 replacement of entire antibody framework regions with those of human

CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 107 AA;

Query Match 77.6%; Score 45; DB 7; Length 107;
Best Local Similarity 66.7%; Pred. No. 7.32e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 89 qgysspxt 97
|||:|:|
QY 1 QQYNSAPDT 9

RESULT 8
ID W58499 standard; protein; 107 AA.
AC W58499;
PT 18-AUG-1998 (first entry)
DE Human kappa light chain subgroup 4 consensus sequence hK4.
KW Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunocongulate; fusion protein; psoriasis;
KW autoimmune disease; rheumatoid arthritis; type I diabetes.
OS Synthetic.
FH Homo sapiens.
FT Key Location/Qualifiers
FT MISC_difference 96 /note= "not specified"
FT MISC_difference 104 /note= "not specified"
FT US5770196-A.
PN 23-JUN-1998.
PF 07-JUN-1995; 472788.
PR 23-JUN-1993; US-082842.
PR 13-DEC-1991; US-808464.
PR 14-DEC-1992; WO-010906.
PR 07-JUN-1995; US-472788.
PA (XOMA) XOMA CORP.
PI Studnicka GM;
DR WPI: 98-376744/32.
PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
PT with humanised variable regions
PS Disclosure: Column 57-58; 77pp; English.
CC A method has been developed of depleting CD5+ cells in an animal. The
CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC molecule or an immunocongulate or fusion protein containing an anti-CD5
CC Ig molecule, and where the modified Ig variable domain comprises at
CC least one of (a) a modified light chain variable region (see W58478 or
CC W58480), and (b) a modified heavy chain variable region (see W58479 or
CC W58481), where W58478 and W58479 are humanised forms of the H65 light
CC and heavy chain variable domains with low risk amino acid substitutions
CC [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
CC W58481 are humanised forms of the H65 light and heavy chain variable
CC domains with moderate risk amino acid substitutions and are present in
CC humanised H65 antibody h63 (ATCC HB 11206). The method is useful for
CC treating autoimmune diseases, especially systemic lupus erythematosus,
CC rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
CC represents a consensus amino acid sequence for light chain subgroups of
CC human antibody variable domains, from the present invention.
SQ Sequence 107 AA;

Query Match 74.1%; Score 43; DB 31; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.28e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 89 qgysspxt 97
|||:|:|
QY 1 QQYNSAPDT 9

RESULT 9
ID R38599 standard; peptide; 107 AA.

AC R38599;
DE 28-OCT-1993 (first entry) 1 (hhl).
PT Human heavy chain subgroup 1 (hhl).
KW Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
FH Key Location/Qualifiers
FT MISC_difference 96 /note= "residue conserved in less than 50% of the
FT MISC_difference 104 known sequences of hhl"
FT MISC_difference 104 /note= "residue conserved in less than 50% of the
FT MISC_difference 104 known sequences of hhl"
FT W09311794-A.
PN 24-JUN-1993.
PF 14-DEC-1992; U10906.
PR 13-DEC-1991; US-808464.
PA (XOMA) XOMA CORP.
PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
DR WPI: 93-213827/26.
PT Antibodies prep. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
PS Claim 2; Page 98-99; 160pp; English.
CC The consensus amino acid sequences for the subgroups of light
CC chains (hK1 - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 -
CC R38592, hL3 - R38593, hL6 - R38594, hK4 - R38595, hL4 - R38596,
CC hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
CC hH2 - R38600) of human variable domains may be used to prepare, for
CC example, a modified mouse antibody variable domain that retains the
CC affinity of the natural domain for antigen while exhibiting reduced
CC immunogenicity in humans.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
SQ Sequence 107 AA;

Query Match 74.1%; Score 43; DB 7; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.28e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 89 qgysspxt 97
|||:|:|
QY 1 QQYNSAPDT 9

RESULT 10
ID R29651 standard; protein; 464 AA.
AC R29651;
DE 12-FEB-1993 (first entry)
DE AMEPY Spheroidin associated protein GIL.
KW Entomopoxvirus; non-essential; regulatory sequences; vector.
OS Amsacta moorei.
PN W09214818-A.
PD 03-SEP-1992.
PF 12-FEB-1992; U00855.
PR 19-FEB-1991; US-657584.
PR 30-JAN-1992; US-827685.
PA (UYFL) UNIV FLORIDA.
PI Grudl ME, Hall RL, Moyer RW;
DR WPI: 92-316172/38.
N-PSDB: Q28301.
PT New viral vectors and chimeric vaccines - comprise entomopoxvirus
PT expression system contg. spheroidin or thymidine kinase sequences
PS Disclosure: Fig 2; 110pp; English.
CC The sequences given in R29646-51 are encoded by a DNA fragment derived
CC from the Entomopoxvirus Amsacta moorei (AMEPY) around the spheroidin
CC DNA sequence. The open reading frames encode the spheroidin protein
CC itself and also other structural or regulatory genes associated with
CC spheroidin. BPV spheroidin has no significant amino acid homology to

CC any previously reported protein. It is a non-essential protein which
 CC makes the coding region desirable as a site for the insertion of
 CC exogenous DNA. The spheroidin gene is naturally expressed at high
 CC levels. Small fragments of the surrounding DNA can be used as
 CC regulatory sequences if placed in operative association with foreign
 CC DNA.

SO Sequence 464 AA;

Query Match 74.1%; Score 43; DB 5; Length 464;

Best Local Similarity 62.5%; Pred. No. 1.28e+02; Indels 0; Gaps 0;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 308 hynstpt 315

OY 2 QYNSAPDR 9

RESULT 11
 ID R55572 standard; Protein; 464 AA.
 R55572;

18-JAN-1995 (first entry)

AmPV spheroidin GIL.

KW Spheroidin; gene expression; vector; insect cell culture;

OS Amascta moorei entomopoxvirus.

PN MO9413812-A.

PD 23-JUN-1994.

PF 07-DEC-1993; U11907.

PR 07-DEC-1992; US-991867.

PA (UYFL) UNIV FLORIDA.

PI Gruidl ME, Hall RL, Moyer RW;

DR WPI: 94-217887/26.

DR N-PSDB: 066812.

PT New entomopoxvirus polynucleotide sequences, proteins and vectors

PT - are used for expression of heterologous proteins in both insect

PT and mammalian host cells

PS Disclosure; Page 66-67; 118pp; English.

CC The sequence of the Amascta moorei entomopoxvirus spheroidin gene

CC and its flanking regions is given in 066797. The protein encoded

CC by GIL OR of this sequence was determined. The spheroidin gene

CC can be used as the location for the insertion of heterologous DNA

CC in insect and mammalian expression systems.

SO Sequence 464 AA;

Query Match 74.1%; Score 43; DB 10; Length 464;

Best Local Similarity 62.5%; Pred. No. 1.28e+02; Indels 0; Gaps 0;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

308 hynstpt 315

OY 2 QYNSAPDR 9

RESULT 12
 ID W41297 standard; Protein; 464 AA.
 W41297;

20-MAY-1998 (first entry)

DE AmPV entomopoxvirus spheroidin protein GIL.

KW Entomopoxvirus; spheroidin gene; AmPV; thymidine kinase; promoter;

KW Insect control; viral vaccine.

OS Amascta moorei.

PN US5721352-A.

PD 24-FEB-1998.

PF 22-NOV-1993; 107755.

PR 22-NOV-1993; US-107755.

PR 19-FEB-1991; US-657584.

PR 30-JAN-1992; US-827685.

PR 12-FEB-1992; WO-000855.

PA (UYFL) UNIV FLORIDA RES FOUND.

PI Gruidl ME, Hall RL, Moyer RW;

DR WPI: 98-168476/15.

DR N-PSDB: V14507, V14517.

PT New entomopoxvirus nucleic acid sequences - used in DNA constructs

PT and vectors for expression of heterologous genes in, e.g. insect
 PT cells

PS Disclosure; Columns 39-42; 55pp; English.

CC This sequence is encoded by the Amascta moorei entomopoxvirus (AmPV)

CC spheroidin gene, which is an example of the gene of the

CC invention, which encodes a 115 kDa protein. EPV spheroidin and

CC thymidine kinase promoters can be used in DNA constructs and vectors for

CC expression of heterologous genes in insects or mammalian cells,

CC e.g. vectors containing Bacillus thuringiensis toxin genes for use in

CC insect control, or recombinant vaccinia or swinepox viruses for use as

CC viral vaccines.

SO Sequence 464 AA;

Query Match 74.1%; Score 43; DB 28; Length 464;

Best Local Similarity 62.5%; Pred. No. 1.28e+02; Indels 0; Gaps 0;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 308 hynstpt 315

OY 2 QYNSAPDR 9

RESULT 13

ID R54308 standard; protein; 107 AA.

AC R54308;

DT 10-NOV-1994 (first entry)

DE Anti-HIV gp120 immunoglobulin light chain variable region b30.

KW Human Immunodeficiency Virus; HIV1; glycoprotein gp120; epitope;

KW neutralisation; monoclonal antibody; kappa light chain;

RW variable region; framework; complementarity determining region.

OS Homo sapiens.

FT Key

FT region

FT 1.21

FT /label= FR1

FT 22.33

FT /label= CDRI

FT 34.48

FT /label= FR2

FT 49.55

FT /label= CDR2

FT 56.87

FT /label= FR3

FT 88.96

FT /label= CDR3

FT 97.107

FT /label= FR4

FT region

PN MO9407922-A.

PD 14-APR-1994.

PF 30-SEP-1993; U09328.

PR 30-SEP-1992; US-954148.

PA (SCRT) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 94-135516/16.

PT New human monoclonal antibodies neutralising HIV - react with

PT gp120 or gp41 and nucleic acid encoding them, useful for in vitro

PT or in vitro diagnosis and for passive immuno-therapy

PS Example; Page 178; 248pp; English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR

CC amplification using primers specific for heavy and light chain

CC variable regions. The amplification products were inserted into a

CC distronic vector to produce a library of fragments. E.coli XL1

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAb regions on their surface. Panning

CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VR region sequence R54308 is from a gp120-

CC specific clone.

SO Sequence 107 AA;

Query Match 72.4%; Score 42; DB 10; Length 107;

Best Local Similarity 71.4%; Pred. No. 1.70e+02; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 88 qgynasp 94

OY 1 COYNSAP 7

RESULT 14
ID W01266 standard; Protein: 107 AA.

AC W01266;

DT 28-JAN-1997 (first entry)

DE VL region of HIV neutralizing MAb, clone B30.

KW Heavy chain; light chain; variable region; VH: monoclonal antibody;

KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;

KW Virus infectivity assay; precursor gp160; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

FT Key

FT region

FT region

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Query Match 72.4%; Score 42; DB 19; Length 107;
Best Local Similarity 71.4%; Pred. No. 1.70e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 88 gqyhasp 94
OY 1 COYNSAP 7

RESULT 15
ID R10281 standard; Protein: 214 AA.
AC R10281;
DT 04-APR-1991 (first entry)
DE Simian immunodeficiency virus nef protein.
KW SIVmd; HIV; AIDS; vaccine; PSMH103.
OS Simian immunodeficiency virus.
PN J02299587-A.
PD 11-DEC-1990.
PE 11-MAY-1989; 116129.
PR 11-MAY-1989; JP-116129.
PA (TOFU) TONEN CORP.
DR WPI: 91-027566/04.

DR N-PSDB; Q10203.
PT New complementary DNA to RNA gene of simian immuno-deficiency
PT virus - used for preparing vaccine and diagnosis agent for AIDS
PS Clam 2; Fig 4; 14pp, Japanese.
CC SIV proteins may be produced from an E.coli expression system
CC transformed with plasmid PSMH103.
CC These may be used in diagnosis, treatment, and development of a vaccine
CC against AIDS, as the sequence has the same structure as HIV-1 (but
CC lacking the vpx gene).
SQ Sequence 214 AA;

Query Match 72.4%; Score 42; DB 2; Length 214;
Best Local Similarity 55.6%; Pred. No. 1.70e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 146 gqytcgpt 154
OY 1 COYNSAPDT 9

Search completed: Thu Sep 2 12:03:03 1999
Job time : 20 secs.

(TM)

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In - protein database search, using Smith-Waterman algorithm

t generated.

1 QOYNSAPDT 9

PAM 150

179066 seqs, 54579741 residues

Listing first 45 summaries

13:sp_vertebrate 14:sp_virus

Mean 20.711; Variance 19.361; scale 1.070

ved by analysis of the total score distribution.

SUMMARIES

9.0	198	2	P70935	SDHC, SDHA, SDHB GENES	3.51e+01
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45	39	67.2	2241	5	015850	L3162.1	PROTEIN.	6.12e+01
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ALIGNMENTS

SQ SEQUENCE 559 AA; 63609 MW; 265E97F2 CRC32;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

[illegible]

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Query Match      79.3%      Score 46; DB 5; Length 446;
Best Local Similarity 62.5%; Pred. No. 9.91e-01;
Matches      5; Conservative      3; Mismatches      0; Indels      0; Gaps      0

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Query Match          75.9%  Score 44:  DB 5:  Length 434;
Best Local Similarity 50.0%  Pred. No. 3,39e+00;
Matches          4;  Conservative          4;  Mismatches 0;  Indels 0;  Gaps 0;

Db          82  QOYHPSPE 89
            |||:::|:
QY          1  QOYNSAPD 8

RESULT
ID  092315          PRELIMINARY;          PRT; 1726 AA.
AC  092315;
DT  01-FEB-1997 (TREMBL.REL. 02, CREATED)
DT  01-FEB-1997 (TREMBL.REL. 02, LAST SEQUENCE UPDATE)
DT  01-NOV-1998 (TREMBL.REL. 08, LAST ANNOTATION UPDATE)
DE  RNA POLYMERASE II LARGE SUBUNIT.
GN  RPO21.
OS  SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
OC  EIKAROTIA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES: SACCCHAROMYCETALES;
OC  SACCCHAROMYCETACEAE: SACCCHAROMYCES

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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 85282617.
RX ALLISON L.A., MOTIE M., SHALES M., INGLES C.J.:
RT "Extensive homology among the largest subunits of eukaryotic and
RT prokaryotic RNA polymerases.";
RL CELL 42:599-610(1985).
RN [2]
RN SEQUENCE FROM N.A.
RP INGLES C.J.:
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: M1190; G172492;
DR SCD: L0001744; RPO21.
DR PFAM: PF00623; RNA_POL_A: 1.
SQ SEQUENCE 1726 AA; 190962 MW; C278A93A CRC32;

Query Match 74.1%; Score 43; DB 3; Length 1726;
Best Local Similarity 85.7%; Pred. No. 6.18e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 4 OQYSSAPT 10
OY 1 OQYNSAPT 7

RESULT 7
ID 079455 PRELIMINARY: PRT: 16 AA.
AC 079455:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LIGHT-CHAIN COMPLEMENTARITY-DETERMINING REGION 3 MRAA
DE (CLONE 14), PARTIAL CDS (FRAGMENT).
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRUSES: RETROVIRIDAE; LENTIVIRUS.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 92052225.
RA BURTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
RA LERNER R.A.:
RT "A large array of human monoclonal antibodies to type 1 human
RT immunodeficiency virus from combinatorial libraries of asymptomatic
RT seropositive individuals.";
RL PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
DR EMBL: M80720; G327942;
FT NON_TER 1
FT 16
SQ SEQUENCE 16 AA; 1883 MW; 5462C8DD CRC32;

Query Match 70.7%; Score 41; DB 14; Length 16;
Best Local Similarity 77.8%; Pred. No. 1.99e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 4 OQYNSAPT 12
OY 1 OQYNSAPT 9

RESULT 8
ID 079461 PRELIMINARY: PRT: 16 AA.
AC 079461:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LIGHT-CHAIN COMPLEMENTARITY-DETERMINING REGION 3 MRAA
DE (CLONE 31), PARTIAL CDS (FRAGMENT).
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRUSES: RETROVIRIDAE; LENTIVIRUS.
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 92052225.
RA BURTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
RA LERNER R.A.;

"A large array of human monoclonal antibodies to type 1 human
RT immunodeficiency virus from combinatorial libraries of asymptomatic
RT seropositive individuals.";
RL PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
DR EMBL: M80726; G327954;
FT NON_TER 1
FT 16
SQ SEQUENCE 16 AA; 1883 MW; 5462C8DD CRC32;

Query Match 70.7%; Score 41; DB 14; Length 16;
Best Local Similarity 77.8%; Pred. No. 1.99e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 4 OQYNSAPT 12
OY 1 OQYNSAPT 9

RESULT 9
ID 083941 PRELIMINARY: PRT: 56 AA.
AC 083941:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE COMPLETE GENOME.
OS OLIVE LATENT VIRUS 1.
OC VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; SOBEMOVIRUS.
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-CITRUS:
RX MEDLINE: 96265016.
RA GRIECO F., SAYINO V., MARTELLI G.P.:
RT "Nucleotide sequence of the genome of a citrus isolate of olive
RT latent virus 1.";
RL ARCH. VIROL. 141:825-838(1996).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-CITRUS:
RA GRIECO F.:
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85989; E145110;
SQ SEQUENCE 56 AA; 6268 MW; 985E185B CRC32;

Query Match 70.7%; Score 41; DB 14; Length 56;
Best Local Similarity 55.6%; Pred. No. 1.99e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 36 OQYHSPST 44
OY 1 OQYNSAPT 9

RESULT 10
ID 088610 PRELIMINARY: PRT: 56 AA.
AC 088610:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE (NEBRASKA) RNA-DEPENDENT RNA POLYMERASE.
GN P6.2.
OS TOBACCO NECROSIS VIRUS (TNV).
OC VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; NECROVIRUS.
RN [1]
RN SEQUENCE FROM N.A.
RP ZHANG L.:
RA THESIS (1993), UNIVERSITY OF NEBRASKA, LINCOLN, NB.
DR EMBL: I04261; E95571;
SQ SEQUENCE 56 AA; 6226 MW; 83A12A8D CRC32;

Query Match 70.7%; Score 41; DB 14; Length 56;
Best Local Similarity 55.6%; Pred. No. 1.99e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 36 QOYHSPST 44
 ID 111:111
 QY 1 QOYNSAPDT 9

RESULT 11
 ID 033074 PRELIMINARY: PRT: 174 AA.

AC 033074;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 18.2 KD PROTEIN.

GN MLC8628.01.

OS MYCOBACTERIUM LEPRAE.

OC BACTERIA: FIRMICUTES: ACTINOBACTERIA: ACTINOBACTERIDAE:

OC ACTINOMYCETALES: CORINEBACTERIINEAE: MYCOBACTERIACEAE: MYCOBACTERIUM.

RN [1]

RP SEQUENCE FROM N.A.

RA EIGLMEIER K., GARNIER T., DE ROSSI E., FSIHI H., COLE S.T.;

RT SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RP [2]

RP SEQUENCE FROM N.A.

RA EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.;

RT "Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae."

RT MOL. MICROBIOL. 7:197-206(1993).

RL EMBL: Y14967; E339078; -.

DR HYPOTHETICAL PROTEIN

KW

SO SEQUENCE 174 AA; 18217 MW; A6B6A827 CRC32;

Query Match 70.7%; Score 41; DB 2; Length 174;
 Best Local Similarity 62.5%; Pred. No. 1.99e+01;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 111 QOYHSPST 118
 ID 111:111:111

QY 1 QOYNSAPDT 8

RESULT 12
 ID 026445 PRELIMINARY: PRT: 228 AA.

AC 026445;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE LOX4-ULTRABITHORAX/ABDOMINAL-A HOMOLOG.

RN [1]

RP HIRUDO MEDICINALIS (MEDICINAL LEECH).

OC EUKARYOTA: METAZOA: ANNELIDA: CLITELLATA: HIRUDINIDA: HIRUDINEA;

OC ARYNCBODELLIDA: HIRUDINIFORMES; HIRUDINIDAE; HIRUDO.

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE: 95370922.

RT WONG V.Y., AISMENBERG G.O., GAN W.B., MACAGNO E.R.;

RT "The leech homeobox gene lox4 may determine segmental differentiation of identified neurons."

RT J. NEUROSCI. 15:5551-5559(1995).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL: S79240; G1086953; -.

DR PROSITE: PS00027; HOMEBOX_1; 1.

DR PFAM: PF00046; homeobox; 1.

KW HOMEBOX; DNA-BINDING; NUCLEAR PROTEIN.

SO SEQUENCE 228 AA; 26518 MW; A8D3850 CRC32;

Query Match 70.7%; Score 41; DB 5; Length 228;
 Best Local Similarity 55.6%; Pred. No. 1.99e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 79 ROYNSPSS 87
 ID 111:111:111

QY 1 QOYNSAPDT 9

RESULT 13
 ID 030879 PRELIMINARY: PRT: 276 AA.

AC 030879;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE PUTATIVE REPLICATION PROTEIN.

OS PSEUDOMONAS ALICIGENES.

OC PLASMID PR2.

OC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: PSEUDOMONAS GROUP;

OC PSEUDOMONAS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-NCIB 9867;

RA KWONG S.M., YEO C.C., CHUAN D., POH C.L.;

RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF020268; G2429364; -.

KW PLASMID.

SO SEQUENCE 276 AA; 30343 MW; FADBC9B8 CRC32;

Query Match 70.7%; Score 41; DB 2; Length 276;
 Best Local Similarity 66.7%; Pred. No. 1.99e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 51 QOYHSPST 59
 ID 111:111:111

QY 1 QOYNSAPDT 9

RESULT 14
 ID 039116 PRELIMINARY: PRT: 406 AA.

AC 039116;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE DNA-BINDING PROTEIN GT-1.

RN [1]

OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

OC EUKARYOTA: VIRIDIPHYTES: EMBRYOPHYTES: TRACHEOPHYTES;

OC EUPHYLOPHITES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS; ROSIDAE;

OC CAPRALES; BRASSICACEAE; ARABIDOPSIS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA MEDLINE: 95170284.

RT HIRATSUKA K., WU X., FUKUZAMA H., CHUA N.H.;

RT "Molecular dissection of GT-1 from Arabidopsis."

RL PLANT CELL 6:1805-1813(1994).

DR EMBL: L36806; G598073; -.

DR MENDEL: 6984; ARATH.1370.1.

SO SEQUENCE 406 AA; 46633 MW; 41019BF2 CRC32;

Query Match 70.7%; Score 41; DB 10; Length 406;
 Best Local Similarity 62.5%; Pred. No. 1.99e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 182 QYNSPST 189
 ID 111:111:111

QY 2 QYNSAPDT 9

RESULT 15
 ID P90934 PRELIMINARY: PRT: 455 AA.

AC P90934;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE M04C9.4 PROTEIN.

GN M04C9.4

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA: METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;

OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

```

RN [1]
RP SEQUENCE FROM N.A.
RA BURTON J.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STILSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RT NATURE 368:32-38(1994).
EQ EMBL: 283731: E1348145: -
EQ SEQUENCE 455 AA: 52021 MW: 83BF586 CRC32:

Query Match 70.7%; Score 41; DB 5; Length 455;
Best Local Similarity 55.6%; Pred. No. 1.99e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 384 HHYNAARDT 392
OY 1 OQYNSAPDT 9

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Search completed: Thu Sep 2 12:06:32 1999
 Job time : 35 secs.

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CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 100.0%; Score 66; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.24e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysdpyt 9
 1 qkysdpyt 9
 1 QKYNSDPYT 9

W2574: W2574 standard; peptide: 9 AA.
 W2574:

DE 19-MAR-1998 (first entry)
 AC Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 63; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 90.9%; Score 60; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 5.92e+00;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 qkysapyt 9
 1 qkysapyt 9
 1 QKYNSDPYT 9

W2570: W2570 standard; peptide: 9 AA.
 W2570:

DE 19-MAR-1998 (first entry)
 AC Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 67; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 86.4%; Score 57; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.28e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysapya 9
 1 qkysapya 9
 1 QKYNSDPYT 9

W2573: W2573 standard; peptide: 9 AA.
 W2573:

DE 19-MAR-1998 (first entry)
 AC Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

light chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disease; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HIVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 Homo sapiens.
 WO9729131-A1.
 14-AUG-1997.
 10-FEB-1997: U02219.
 25-NOV-1996: US-031476.
 09-FEB-1996: US-599226.
 (BADI) BASF AG.
 Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 Markovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 66; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbance,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 Sequence 9 AA;
 SQ

Query Match 84.8%; Score 56; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.65e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 1 GKYSAPYT 9
 |||||
 1 QKYNSDPT 9

RESULT 5
 W2576 standard; peptide: 9 AA.
 AC W2576:
 DE 19-MAR-1998 (first entry)
 Anti-TNF-alpha antibody light chain CDR3.
 Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 light chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HIVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 Homo sapiens.
 WO9729131-A1.
 14-AUG-1997.
 10-FEB-1997: U02219.

25-NOV-1996: US-031476.
 09-FEB-1996: US-599226.
 (BADI) BASF AG.
 Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 Markovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 66; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbance,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 Sequence 9 AA;
 SQ

Query Match 83.3%; Score 55; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.12e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 GKYSAPYT 8
 |||||
 1 QKYNSDPT 8

RESULT 6
 W2577 standard; peptide: 9 AA.
 AC W2577:
 DE 19-MAR-1998 (first entry)
 Anti-TNF-alpha antibody light chain CDR3.
 Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 light chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HIVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 Homo sapiens.
 WO9729131-A1.
 14-AUG-1997.
 10-FEB-1997: U02219.
 25-NOV-1996: US-031476.
 09-FEB-1996: US-599226.
 (BADI) BASF AG.
 Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 Markovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 70; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 83.3%; Score 55; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.12e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapy 8
 |||||
 QY 1 QKYNSDPY 8

RESULT 7
 ID W2575 standard; peptide: 9 AA.
 AC W2575;
 DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 RA 09-FEB-1996: US-599226.
 (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manokovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 69; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 83.3%; Score 55; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.12e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkynsapy 9
 |||||
 QY 1 QKYNSDPY 9

RESULT 8
 ID W2578 standard; peptide: 9 AA.
 AC W2578;
 DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 RA 09-FEB-1996: US-599226.
 (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manokovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 83.3%; Score 55; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.12e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkynsapy 9
 |||||
 QY 1 QKYNSDPY 9

RESULT 9

ID W27584 standard; peptide: 9 AA.

AC W27584;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997; U02219.

PR 25-NOV-1996; US-031476.

PA 09-FEB-1996; US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 72; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

SQ Sequence 9 AA;

Query Match 80.3%; Score 53; DB 27; Length 9;

Best Local Similarity 77.8%; Pred. No. 3.51e+01;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkynrpyt 9

Y 1 OKYNSDPYT 9

RESULT 10

ID W27583 standard; peptide: 9 AA.

AC W27583;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997; U02219.

PR 25-NOV-1996; US-031476.

PA 09-FEB-1996; US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 72; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

SQ Sequence 9 AA;

Query Match 78.8%; Score 52; DB 27; Length 9;

Best Local Similarity 77.8%; Pred. No. 4.50e+01;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkylsapyt 9

Y 1 OKYNSDPYT 9

RESULT 11

ID W27571 standard; peptide: 9 AA.

AC W27571;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997; U02219.

PR 25-NOV-1996; US-031476.

PA 09-FEB-1996; US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 78.8%; Score 52; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 4.50e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 1 qkyrnpypa 9
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 OY 1 OKYNSDPYT 9

RESULT 12
 ID W27568 standard; Protein: 107 AA.
 AC W27568;

DR 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
 KW light chain; variable region; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 DR N-PSDB; T88403.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 15; Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 107 AA;

Query Match 78.8%; Score 52; DB 27; Length 107;
 Best Local Similarity 66.7%; Pred. No. 4.50e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 89 qkyrnpypa 97
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 OY 1 OKYNSDPYT 9

RESULT 13
 ID R44617 standard; Protein: 533 AA.
 AC R44617;

DR 02-JUN-1994 (first entry)
 DE Human retinol binding protein receptor.
 KW Retinol binding protein receptor; retinitis pigmentosa.
 OS Homo sapiens.

PN WO9323538-A.
 PD 25-NOV-1993.
 PE 14-MAY-1993; U04586.
 PR 15-MAY-1992; US-883539.
 PA (LUDW) LODMIC INST CANCER RES.
 PI BAVIK CO, Eriksson U, Simon A;
 DR WPI: 93-386570/48.
 DR N-PSDB; Q53070.
 PT New retinol binding protein receptor and homologue coding nucleic
 PT acid molecule - useful for diagnosis and treatment of retinoid
 PT linked pathological conditions, for hybridisation in stringent
 PT conditions and treating retinitis
 PS Claim 15; Page 21-24; 44pp; English.
 CC The protein (SEQ. ID NO. 1) may be used to diagnose and treat
 CC retinoid linked conditions such as inability to accumulate
 CC retinoids in the eye, leading to retinitis pigmentosa.
 SQ Sequence 533 AA;

Query Match 77.3%; Score 51; DB 9; Length 533;
 Best Local Similarity 66.7%; Pred. No. 5.77e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 424 qkygktpyt 432
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 OY 1 OKYNSDPYT 9

RESULT 14
 ID W27572 standard; peptide: 9 AA.
 AC W27572;

DR 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.

PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PA 09-FEB-1996: US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 SQ Sequence 9 AA;

Query Match 75.8%; Score 50; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.39e+01;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 qkyrpyrpt 9
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 OY 1 QKYNSDPYT 9

RESULT 15
 ID W27579 standard; peptide: 9 AA.
 AC W27579;
 PT 19-MAR-1998 (first entry)
 PI Anti-TNF-alpha antibody light chain CDR3.
 PI Human: tumour necrosis factor-alpha; TNF-alpha; antibody: CDR3;
 PI light chain; complementarity determining region 3; inhibition;
 PI treatment; sepsis; disease; autoimmune disease; infectious disease;
 PI malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 PI cardiac disorder; inflammatory bone disorder; reperfusion injury;
 PI bone resorption disease; coagulation disturbance; burn; ELAM-1;
 PI keloid formation; scar tissue formation; pyrexia; HVEC;
 PI periodontal disease; obesity; radiation toxicity;
 PI endothelial cell leukocyte adhesion molecule-1;
 PI human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PA 09-FEB-1996: US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 SQ Sequence 9 AA;

Query Match 75.8%; Score 50; DB 27; Length 9;
 Best Local Similarity 75.0%; Pred. No. 7.39e+01;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 qkyrpyrpt 8
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 |||
 OY 1 QKYNSDPYT 8

Search completed: Thu Sep 2 12:08:43 1999
 Job time : 20 secs.

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CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
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CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: proteIn
CC SEQUENCE 107 AA: 11654 MW: 62438 CN;

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Query Match 75.8%; Score 50; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 3.24e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0
Db 88 QOYHSSPYT 96
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QY 1 OKYNSDPYT 9

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XX AC xxxxxx
XX DT
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Sequence 87, Application US/08899575
Sequence 87, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25

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CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;

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DQ Best Local Similarity 75.8%; Score 50; DB 2; Length 107;
DQ Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DQ 1 QKYNSDPYT 9

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AC xxxxxx
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XX DE Sequence 99, Application PC/TUS9508743
XX GENERAL INFORMATION:
XX APPLICANT:
XX TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX NUMBER OF SEQUENCES: 170
XX COMPUTER READABLE FORM:
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XX SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: PCT/US95/08743
XX FILING DATE: 11-JUL-1995
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 08/276,852
XX FILING DATE: 18-JUL-1994
XX INFORMATION FOR SEQ ID NO: 99:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 108 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
XX MOLECULE TYPE: protein
XX SEQUENCE 108 AA; 11738 MW; 63142 CN;

Query Match 69.7%; Score 46; DB 3; Length 108;
Best Local Similarity 55.6%; Pred. No. 8.67e+01;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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 AC xxxxxx
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 CC Sequence 99, Application PC/TUS9508743
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
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 CC COMPUTER: IBM PC compatible
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 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
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 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 108 AA; 11738 MM; 63142 CN;
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 Best Local Similarity 55.6%; Pred.No. 8.67e+01;
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CC	Sequence 99, Application US/08899575		
CC	Patent No. 5804440		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Burton, Dennis R		
CC	APPLICANT: Barbas, Carlos F		
CC	APPLICANT: Lerner, Richard A		
CC	TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES		
CC	TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS		
CC	NUMBER OF SEQUENCES: 170		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: The Scripps Research Institute, Office of		
CC	ADDRESSEE: Patent Counsel		
CC	STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,		
CC	STREET: Mail Drop TPC8		
CC	CITY: La Jolla		
CC	STATE: CA		
CC	COUNTRY: USA		
CC	ZIP: 92037		
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CC	FILING DATE: 30-SEP-1993		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 07/954,148		
CC	FILING DATE: 30-SEP-1992		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Fitting, Thomas		
CC	REGISTRATION NUMBER: 34,163		
CC	REFERENCE/DOCKET NUMBER: SCRI452P		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 619-554-2937		
CC	TELEFAX: 619-554-6312		
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CC	Patent No. 5770440			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Burton, Dennis R			
CC	APPLICANT: Barbas, Carlos F			
CC	APPLICANT: Leher, Richard A			
CC	TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES			
CC	TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS			
CC	NUMBER OF SEQUENCES: 170			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: The Scripps Research Institute, Office of			
CC	ADDRESSEE: Patent Counsel			
CC	STREET: 10656 No. 5770440th Torrey Pines Road, Suite 220,			
CC	STREET: Mail Drop TPC8			
CC	CITY: La Jolla			
CC	STATE: CA			
CC	COUNTRY: USA			
CC	ZIP: 92037			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
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CC	FILING DATE: 30-SEP-1993			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US 07/954,148			
CC	FILING DATE: 30-SEP-1992			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Fitting, Thomas			
CC	REGISTRATION NUMBER: 34,163			
CC	REFERENCE/DOCKET NUMBER: SCRI452P			
CC	TELECOMMUNICATION INFORMATION:			
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CC	TELEFAX: 619-554-6312			
CC	INFORMATION FOR SEQ ID NO: 99:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 108 amino acids			
CC	TYPE: amino acid			
CC	TOPOLOGY: linear			
CC	MOLECULE TYPE: protein			
CC	SEQUENCE 108 AA: 11738 MW; 63142 CN;			
DB	88 QOYGISPT 96			
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XX CC Sequence 99, Application US/08276852
XX CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
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CC CURRENT APPLICATION DATA:
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CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
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CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11738 MW; 63142 CN;
SQ
DB 88 QOYGTSPYT 96
OY 1 OKYNSDPYT 9
Query Match 69.7%; Score 46; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 8.67e+01;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
RESULT 10
ID PCT-US93-07832-3 STANDARD; PRT; 109 AA.
XX xxxxxx
AC
XX
DT
XX
DE Sequence 3, Application PC/TUS9307832
XX Sequence 3, Application PC/TUS9307832
CC GENERAL INFORMATION:
CC

CC APPLICANT: Genentech, Inc.
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 40
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/07832
CC FILING DATE: 19930820
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/715272
CC FILING DATE: 14-JUN-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05126
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/934373
CC FILING DATE: 21-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME:
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 709P2PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE:
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 109 AA; 11850 MW; 69772 CN;
SQ
DB 89 QOYNSLPYT 97
OY 1 OKYNSDPYT 9
Query Match 69.7%; Score 46; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 8.67e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 11
ID US-07-934-373C-3 STANDARD; PRT; 109 AA.
XX xxxxxx
AC
XX
DT
XX
DE Sequence 3, Application US/07934373C
XX Sequence 3, Application US/07934373C
CC Patent No. 5821337
CC GENERAL INFORMATION:
CC APPLICANT: Paul J. Carter
CC APPLICANT: Leonard G. Presta
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 1 DNA Way
CC CITY: South San Francisco
CC STATE: California
CC

CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 23L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
SQ SEQUENCE 109 AA: 11858 MW: 64524 CN:

Query Match 68.2%; Score 45; DB 3; Length 109;
Best Local Similarity 55.6%; Pred. No. 1.11e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 89 QOYGSPT 97
1 1 1 1 1
1 QKNSDPT 9

RESULT 14
ID US-08-162-102C-24 STANDARD: PRT; 109 AA.

Sequence 24, Application US/08162102C
Patent No. 5762305
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
APPLICANT: Barbas, III, Carlos F.
APPLICANT: Chanock, Robert M.
APPLICANT: Murphy, Brian R.
APPLICANT: Crowe, Jr., James E.
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162.102C
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07300/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: rsv 23L
FEATURE:

CC NAME/KEY: Peptide
CC LOCATION: 1..109
SQ SEQUENCE 109 AA: 11858 MW: 64524 CN:

Query Match 68.2%; Score 45; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 1.11e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 89 QOYGSPT 97
1 1 1 1 1
1 QKNSDPT 9

RESULT 15
ID US-08-118-270-59 STANDARD: PRT; 305 AA.

Sequence 59, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118.270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 305 AA: 33985 MW: 525962 CN;

Query Match 68.2%; Score 45; DB 1; Length 305;
Best Local Similarity 62.5%; Pred. No. 1.11e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 153 KYRSEPT 160
1 1 1 1 1
2 KYNSDPT 9

Fri Sep 3 09:53:05 1999

US-08-599-226-23.ra1

Page 8

Search completed: Thu Sep 2 12:10:48 1999
Job time : 7 secs.

 WIRENET (TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:09:02 1999; Maspar time 3.01 Seconds
 119.645 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-599-226-23
 Description: (1-9) from US08599226.pep
 Perfect Score: 66
 Sequence: 1 QKXNSDPY 9

Scoring table: PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues
 Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: PIR60
 1:PIR1 2:PIR2 3:PIR3 4:PIR4

Statistics: Mean 22.440; Variance 29.082; scale 0.772

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	54	81.8	500	2	S64220	hypothetical protein
2	53	80.3	790	2	S27458	SMW2 protein - yeast
3	51	77.3	533	2	A47143	retinal pigment micro
4	50	75.8	794	2	T02171	hypothetical protein
5	50	75.8	820	2	T02152	hypothetical protein - b
6	50	75.8	905	2	T02305	Lu-ECAM-1 protein - b
7	49	74.2	397	2	E70317	hypothetical protein
8	49	74.2	1042	2	G64514	type I restriction en
9	49	74.2	2251	2	B54972	voltage-dependent cal
10	49	74.2	2259	2	S29336	calcium channel prote
11	49	74.2	2270	2	A54972	voltage-dependent cal
12	48	72.7	91	2	S67940	Ig kappa chain V regl
13	48	72.7	92	2	S37513	Ig kappa chain V regl
14	48	72.7	109	2	A30608	Ig kappa chain V-III
15	48	72.7	109	2	H30601	Ig kappa chain V-III
16	48	72.7	259	2	H64699	hypothetical protein
17	48	72.7	259	2	C71820	hypothetical protein
18	48	72.7	469	1	AJZROU	glutamate- ammonia 11
19	48	72.7	3973	2	B71612	hypothetical protein
20	47	71.2	107	2	A28195	Ig kappa chain V regl
21	47	71.2	108	1	K1H0BN	Ig kappa chain V-1 re
22	47	71.2	108	2	PL0204	anti-DNA autoantibody
23	47	71.2	128	1	K3H041	Ig kappa chain precu

24	47	71.2	129	2	S40369	Ig kappa chain - huma	2.10e+01
25	47	71.2	270	2	F63362	conserved hypothetical	2.10e+01
26	47	71.2	348	2	S34494	ccsa protein - Euglen	2.10e+01
27	47	71.2	465	2	H64507	hypothetical protein	2.10e+01
28	47	71.2	651	2	A55100	SEC3 protein - yeast	2.10e+01
29	47	71.2	2249	2	A41477	190K surface antigen	2.10e+01
30	46	69.7	263	1	ASLJMA	nef protein - simian	3.24e+01
31	46	69.7	312	2	S45065	class 3 outer membran	3.24e+01
32	46	69.7	331	2	S28441	outer membrane protei	3.24e+01
33	46	69.7	331	2	S21409	class 3 outer membran	3.24e+01
34	46	69.7	521	2	I39956	neutral proteinase (E	4.98e+01
35	45	68.2	106	2	A49138	Iga kappa rheumatoid	4.98e+01
36	45	68.2	348	1	OOHUB	opsin, blue-sensitive	4.98e+01
37	45	68.2	443	2	G64114	site-specific DNA-met	4.98e+01
38	45	68.2	826	2	A31822	villin - chicken	4.98e+01
39	45	68.2	827	1	A31842	villin - human	4.98e+01
40	45	68.2	956	2	G70327	isoletucyl-tRNA synthe	4.98e+01
41	45	68.2	1254	1	A32686	DNA-directed DNA poly	4.98e+01
42	44	66.7	177	2	A45739	trac protein precu	7.60e+01
43	44	66.7	295	2	S50316	CIN5 protein - yeast	7.60e+01
44	44	66.7	442	1	VJPP2	vitellogenin II precu	7.60e+01
45	44	66.7	2222	2	A37490	voltage-dependent cal	7.60e+01

ALIGNMENTS

RESULT 1
 ENTRY 1
 TITLE S64220 #type complete
 hypothetical protein YGL202w - yeast (Saccharomyces cerevisiae)

ALTERNATE_NAMES
 TITLE S64220 #type complete
 hypothetical protein YGL202w - yeast (Saccharomyces cerevisiae)
 DATE 17-May-1996 #sequence_revision 17-May-1996 #text_change 06-Feb-1998

ACCESSIONS
 S64220
 S64218
 Bjourson, A.J.; McReynolds, A.D.K.; Wright, L.F.
 #authors submitted to the Protein Sequence Database, May 1996
 #accession S64220

#molecule_type DNA
 #residues 1-500 #label BUO
 #cross-references EMBL:272724; NID:g1322833; PID:e243502; PID:g1322834;
 MIPS:YGL202w
 #experimental_source strain S288C

GENETICS
 #gene SGD:ARO8
 #map_position 7L
 SUMMARY #length 500 #molecular-weight 56177 #checksum 3537

Query Match 81.8%; Score 54; DB 2; Length 500;
 Best Local Similarity 100.0%; Pred. No. 8.34e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 415 KYNNDPY 421
 QY 2 KYNNDPY 8

RESULT 2
 ENTRY 2
 TITLE S27458 #type complete
 SMW2 protein - yeast (Saccharomyces cerevisiae)
 ALTERNATE_NAMES
 #formal_name Saccharomyces cerevisiae
 #formal_name Saccharomyces cerevisiae
 DATE 28-May-1993 #sequence_revision 28-May-1993 #text_change 06-Feb-1998
 ACCESSIONS
 S27458
 S27458
 S27458
 #authors Lilliche, S.R.; Brown, S.S.
 #submission submitted to the EMBL Data Library, April 1992
 #description Characterization of a suppressor of the MYO2 gene in yeast.
 #accession S27458
 #molecule_type DNA

##residues 1-790 ##label LIL
#cross-references EMBL:M90654; NID:g172627; PID:g172628
REFERENCE
#authors Schaff-Gerstenschlaeger, I.; Bauer, A.; Boles, E.;
#submission submitted to the EMBL Data Library, July 1993
#description Sequence and function analysis of a 4.3kb fragment of
saccharomyces cerevisiae Chromosome II including three open
reading frames.
#accession S36778
##molecule-type DNA
##residues 323-790 ##label SCH
#cross-references EMBL:X74437; NID:g402607; PID:g402610
REFERENCE
#authors Entian, K.D.; Koetter, P.; Rose, M.; Becker, J.; Grey, M.;
Li, Z.; Niegemann, E.; Schenk-Groeninger, R.; Servos, J.;
Wehner, E.; Wolter, R.; Brendel, M.; Bauer, J.; Braun, H.;
Dern, K.; Duesterhus, S.; Gruenbein, R.; Hedges, D.;
Klesau, P.; Koriol, S.; Krebs, B.; Proft, M.; Slegers, K.;
Baur, A.; Boles, E.; Miosga, T.; Schaff-Gerstenschlaeger,
I.; Zimmermann, F.K.
#submission submitted to the Protein Sequence Database, August 1994
#accession S46043
##molecule-type DNA
##residues 1-790 ##label ENT
#cross-references EMBL:Z36041; NID:g536517; PID:g536518; MIPS:YBR172C
REFERENCE
#authors Schaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.;
Zimmermann, F.K.
#journal Yeast (1993) 9:915-921
#title Yeast sequencing reports. Sequence and function analysis of a
4.3 kb fragment of Saccharomyces cerevisiae chromosome II
including three open reading frames.
#accession S37602
##molecule-type DNA
##residues 323-358,'S',359-394,'S',395-430,'S',431-466,'S',467-502,
'S',503-538,'S',539-573,'S',574-610,'S',611-646,'S',
647-682,'S',683-718,'S',719-754,'S',755-790,'S'
##label SC2
#note In reference S46617 the authors state: In Fig. 3 the 'S'
at the end of each line is not part of the amino acid
sequence and has to be removed
REFERENCE
#authors Schaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.;
Zimmermann, F.K.
#journal Yeast (1994) 10:1257
#title Erratum to: sequence and function analysis of a 4.3 kb
fragment of Saccharomyces cerevisiae chromosome II
including three open reading frames.
#description erratum; correction to sequence display
GENETICS
#gene SCD:SMY2
#cross-references SGD:S0000376; MIPS:YBR172C
#map-position 2R
SUMMARY #length 790 #molecular-weight 87098 #checksum 5821
Query Match 80.3%; Score 53; DB 2; Length 790;
Best Local Similarity 55.6%; Pred. No. 1.34e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Db 318 EXDTPPT 326
OY 1 QKXNDPPT 9
RESULT 3
ENTRY A47143 #type complete
TITLE retinal pigment microsomal protein RPE65, epithelium-specific
- bovine
ALTERNATE_NAMES membrane receptor p63; retinol-binding protein receptor
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change
10-Sep-1997

ACCESSIONS A47143; A48017; S28503
REFERENCE
#authors Hamel, C.P.; Tsiou, E.; Pfeiffer, B.A.; Hooks, J.J.; Detrick,
B.; Redmond, T.M.
#journal J. Biol. Chem. (1993) 268:15751-15757
#title Molecular cloning and expression of RPE65, a novel retinal
pigment epithelium-specific microsomal protein that is
post-translationally regulated in vitro.
#cross-references MVID:93340181
#accession A47143
##status preliminary
##molecule-type mRNA
##residues 1-533 ##label HAM
#cross-references GB:L11356; NID:g163656; PID:g163657
REFERENCE
#authors Bavik, C.O.; Levy, F.; Hellman, U.; Wernstedt, C.; Eriksson,
U.
#journal J. Biol. Chem. (1993) 268:20540-20546
#title The retinal pigment epithelial membrane receptor for plasma
retinol-binding protein. Isolation and cDNA cloning of the
63-KDa protein.
#cross-references MVID:93386633
#accession A48017
##status preliminary
##molecule-type mRNA
##residues 1-340,'U',342-533 ##label BA2
#cross-references EMBL:X66277; NID:g563; PID:g564
KEYWORDS membrane protein
SUMMARY #length 533 #molecular-weight 60944 #checksum 3885
Query Match 77.3%; Score 51; DB 2; Length 533;
Best Local Similarity 66.7%; Pred. No. 3.44e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 424 QKXGKPYT 432
OY 1 QKXNDPPT 9
RESULT 4
ENTRY T02171 #type complete
TITLE hypothetical protein lu-ECAM-1 - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change
05-Mar-1999
ACCESSIONS T02171
REFERENCE Z14590
#authors Eblen, R.C.; Widom, J.; Gruber, A.D.; Abdel-Chany, M.;
Levine, R.; Goodwin, A.; Paul, B.U.
#submission submitted to the EMBL Data Library, April 1997
#description Cloning and characterization of lu-ECAM-1 suggest it is an
endothelial chloride channel.
#accession T02171
##status preliminary; translated from GB/EMBL/DBJ
##molecule-type mRNA
##residues 1-794 ##label ELB
#cross-references EMBL:AF001262; NID:g2623764; PID:g2623765
#experimental_source lung
SUMMARY #length 794 #molecular-weight 88509 #checksum 6853
Query Match 75.8%; Score 50; DB 2; Length 794;
Best Local Similarity 75.0%; Pred. No. 5.45e+00;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 111 KYGDDPYT 118
OY 2 KYNSDPYT 9
RESULT 5
ENTRY T02152 #type complete
TITLE lu-ECAM-1 protein - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle

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DATE      05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change
ACCESSIONS
REFERENCE  T02152
#authors   Elble, R.C.; Widom, J.; Gruber, A.D.; Abdel-Ghany, M.;
            Levine, R.; Goodwin, A.; Pauli, B.U.
#submission submitted to the EMBL Data Library, April 1997
#description Cloning and characterization of lu-ECAM-1 suggest it is an
            endothelial chloride channel.
#accession  T02152
#status     preliminary; translated from GB/EMBL/DDBT
#molecule_type mRNA
#residues   1-820 #label E1B
#cross-references EMBL:AF001263; NID:g2623766; PID:g2623767
#experimental_source lung
SUMMARY    #length 820 #molecular-weight 91464 #checksum 3104

Query Match 75.8%; Score 50; DB 2; Length 820;
Best Local Similarity 75.0%; Pred. No. 5.45e+00;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 111 KYGDPYT 118
|||
OY 2 KYNSDPYT 9

RESULT 6
ENTRY  T02205 #type complete
TITLE  lu-ECAM-1 protein - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change

ACCESSIONS
REFERENCE  T02205
#authors   Elble, R.C.; Widom, J.; Gruber, A.D.; Abdel-Ghany, M.;
            Levine, R.; Goodwin, A.; Pauli, B.U.
#submission submitted to the EMBL Data Library, April 1997
#description Cloning and characterization of lu-ECAM-1 suggest it is an
            endothelial chloride channel.
#accession  T02205
#status     preliminary; translated from GB/EMBL/DDBT
#molecule_type mRNA
#residues   1-905 #label E1B
#cross-references EMBL:AF001261; NID:g2623762; PID:g2623763
#experimental_source lung
SUMMARY    #length 905 #molecular-weight 101005 #checksum 5557

Query Match 75.8%; Score 50; DB 2; Length 905;
Best Local Similarity 75.0%; Pred. No. 5.45e+00;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 111 KYGDPYT 118
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OY 2 KYNSDPYT 9

RESULT 7
ENTRY  E70317 #type complete
TITLE  Hypothetical protein ag_183 - Aquifex aeolicus
ORGANISM #formal_name Aquifex aeolicus
DATE 08-May-1998 #sequence_revision 08-May-1998 #text_change

ACCESSIONS
REFERENCE  E70317
#authors   Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
            Lenox, A.L.; Graham, D.E.; Overbeek, R.; Speed, M.A.;
            Keller, M.; Aulay, M.; Huber, R.; Feldman, R.A.; Short,
            J.M.; Olson, G.J.; Swanson, R.V.
#journal    Nature (1998) 392:353-358
#title      The complete genome of the hyperthermophilic bacterium
            Aquifex aeolicus.
#cross-references MVID:98196666
#accession  E70317

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#status     preliminary; nucleic acid sequence not shown;
            translation not shown
#molecule_type DNA
#residues   1-397 #label AOF
#cross-references GB:AE000677; NID:g2982900; PID:g2982913; GB:AE000657
#experimental_source strain VFS
GENETICS
#gene       ag_183
SUMMARY    #length 397 #molecular-weight 46821 #checksum 9057

Query Match 74.2%; Score 49; DB 2; Length 397;
Best Local Similarity 66.7%; Pred. No. 8.59e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 362 KYRSPYTS 370
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OY 1 KYNSDPYT 9

RESULT 8
ENTRY  G64514 #type complete
TITLE  type I restriction enzyme homolog - Methanococcus jannaschii
ORGANISM #formal_name Methanococcus jannaschii
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change

ACCESSIONS
REFERENCE  G64514
#authors   Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann,
            R.D.; Sutton, G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton,
            R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.;
            Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
            Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodok, A.;
            Scott, J.L.; Geoghegan, N.S.M.; Weidman, J.F.; Fuhrmann,
            J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson,
            J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts,
            K.M.; Hurst, M.A.; Kalne, B.P.; Bordovsky, M.; Klenk,
            H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
#journal    Science (1996) 273:1058-1073
#title      Complete genome sequence of the methanogenic archaeon,
            Methanococcus jannaschii.
#cross-references MVID:96337999
#accession  G64514
#status     preliminary; nucleic acid sequence not shown;
            translation not shown
#molecule_type DNA
#residues   1-1042 #label BUL
#cross-references GB:U77118; NID:g1500644; TIGR:MJEC140; PID:g1522673
GENETICS
#map_position BCLREY52581-49453
#genome     plasmid
#note       this stable 58-kilobase pair plasmid is also designated ECL
            (large extrachromosomal element) and contains 44 predicted
            coding regions
CLASSIFICATION
#superfamily unassigned DEAD/H box helicases; DEAD/H box
            helicase homology
KEYWORDS   ATP; P-loop
FEATURE
336-684    #domain DEAD/H box helicase homology #label DEAD\
336-343    #region nucleotide-binding motif A (P-loop)\
435-440    #region nucleotide-binding motif B\
439-442    #region DEAD motif
SUMMARY    #length 1042 #molecular-weight 121522 #checksum 7313

Query Match 74.2%; Score 49; DB 2; Length 1042;
Best Local Similarity 62.5%; Pred. No. 8.59e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 262 KYGNPYT 269
|||
OY 2 KYNSDPYT 9

```

```

RESULT 9
ENTRY B54972 #type complete
TITLE voltage-dependent calcium channel alpha 1E-1 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE B54972
#authors Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust,
P.F.; Philipson, L.H.; Miller, R.J.; Johnson, E.C.;
#journal J. Biol. Chem. (1994) 269:22347-22357
#title Structure and functional characterization of neuronal
#alpha-1E calcium channel subtypes.
#cross-references MVID:94350992
#accession B54972
#status preliminary; nucleic acid sequence not shown;
translation not shown

#molecule_type mRNA
#residues 1-2251 #label WIL
#cross-references GB:L29384; NID:9495867; PID:9495868
CLASSIFICATION #superfamily voltage-dependent calcium channel protein
alpha-1 chain
SUMMARY #length 2251 #molecular_weight 254636 #checksum 4202

Query Match 74.2%; Score 49; DB 2; Length 2251;
Best Local Similarity 62.5%; Pred. No. 8.59e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2163 QRYISEPY 2170
1:1:1:1:1
QY 1 QKYNDDPY 8

RESULT 10
ENTRY S29236 #type complete
TITLE calcium channel protein BII-1, brain - rabbit
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic
rabbit
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Sep-1998
ACCESSIONS S29236
REFERENCE S29236
#authors Nildome, T.; Kim, M.S.; Friedrich, T.; Morl, Y.
#journal FEBS Lett. (1992) 308:7-13
#title Molecular cloning and characterization of a novel calcium
channel from rabbit brain.
#cross-references MVID:92354772
#accession S29236
#status preliminary
#molecule_type mRNA
#residues 1-2259 #label NII
#cross-references EMBL:X67855; NID:91473; PID:91473
CLASSIFICATION #superfamily voltage-dependent calcium channel protein
alpha-1 chain
KEYWORDS transmembrane protein
SUMMARY #length 2259 #molecular_weight 254250 #checksum 5523

Query Match 74.2%; Score 49; DB 2; Length 2259;
Best Local Similarity 62.5%; Pred. No. 8.59e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2172 QRYISEPY 2179
1:1:1:1:1
QY 1 QKYNDDPY 8

RESULT 11
ENTRY A54972 #type complete
TITLE voltage-dependent calcium channel alpha 1E-3 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change
17-Mar-1999

```

```

ACCESSIONS A54972
REFERENCE A54972
#authors Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust,
P.F.; Philipson, L.H.; Miller, R.J.; Johnson, E.C.;
#journal J. Biol. Chem. (1994) 269:22347-22357
#title Structure and functional characterization of neuronal
#alpha-1E calcium channel subtypes.
#cross-references MVID:94350992
#accession A54972
#status preliminary
#molecule_type mRNA
#residues 1-2270 #label WIL
#cross-references GB:L29385; NID:9495869; PID:9495870
CLASSIFICATION #superfamily voltage-dependent calcium channel protein
alpha-1 chain
SUMMARY #length 2270 #molecular_weight 257348 #checksum 387

Query Match 74.2%; Score 49; DB 2; Length 2270;
Best Local Similarity 62.5%; Pred. No. 8.59e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2182 QRYISEPY 2189
1:1:1:1:1
QY 1 QKYNDDPY 8

RESULT 12
ENTRY S67940 #type fragment
TITLE Ig kappa chain V region, subgroup III (clone MH52) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Mar-1997 #sequence_revision 09-May-1997 #text_change
20-Mar-1998
ACCESSIONS S67940
REFERENCE S67940
#authors Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith,
B.R.
#journal Autoimmunity (1992) 12:135-141
#title Cloning of a human autoimmune response: preparation and
sequencing of a human anti-thyroglobulin autoantibody using
a combinatorial approach.
#cross-references MVID:92314301
#accession S67940
#status preliminary
#molecule_type mRNA
#residues 1-91 #label HEX
#cross-references EMBL:X73852
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 91 #checksum 3259

Query Match 72.7%; Score 48; DB 2; Length 91;
Best Local Similarity 66.7%; Pred. No. 1.35e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 71 QOYSSPYT 79
1:1:1:1:1
QY 1 QKYNDDPYT 9

RESULT 13
ENTRY S37513 #type fragment
TITLE Ig kappa chain V region (V-kappa 3) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
08-Sep-1997
ACCESSIONS S37513
REFERENCE S37501
#authors Klein, U.; Kneppers, R.; Rajewsky, K.
#submission submitted to the EMBL Data Library, September 1993
#description Human Igk(+)IgD(+) cells, the major B cell subset in the
peripheral blood, expresses V(kappa) genes with no or
little somatic mutation throughout life.

```

```
#accession      S37513
#status          preliminary
#molecule_type mRNA
#residues        1-92 #label KLE
#cross-references EMBL:265598; NID:9405668; PID:9405669
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS         heterotetramer; immunoglobulin
SUMMARY          #length 92 #checksum 6096

Query Match      72.7%; Score 48; DB 2; Length 92;
Best Local Similarity 66.7%; Pred. No. 1.35e+01;
Matches          6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db              73 OQYSSPYT 81
               1 1 1 1 1 1
               1 OKYNSDPYT 9

RESULT 14
ENTRY      A30608      #type fragment
TITLE      Ig kappa chain V-III region (Son) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996

ACCESSIONS  A30608
REFERENCE    A30601
AUTHORS      Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
             Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
             Frangione, B.
#journal     J. Immunol. (1989) 142:3158-3163
#title       Structural and idiotypic characterization of the L chains of
             human IgM autoantibodies with different specificities.
#cross-references MIMD:89215279
#accession   A30608
#status      preliminary
#molecule_type protein
#residues    1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
SUMMARY       #length 109 #checksum 6031

Query Match      72.7%; Score 48; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.35e+01;
Matches          6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db              90 OQYSSPYT 98
               1 1 1 1 1 1
               1 OKYNSDPYT 9

RESULT 15
ENTRY      H30601      #type fragment
TITLE      Ig kappa chain V-III region (Gar and Flo) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996

ACCESSIONS  H30601; E30601
REFERENCE    A30601
AUTHORS      Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
             Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
             Frangione, B.
#journal     J. Immunol. (1989) 142:3158-3163
#title       Structural and idiotypic characterization of the L chains of
             human IgM autoantibodies with different specificities.
#cross-references MIMD:89215279
#accession   H30601
#status      preliminary
#molecule_type protein
#residues    1-109 #label GON1
#accession   E30601
#status      preliminary
#molecule_type protein
#residues    1-109 #label GON2
```

```
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS         heterotetramer; immunoglobulin
SUMMARY          #length 109 #checksum 5951

Query Match      72.7%; Score 48; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.35e+01;
Matches          6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db              90 OQYSSPYT 98
               1 1 1 1 1 1
               1 OKYNSDPYT 9

Search completed: Thu Sep 2 12:09:18 1999
Job time : 16 secs.
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RESULT 2
ID SMY2 YEAST STANDARD; PRT; 790 AA.
AC P32909;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE SMY2 PROTEIN.
GN SMY2 OR YBR172C OR YBR1233.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
OC SACCCHAROMYCETACEAE; SACCCHAROMYCSES.
RN [1]
RP SEQUENCE FROM N.A.
RA LITTLE S.H., BROWN S.S.;
RL SUBMITTED (APR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 323-790 FROM N.A.
RA STRAIN-5288C;
RL MEDLINE: 94025982.
RA SCHAEFF-GERSTENSCHLAGER I., BAUER A., BOLES E., ZIMMERMANN F.K.;
RT "Sequence and function analysis of a 4.3 kb fragment of Saccharomyces cerevisiae chromosome II including three open reading frames.";
RT YEAST 9:915-921(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-5288C;
RC ERTIAN K.-D., KOETTER P., ROSE M., BECKER J., GREY M., LI Z.,
RA NIEGEMANN E., SCHEENK-GROENINGER R., SERVOS J., WEHNER E.,
RA WOLTER R., BRENDLE M., BAUER J., BRAUN H., DERN K., DUESTERHUS S.,
RA GUENBEIN R., HEDGES D., KIESAU P., KOROL S., KREMS B., PROFT M.,
RA STEIGERS K., BAUR A., BOLES E., MIOGA T.,
RA SCHAEFF-GERSTENSCHLAGER I., ZIMMERMANN F.K.;
RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: SUPPRESSOR OF THE MYO2 GENE.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M90654; G172628; -;
DR EMBL: X74437; G402610; -;
DR EMBL: Z36041; G536518; -;
DR PIR: S27458; S27458.
DR SGD: L0001941; SMY2.
SQ SEQUENCE 790 AA; 87098 MW; E3543AC2 CRC32;
Query Match 80.3%; Score 53; DB 1; Length 790;
Best Local Similarity 55.6%; Pred. No. 3,33e-01;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Db 318 EKYDTPPT 326
QY 1 QKXNSDPT 9

RESULT 3
ID CB21_RABIT STANDARD; PRT; 2259 AA.
AC 002343;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE BRAIN CALCIUM CHANNEL BII-1 PROTEIN.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
RX MEDLINE: 92354772.
RA NIIDOME T., KIM M.S., FRIEDRICH T., MORI Y.;
RT "Molecular cloning and characterization of a novel calcium channel
RT from rabbit brain."
RL FEBS LETT. 308:7-13(1992).
CC -1- FUNCTION: BRAIN CALCIUM CHANNEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BRAIN CALCIUM CHANNEL ARE
CC PRODUCED FROM A SINGLE GENE. BII-1 AND BII-2 DIFFER ONLY IN THEIR
CC C-TERMINAL REGION FROM AA 2101.
CC -1- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X67855; G1473; -;
DR PIR: S29236; S29236.
DR PFAM: PF00520; ION_trans: 4.
KW IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; VOLTAGE-GATED CHANNEL;
KW CALCIUM CHANNEL; GLYCOPROTEIN; DUPLICATION; PHOSPHORYLATION;
KW ALTERNATIVE SPLICING.
FT REPEAT 76 354
FT REPEAT 464 706
FT REPEAT 1130 1414
FT REPEAT 1453 1716
FT TRANSMEM 90 108
FT TRANSMEM 127 146
FT TRANSMEM 159 176
FT TRANSMEM 186 204
FT TRANSMEM 224 243
FT TRANSMEM 327 351
FT TRANSMEM 477 495
FT TRANSMEM 511 530
FT TRANSMEM 539 557
FT TRANSMEM 568 586
FT TRANSMEM 606 625
FT TRANSMEM 679 703
FT TRANSMEM 1144 1162
FT TRANSMEM 1179 1198
FT TRANSMEM 1211 1229
FT TRANSMEM 1244 1262
FT TRANSMEM 1282 1301
FT TRANSMEM 1389 1413
FT TRANSMEM 1469 1487
FT TRANSMEM 1503 1522
FT TRANSMEM 1531 1549
FT TRANSMEM 1562 1580
FT TRANSMEM 1600 1619
FT TRANSMEM 1689 1713
FT CARBOHYD 254 254
FT CARBOHYD 1556 1556
FT CARBOHYD 1561 1561
SQ SEQUENCE 2259 AA; 254250 MW; 3466267E CRC32;
Query Match 74.2%; Score 49; DB 1; Length 2259;
Best Local Similarity 62.5%; Pred. No. 2,69e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 2172 QRYTSEPY 2179
QY 1 QKXNSDPT 8

RESULT 4
ID GNL1_RHIV STANDARD; PRT; 469 AA.
AC P09826;

DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE GLUTAMINE SYNTHETASE I (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE I)
DE (GSI).
GN GLNA.
OS RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE).
OC BACTERIA: PROTEOBACTERIA: ALPHA SUBDIVISION: RHIZOBIACEAE GROUP;
OC RHIZOBIACEAE: RHIZOBIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RC1001;
RX MEDLINE: 87174729.
RA COLOMNA-ROMANO S., RICCIO A., GUIDA M., DEFEZ R., LAMBERTI A.,
RA IACCARINO M., ARNOLD W., PRIERER U., PUHLER A.;
RT "tight linkage of glna and a putative regulatory gene in Rhizobium
leguminosarum".
RL NCCLC ACIDS RES. 15:1951-1964(1987).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) - ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED
CC BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE.
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII) CAN BE FOUND IN
CC THIS NITROGEN FIXING BACTERIA. GSI IS A TYPICAL PROKARYOTIC
CC GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE EUKARYOTIC
CC ENZYME.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X04880; G46193; -.
DR PIR: A26367; AJZKOL.
DR PROSITE: PS00180; GLNA_1; FALSE_NEG.
DR PROSITE: PS00181; GLNA_ATP; 1.
DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
DR PFAM: PF00120; gln-synt; 1.
DR HSP: P06201; 2IGS.
DR NITROGEN FIXATION; LIGASE: MULTIGENE FAMILY.
DR BINDING 398 AMP (UNDER CONDITIONS OF ABUNDANT
SEQUENCE 469 AA; 52232 MW; 9859505D CRC32;
GLUTAMINE) (BY SIMILARITY).
Query Match 72.7%; Score 48; DB 1; Length 469;
Best Local Similarity 71.4%; Pred. No. 4.45e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 141 KYRADPY 147
||:||||
QY 2 KYNSDPY 8
RESULT 5
ID GLNI_RHIME STANDARD; PRT: 469 AA.
AC 059747;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE GLUTAMINE SYNTHETASE I (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE I)
DE (GSI).
GN GLNA.
OS RHIZOBIUM MELLIOTI.
OC BACTERIA: PROTEOBACTERIA: ALPHA SUBDIVISION: RHIZOBIACEAE GROUP;
OC RHIZOBIACEAE: SINORHIZOBIUM.
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-2011;
RX MEDLINE: 97085050.
RA ARCONDEGUY T., HUEZ I., FOURMENT J., KAHN D.;
RT "Symbolic nitrogen fixation does not require adenylation of
RT glutamine synthetase I in Rhizobium melliotti".
RL FEBS MICROBIOL. LETT. 145:33-40(1996).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) - ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED
CC BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE
CC (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII) CAN BE FOUND IN
CC THIS NITROGEN FIXING BACTERIA. GSI IS A TYPICAL PROKARYOTIC
CC GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE EUKARYOTIC
CC ENZYME.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U50385; G1245379; -.
DR PROSITE: PS00180; GLNA_1; 1.
DR PROSITE: PS00181; GLNA_ATP; 1.
DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
DR PFAM: PF00120; gln-synt; 1.
DR HSP: P06201; 2IGS.
DR NITROGEN FIXATION; LIGASE: MULTIGENE FAMILY.
DR BINDING 397 AMP (UNDER CONDITIONS OF ABUNDANT
SEQUENCE 469 AA; 52035 MW; 7E3044A9 CRC32;
GLUTAMINE) (BY SIMILARITY).
Query Match 72.7%; Score 48; DB 1; Length 469;
Best Local Similarity 71.4%; Pred. No. 4.45e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 141 KYRADPY 147
||:||||
QY 2 KYNSDPY 8
RESULT 6
ID KYIV_HUMAN STANDARD; PRT: 108 AA.
AC P04430;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (BAN).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA;
OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
RN [1]
RP SEQUENCE.
RX MEDLINE: 86174817.
RA DWOLET F.E., O'CONNOR T.P., BENSON M.D.;
RT "Polymorphism in a kappa (AL) amyloid protein (BAN)".
RL MOL. IMMUNOL. 23:73-78(1986).
DR PIR: A01878; KIHUBN.
DR PFAM: PF00047; 1g; 1.
DR HSP: P80362; 1WTL.
DR IMMUNOGLOBULIN V REGION; AMYLOID.
DR DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 GN DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 0D44DA0A CRC32;

Query Match 71.2%; Score 47; DB 1; Length 108;
 Best Local Similarity 77.8%; Pred. No. 7.31e+00;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 89 OQYNSDPYT 97
 1 OQYNSDPYT 9

RESULT 7
 ID KVK_HUMAN STANDARD; PRT: 128 AA.

AC P06311;
 01-JAN-1988 (REL. 06, CREATED)
 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA KLOBECK H.G., MEINDL A., COMERIATO G., SOLOMON A., ZACHAU H.G.;
 RT "Human Immunoglobulin Kappa light chain genes of subgroups II and III."
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
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CC EMBL: 200021; G33179; -.
 DR PIR: A01899; K3H041.
 DR PFAM: PF00047; 19; 1.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 118 128
 FT NON_TER 108 128 BY SIMILARITY.
 FT SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match 71.2%; Score 47; DB 1; Length 128;
 Best Local Similarity 55.6%; Pred. No. 7.31e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 109 OQYNSDPYT 117
 1 OQYNSDPYT 9

RESULT 8
 ID YX01_CAEEL STANDARD; PRT: 297 AA.
 AC Q11108;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 35.0 KD PROTEIN C03B1.1 IN CHROMOSOME X.
 GN C03B1.1.

OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MARTIN J.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

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 CC -----

DR EMBL: U40952; G1072246; -.
 DR WORMPEP: C03B1.1; C803903.
 KM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 297 AA; 35049 MW; 11C549A6 CRC32;

Query Match 71.2%; Score 47; DB 1; Length 297;
 Best Local Similarity 55.6%; Pred. No. 7.31e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 186 EXYEDQYT 194
 1 OQYNSDPYT 9

RESULT 9
 ID CHLI_EUGGR STANDARD; PRT: 348 AA.

AC P31205;
 01-JUL-1993 (REL. 26, CREATED)
 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE MAGNESIUM-CHELATASE SUBUNIT CHLI (MG-PROTOPORPHYRIN IX CHELATASE).
 GN CHLI OR CCSA.

OS EUGLENA GRACILIS.
 OC EUKARYOTA; EUGLENOZOA; EUGLENIDA; EUGLENALES; EUGLENA.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-Z;
 RX MEDLINE: 92299087.
 RA ORSAT B., MONFORT A., CHATELLARD P., STUTZ E.;
 RT "Mapping and sequencing of an actively transcribed Euglena gracilis
 RT chloroplast gene (ccsa) homologous to the Arabidopsis thaliana
 RT nuclear gene csi(ch-42)."
 RL FEBS LETT. 303:181-184(1992).
 -1- FUNCTION: INVOLVED IN CHLOROPLAST PIGMENT BIOSYNTHESIS; INTRODUCES
 A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-
 PROTOPORPHYRIN IX.

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 CC -----

CC EMBL: 211874; -; NOT_ANNOTATED_CDS.
 DR EMBL: X65484; G12570; -.
 DR EMBL: X70810; G285952; -.
 DR PIR: S21383; S21383.
 DR PIR: S34494; S34494.

DR EMBL: 211874; -; NOT_ANNOTATED_CDS.
 DR EMBL: X65484; G12570; -.
 DR EMBL: X70810; G285952; -.
 DR PIR: S21383; S21383.
 DR PIR: S34494; S34494.

DR PFAM: PF01078; Mg-chelatase; 1.
 DR MENDEL; 4351; EDGAR; CHL1.
 KN PHOTOSYNTHESIS; CHLOROPHYLL BIOSYNTHESIS; CHLOROPLAST;
 KW ATP-BINDING.
 FT NP_BIND 42 49 ATP (POTENTIAL).
 SQ SEQUENCE 348 AA; 39307 MW; 34368573 CRC32;

Query Match 71.2%; Score 47; DB 1; Length 348;
 Best Local Similarity 100.0%; Pred. No. 7.31e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 YNSDPY 75
 |||||
 QY 3 YNSDPY 8

RESULT 10
 ID SEQ_YEAST STANDARD; PRT; 651 AA.
 AC P40357;
 DT 01-FEB-1995 (REL. 31, CREATED)
 RT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROTEIN TRANSPORT PROTEIN SEC9.
 GN SEC9 OR HSB7 OR YGR009C.
 OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACHAROMYCETALES;
 CC SACHAROMYCEAE; SACHAROMYCES.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95042722.
 RA BRENNEMAN P.J., KEARNS B.G., CHAMPION K.M., KERANEN S.,
 RA BANKAITIS V., NOYICK P.;
 RT "Sec9 is a SNAP-25-like component of a yeast SNARE complex that may
 be the effector of Sec4 function in exocytosis.";
 RL CELL 79:245-258(1994).
 [2]
 RN SEQUENCE FROM N.A.
 RP HEBLING U., HOFMANN B., DELIUS H.;
 RA SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDJ DATA BANKS.

CC -1- FUNCTION: COMPONENT OF A SNARE COMPLEX THAT MAY BE THE EFFECTOR OF
 SEC4 FUNCTION IN EXOCYTOSIS.
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
 CC -1- SIMILARITY: TO YEAST YMR017W.

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CC EMBL: L34336; G508620; -
 DR EMBL: Z72794; E243918; -
 DR PIR: S48526; S48526.
 DR PIR: A55100; A55100.
 DR SGD: L0001835; SEC9.
 DR PFAM: PF00835; SNAP-25; 1.
 KW PROTEIN TRANSPORT.
 SQ SEQUENCE 651 AA; 73623 MW; 19BA1CBD CRC32;

Query Match 71.2%; Score 47; DB 1; Length 651;
 Best Local Similarity 50.0%; Pred. No. 7.31e+00;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 123 RYDDPYA 130
 ||:||||
 QY 2 KYNSDPY 9

RESULT 11
 ID 190K_RICRI STANDARD; PRT; 2249 AA.
 AC P15921;

DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE 190 KD ANTIGEN PRECURSOR (CELL SURFACE ANTIGEN).
 OS RICKETTSIA RICKETTSII.
 OC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
 OC RICKETTSIACEAE; RICKETTSIENAE; RICKETTSIA.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R.
 RX MEDLINE: 90354033.
 RA ANDERSON B.E., McDONALD G.A., JONES D.C., REGNERY R.L.;
 RT "A protective protein antigen of Rickettsia rickettsii has tandemly
 repeated, near-identical sequences.";
 RL INFECT. IMMUN. 58:2760-2769(1990).
 CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
 CC -1- PTM: GLYCOSYLATED (POSSIBLE).
 CC -1- DISEASE: PROBABLY PLAYS AN IMPORTANT ROLE IN THE PATHOGENESIS OF
 AND IMMUNITY TO ROCKY MOUNTAIN SPOTTED FEVER.

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CC EMBL: M31227; G152466; -
 DR PIR: A41477; A41477.
 KW ANTIGEN; REPEAT; SIGNAL; S-LAYER; GLYCOPROTEIN.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 2249 190 KD ANTIGEN.
 FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 212 286 A (TYPE I).
 FT REPEAT 287 358 B (TYPE II).
 FT REPEAT 359 430 C (TYPE II).
 FT REPEAT 431 505 D (TYPE I).
 FT REPEAT 506 577 E (TYPE II).
 FT REPEAT 578 652 F (TYPE I).
 FT REPEAT 653 724 G (TYPE II).
 FT REPEAT 725 799 H (TYPE I).
 FT REPEAT 800 874 I (TYPE I).
 FT REPEAT 875 949 J (TYPE I).
 FT REPEAT 950 1021 K (TYPE II).
 FT REPEAT 1022 1093 L (TYPE II).
 FT REPEAT 1094 1165 M (TYPE II).
 FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
 SQ SEQUENCE 2249 AA; 224333 MW; 586DE285 CRC32;

Query Match 71.2%; Score 47; DB 1; Length 2249;
 Best Local Similarity 62.5%; Pred. No. 7.31e+00;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 2088 KYKSESYT 2095
 ||:||||
 QY 2 KYNSDPY 9

RESULT 12
 ID NEF_SIVMA STANDARD; PRT; 263 AA.
 AC P31818;
 DT 01-JUL-1993 (REL. 26, CREATED)
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DE 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KD PROTEIN) (3'ORF).
 GN NEF.
 OS SIMIAN IMMUNODEFICIENCY VIRUS (IALL ISOLATE) (SIV-MAC).
 OC VIROSES; RETROVIRUSES; RETROVIRIDAE; LENTIVIRUS.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92365133.
 RA UNGER R.E., MARTIAS M.L., PRATT-LOWE E., PADRID P.A., LUCIW P.A.;

ID OPSE_HUMAN STANDARD: PRT: 348 AA.
AC P03999: Q13877;
DT 23-OCT-1986 (REL. 02, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE BLUE-SENSITIVE OPSIN (BLUE CONE PHOTORECEPTOR PIGMENT).
GN BCP.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-RETINAL CONE CELL;
RX MEDLINE: 86151699.
RA NATHANS J., THOMAS D., HOGNESS D.S.;
RT "Molecular genetics of human color vision: the genes encoding blue,
RL green, and red pigments.";
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE: 97250263.
RA SHIMMIN L.C., MAI P., LI W.H.;
RT "Sequences and evolution of human and squirrel monkey blue opsin
RL genes.";
RN [3]
RP SEQUENCE OF 272-310 FROM N.A.
RC MEDLINE: 89222444.
RA SARKAR G., SOMMER S.S.;
RT "Access to a messenger RNA sequence or its protein product is not
RL limited by tissue or species specificity.";
RN [4]
RP REVIEW
RC MEDLINE: 87293932.
RA APPLEBURY M.L., HARGRAVE P.A.;
RT "Molecular biology of the visual pigments.";
RL VISION RES. 26:1881-1895(1986).
RN [5]
RP VARIANTS TRITANOPIA ARG-79 AND PRO-214.
RC MEDLINE: 92170786.
RA WEITZ C.J., MIYAKE Y., SHINZATO K., MONTAG E., ZRENNER E., WENT L.N.,
RT NATHANS J.;
RT "Human tritanopia associated with two amino acid substitutions in the
RL blue-sensitive opsin.";
RN [6]
RP VARIANT TRITANOPIA SER-264.
RC MEDLINE: 92351946.
RA WEITZ C.J., WENT L.N., NATHANS J.;
RT "Human tritanopia associated with a third amino acid substitution in
RL the blue-sensitive visual pigment.";
RN [7]
RP AM. J. HUM. GENET. 51:444-446(1992).
RT -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: THE THREE COLOR PIGMENTS ARE FOUND IN THE CONE
CC PHOTORECEPTOR CELLS.
CC -1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED.
CC -1- DISEASE: DEFECTS IN BCP ARE THE CAUSE OF TRITAN COLOR BLINDNESS
CC (TRITANOPIA).
CC -1- THIS OPSIN HAS AN ABSORPTION MAXIMA AT 420 NM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC BELONGS TO THE OPSIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: M13299: G180685; -;
DR EMBL: M13295: G180685; JOINED.
DR EMBL: M13296: G180685; JOINED.
DR EMBL: M13297: G180685; JOINED.
DR EMBL: M13298: G180685; JOINED.
DR EMBL: U53874: G2138076; -;
DR EMBL: M26172: G553205; -;
DR PIR: A03156; COHOB.
DR GCRDB: GCR_0057; -;
DR MIM: 190900; -;
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
DR PROSITE: PS00238; OPSIN; 1.
DR PFAM: PF00001: 7tm_1; 1.
KM PHOTORECEPTOR; RETINAL PROTEIN; TRANSMEMBRANE; GLYCOPROTEIN; VISION;
KN PHOSPHORYLATION; G-PROTEIN COUPLED RECEPTOR; DISEASE MUTATION.
FT DOMAIN 1 33
FT TRANSMEM 34 58
FT DOMAIN 59 70
FT TRANSMEM 71 96
FT DOMAIN 97 110
FT TRANSMEM 111 130
FT DOMAIN 131 149
FT TRANSMEM 150 173
FT DOMAIN 174 199
FT TRANSMEM 200 227
FT DOMAIN 228 249
FT TRANSMEM 250 273
FT DOMAIN 274 281
FT TRANSMEM 282 306
FT DOMAIN 307 348
FT CARBOHYD 14 14
FT DISULFID 107 184
FT BINDING 293 293
FT VARIANT 79 79
FT VARIANT 214 214
FT VARIANT 264 264
FT VARIANT 308 310
SQ SEQUENCE 348 AA: 39135 MW: 3700502 CRC32;
Query Match 68.2%; Score 45; DB 1; Length 348;
Best Local Similarity 62.5%; Pred. No. 1,93e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
DB 194 KYRSESYT 201
QY 2 KYNSDPT 9
Search completed: Thu Sep 2 12:09:42 1999
Job time : 8 secs.

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 W P E R E H (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:10:00 1999; Maspar time 4.27 Seconds

Abular output not generated. 115.143 Million cell updates/sec

Title: >US-08-599-226-23

Description: (1-9) from US08599226.pep

Sequence: 66
 1 QKXNSDPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

Sptrembl9
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mnc 8:sp_orananelle
 9:sp_phase 10:sp_plant 11:sp_protent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 22.085; Variance 26.114; scale 0.846

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	52	78.8	337	2	034232	ORF40X1 PROTEIN.	1.04e+00
2	52	78.8	337	2	087136	ORF139-17 PROTEIN.	1.04e+00
3	51	77.3	533	6	028175	RETINAL PIGMENT EPTTHE	1.74e+00
4	51	77.3	533	6	005661	RETINAL PIGMENT EPTTHE	1.74e+00
5	50	75.8	342	6	018744	LO-ECAM-1.	2.89e+00
6	50	75.8	342	6	018742	LO-ECAM-1.	2.89e+00
7	50	75.8	342	6	018743	LO-ECAM-1.	2.89e+00
8	50	75.8	342	6	018741	LO-ECAM-1.	2.89e+00
9	49	74.2	397	2	066569	HYPOHETICAL 46.8 KD P	4.77e+00
10	49	74.2	1042	1	060295	PUTATIVE TYPE 1 RESTR	4.77e+00
11	49	74.2	2098	5	P91443	STIMILAR TO MYOSIN.	4.77e+00
12	49	74.2	2270	4	014581	DIHYDROPYRIDINE-SENSIT	4.77e+00
13	49	74.2	2312	4	015878	VOLTAGE-OPERATED CALCI	4.77e+00
14	48	72.7	259	2	025981	HYPOHETICAL 29.4 KD P	7.83e+00
15	47	71.2	270	1	029360	CONSERVED HYPOHETICAL	1.28e+01
16	47	71.2	465	1	059060	HYPOHETICAL PROTEIN M	1.28e+01
17	47	71.2	583	2	P97082	GLUCAN-BINDING PROTEIN	1.28e+01
18	47	71.2	1053	2	P95632	ROMPA (FRAGMENT).	1.28e+01
19	47	71.2	1058	2	P95661	ROMPA (FRAGMENT).	1.28e+01
20	47	71.2	1058	2	P96141	ROMPA (FRAGMENT).	1.28e+01

21	47	71.2	1060	2	P95592	ROMPA (FRAGMENT).	1.28e+01
22	47	71.2	1060	2	P95594	ROMPA (FRAGMENT).	1.28e+01
23	47	71.2	1060	2	P95638	ROMPA (FRAGMENT).	1.28e+01
24	47	71.2	1060	2	P95593	ROMPA (FRAGMENT).	1.28e+01
25	47	71.2	1060	2	P95585	ROMPA (FRAGMENT).	1.28e+01
26	47	71.2	1060	2	P95660	ROMPA (FRAGMENT).	1.28e+01
27	47	71.2	1060	2	P95659	ROMPA (FRAGMENT).	1.28e+01
28	47	71.2	1060	2	P95591	ROMPA (FRAGMENT).	1.28e+01
29	47	71.2	1060	2	P95642	ROMPA (FRAGMENT).	1.28e+01
30	47	71.2	1061	2	P94174	ROMPA (FRAGMENT).	1.28e+01
31	47	71.2	1061	2	P94855	ROMPA (FRAGMENT).	1.28e+01
32	47	71.2	1062	2	P95641	ROMPA (FRAGMENT).	1.28e+01
33	47	71.2	1062	2	P97237	ROMPA (FRAGMENT).	1.28e+01
34	47	71.2	2021	2	052657	190-RDA ANTIGEN (ROMPA	1.28e+01
35	46	69.7	294	2	053988	PARTIAL POB CLASS 3 O	2.06e+01
36	46	69.7	300	2	066051	CLASS 3 PORIN PROTEIN	2.06e+01
37	46	69.7	301	2	068155	PORIN PROTEIN (FRAGMEN	2.06e+01
38	46	69.7	326	2	051946	OUTER MEMBRANE PROTEIN	2.06e+01
39	46	69.7	326	2	051944	OUTER MEMBRANE PROTEIN	2.06e+01
40	46	69.7	326	2	051945	OUTER MEMBRANE PROTEIN	2.06e+01
41	46	69.7	521	2	044677	NEURAL PROTEASE.	2.06e+01
42	46	69.7	560	5	044626	KLID12.1 PROTEIN.	2.06e+01
43	46	69.7	642	10	064397	RECEPTOR-LIKE PROTEIN	2.06e+01
44	46	69.7	819	5	023004	SIMILAR TO G-PROTEIN C	2.06e+01
45	46	69.7	2543	5	P90649	156D SURFACE ANTIGEN.	2.06e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	337 AA.
AC	034232			
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	ORF40X1 PROTEIN.			
OS	VIBRIO CHOLERAE.			
OC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-AI-1837;			
RX	MEDLINE; 97252505.			
RA	STROEHER U.H., PARASIVAM G., DREDEGE B.K., MANNING P.A.;			
RT	"Novel Vibrio cholerae O139 genes involved in lipopolysaccharide			
RT	biosynthesis."			
RL	J. BACTERIOL. 179:2740-2747(1997).			
DR	EMBL; Y07786; E274690;			
SQ	SEQUENCE 337 AA; 40132 MW; 204A7939 CRC32;			

Query Match 78.8%; Score 52; DB 2; Length 337;
 Best Local Similarity 75.0%; Pred. No. 1.04e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB	147 QKXNSAPY 154	
OY	1 QKXNSDPY 8	
RESULT	2	
ID	087136	PRELIMINARY; PRT; 337 AA.
AC	087136	
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)	
DE	ORF139-17 PROTEIN.	
OS	VIBRIO CHOLERAE.	
OC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-MO45;	
RA	YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,	
RA	TAKEDA Y.;	
RT	"The genes responsible for O-antigen synthesis of Vibrio cholerae	

RT 0139 are closely related to those of Vibrio cholerae 022.";
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567; -;
 SQ SEQUENCE 337 AA; 40147 MW; 176B46EB CRC32;

Query Match 78.8%; Score 52; DB 2; Length 337;
 Best Local Similarity 75.0%; Pred. No. 1.04e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 147 OKYHSAVY 154
 111:111
 QY 1 OKYNSDPY 8

RESULT 3
 ID 028175 PRELIMINARY; PRT; 533 AA.
 AC 028175;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE RETINAL PIGMENT EPITHELIUM-SPECIFIC PROTEIN.
 OS BOS TAURUS (BOVINE).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC ARTIODACTYLIA: RUMINANTIA: PECORA: BOVIDAE: BOVINAE: BOS.

RP SEQUENCE FROM N.A.
 RC TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 93340181.

RA HAMEL C.P., TSILOU E., PEEFER B.A., HOOKS J.J., DETRICK B.,
 RA REDMOND T.,

RT "Molecular cloning and expression of RPE65, a novel retinal pigment
 epithelium-specific microsome protein that is post-transcriptionally
 regulated in vitro."

RL J. BIOL. CHEM. 268:15751-15757(1993).

RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 9323190.

RA HAMEL C.P., TSILOU E., HARRIS E.D., PEEFER B.A., HOOKS J.J.,
 RA DETRICK B., REDMOND T.,

RT "A developmentally regulated microsome protein specific for the
 pigment epithelium of the vertebrate retina."

RL J. NEUROSCI. RES. 34:414-425(1993).

DR EMBL: L11356; G163657; -;
 KW PIGMENT.

SQ SEQUENCE 533 AA; 60944 MW; 91D0716 CRC32;

Query Match 77.3%; Score 51; DB 6; Length 533;
 Best Local Similarity 66.7%; Pred. No. 1.74e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 424 OKYGRPYT 432
 111:111
 QY 1 OKYNSDPY 9

RESULT 4
 ID 005661 PRELIMINARY; PRT; 533 AA.
 AC 005661;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE RETINAL PIGMENT EPITHELIUM MEMBRANE RECEPTOR P63.
 OS BOS TAURUS (BOVINE).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC ARTIODACTYLIA: RUMINANTIA: PECORA: BOVIDAE: BOVINAE: BOS.

RP SEQUENCE FROM N.A., AND SEQUENCE OF 365-382 AND 407-423.
 RC STRAIN-STEINHOLZ; TISSUE-EYE;
 RX MEDLINE: 93386633.

RA BAYK C.O., HELLMAN U., WERNSTEDT C., ERIKSSON U.,
 RT "The retinal pigment epithelial membrane receptor for plasma

retinol-binding protein. Isolation and cDNA cloning of the 63-kDa

RT protein.";
 RL J. BIOL. CHEM. 268:20540-20546(1993).
 CC -1- FUNCTION: THIS RECEPTOR BINDS PLASMA RETINOL BINDING PROTEIN.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN RETINAL PIGMENT
 EPITHELIUM.

DR EMBL: X66277; G564; -;
 KW RECEPTOR; RETINOL-BINDING; PLASMA; MEMBRANE.
 FT MOD RES 21
 SQ SEQUENCE 533 AA; 60970 MW; F77E22D7 CRC32;

Query Match 77.3%; Score 51; DB 6; Length 533;
 Best Local Similarity 66.7%; Pred. No. 1.74e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 424 OKYGRPYT 432
 111:111
 QY 1 OKYNSDPY 9

RESULT 5
 ID 018744 PRELIMINARY; PRT; 342 AA.
 AC 018744;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE LU-ECAM-1.

OS BOS TAURUS (BOVINE).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC ARTIODACTYLIA: RUMINANTIA: PECORA: BOVIDAE: BOVINAE: BOS.

RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RX ELBE R.C., WIDOM J., GRUBER A.D., ABDEL-GHANY M., LEVINE R.,

RA GOODMAN A., PAULI B.U.,
 RA SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF001264; G2623769; -;
 SQ SEQUENCE 342 AA; 39037 MW; 0DF25F74 CRC32;

Query Match 75.8%; Score 50; DB 6; Length 342;
 Best Local Similarity 75.0%; Pred. No. 2.89e+00;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 111 KYGDPPYT 118
 11:111
 QY 2 KYNSDPY 9

RESULT 6
 ID 018742 PRELIMINARY; PRT; 794 AA.
 AC 018742;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE LU-ECAM-1.

OS BOS TAURUS (BOVINE).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC ARTIODACTYLIA: RUMINANTIA: PECORA: BOVIDAE: BOVINAE: BOS.

RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RX ELBE R.C., WIDOM J., GRUBER A.D., ABDEL-GHANY M., LEVINE R.,

RA GOODMAN A., PAULI B.U.,
 RA SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF001264; G2623765; -;
 SQ SEQUENCE 794 AA; 88509 MW; 2D450EEB CRC32;

Query Match 75.8%; Score 50; DB 6; Length 794;
 Best Local Similarity 75.0%; Pred. No. 2.89e+00;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 111 KYGDPPYT 118
 11:111

QY 2 KYNSDPYT 9

RESULT 7
ID 018743 PRELIMINARY; PRT: 820 AA.
AC 018743;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE LU-ECAM-1.
OS BOS TAUROS (BOVINE).
OC EURAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC ARTIOACETYLIA; ROMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA EBLE R.C., WIDOM J., GRUBER A.D., ABDEL-GHANY M., LEVINE R.,
RA GOODWIN A., PAULI B.U.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL: AF001263; G2623767; -
SEQUENCE 820 AA; 91464 MW; 171ED21C CRC32;

Query Match 75.8%; Score 50; DB 6; Length 820;
Best Local Similarity 75.0%; Pred. No. 2.89e+00;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 111 KYGDDPYT 118
QY 2 KYNSDPYT 9

RESULT 8
ID 018741 PRELIMINARY; PRT: 905 AA.
AC 018741;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LU-ECAM-1.
OS BOS TAUROS (BOVINE).
OC EURAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC ARTIOACETYLIA; ROMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA EBLE R.C., WIDOM J., GRUBER A.D., ABDEL-GHANY M., LEVINE R.,
RA GOODWIN A., PAULI B.U.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL: AF001261; G2623763; -
PFAM: PF00041; fn3; 1.
SEQUENCE 905 AA; 101005 MW; 86E5459 CRC32;

Query Match 75.8%; Score 50; DB 6; Length 905;
Best Local Similarity 75.0%; Pred. No. 2.89e+00;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 111 KYGDDPYT 118
QY 2 KYNSDPYT 9

RESULT 9
ID 066569 PRELIMINARY; PRT: 397 AA.
AC 066569;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 46.8 KD PROTEIN.
GN AQ.183.
OS ACUIFEX ABOLICUS.
CC BACTERIA; ACUIFICALES; ACUIFICACEAE; ACUIFEX.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;

EX MEDLINE; 98196666.
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUYAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL NATURE 392:353-358(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUYAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AE000677; G2982913; -
RW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 397 AA; 46821 MW; 29F9AF24 CRC32;

Query Match 74.2%; Score 49; DB 2; Length 397;
Best Local Similarity 66.7%; Pred. No. 4.77e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 362 QKXSDPYT 370
QY 1 QKXSDPYT 9

RESULT 10
ID 060295 PRELIMINARY; PRT: 1042 AA.
AC 060295;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PUTATIVE TYPE I RESTRICTION ENZYME R PROTEIN (EC 3.1.21.3).
GN MJECL40.
OS METHANOCOCCLUS JANNASCHII.
OC ARCHAEA; EURARCHAEOTA; METHANOCOCCELES; METHANOCOCCEACEAE;
CC METHANOCOCCLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96337999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.F., ADAMS M.D., REICH C.I.,
RA OVERBECK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
RA SCOTT J.L., GEORGHAEN N.S.M., WEIDMAN J.F., FUHRMAN J.L., NGUYEN D.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS R.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
RA KLEIN H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL SCIENCE 273:1058-1073(1996).
CC -1- FUNCTION: SUBUNIT R IS REQUIRED FOR BOTH NUCLEASE AND ATPASE
CC ACTIVITIES, BUT NOT FOR MODIFICATION (BY SIMILARITY).
CC -1- TYPE I RESTRICTION AND MODIFICATION ENZYMES ARE COMPLEX,
CC MULTI-FUNCTIONAL SYSTEMS WHICH REQUIRE ATP, S-ADENOSYL METHIONINE
CC AND MG(2+) AS CO-FACTORS AND, IN ADDITION TO THEIR
CC ENDONUCLEOLYTIC AND METHYLASE ACTIVITIES, ARE POTENT
CC DNA-DEPENDENT ATPASES (BY SIMILARITY).
CC -1- SUBUNIT: THE TYPE I RESTRICTION & MODIFICATION SYSTEM IS COMPOSED
CC OF THREE POLYPEPTIDES R,M AND S (BY SIMILARITY).
CC -1- SIMILARITY: WITH ATPASES.
DR EMBL: U77118; G1522673; -
DR PFAM: PF00271; helicase_C; 1.
RW HYPOTHETICAL PROTEIN; RESTRICTION SYSTEM; DNA-BINDING; ATP-BINDING.
SQ SEQUENCE 1042 AA; 121522 MW; 9FA7EE8 CRC32;

Query Match 74.2%; Score 49; DB 1; Length 1042;
Best Local Similarity 62.5%; Pred. No. 4.77e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 262 KYGDDPYT 269
QY 1 KYGDDPYT 9

OY 2 KYNSDPYT 9

RESULT 11 PRELIMINARY: PRT: 2098 AA.

AC P91443: 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE SIMILAR TO MYOSIN.

GN T10H10.1.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTERA; RHADITIDA; RHADITIDA;

OC RHADITIDA; RHADITIDEA; RHADITIDAE; PELODERINAE; CAENORHABDITIS.

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2:

RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRATON M., DEAR S., DU Z., DURBIN R., FAVELL A., FULTON L., GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCINTYRE A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFEK L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STULSTON J., THIRRY-MING J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLMAN P.; 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.

RT NATURE 368:32-38(1994).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2:

RA NELSON J., LANGSTON Y.;

RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]

RN SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2:

RA WATERSTON R.;

RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U80848; G1707260; 1.

DR PFAM: PF00063; myosin_head; 1.

DR PFAM: PF00784; MYTH4; 2.

DR SEQUENCE 2098 AA; 239782 MW; 3A668091 CRC32;

SO Query Match 74.2%; Score 49; DB 5; Length 2098; Best Local Similarity 71.4%; Pred. No. 4.77e+00; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1581 YNAEPT 1587

OY 3 YNSDPYT 9

RESULT 12 PRELIMINARY: PRT: 2270 AA.

AC 014581: 014580; 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE DIHYDROXYRINDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-1D SUBUNIT (ALPHA-1E).

GN CACNA1D.

OS HOMO SAPIENS (HUMAN)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CARNIVORINIA; HOMINIDAE; HOMO.

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE-HIPOCAMPUS;

RX MEDLINE: 94350992;

RA WILKINS M.E., MARUBIO L.M., DEAL C.R., HANS M., BRUST P.F.,

RA PHILIPSON L.H., MILLER R.J., JOHNSON E.C., HARPOLD M.M., ELLIS S.B.; "Structure and functional characterization of neuronal alpha 1E calcium channel subtypes";

RT J. BIOL. CHEM. 269:22347-22357(1994).

CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.

CC (DHP), A CALCIUM CHANNEL BLOCKER.

CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: BRAIN, RETINA AND SPLEN.

CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN (ALPHA-1E-1 AND ALPHA-1E-3) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ALPHA-1E-3.

CC -1- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.

DR EMBL: U29385; G495870; -.

DR EMBL: U29384; G495868; -.

DR MIM: 114206; -.

DR PFAM: PF00520; Ion. trans; 4.

RA IONIC CHANNEL; GLYCOPROTEIN; REPEAT; PHOSPHORYLATION; ALTERNATIVE SPLICING.

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2:

RX MEDLINE: 94350992;

RA WILKINS M.E., MARUBIO L.M., DEAL C.R., HANS M., BRUST P.F.,

RT NATURE 368:32-38(1994).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2:

RA NELSON J., LANGSTON Y.;

RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]

RN SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2:

RA WATERSTON R.;

RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U80848; G1707260; 1.

DR PFAM: PF00063; myosin_head; 1.

DR PFAM: PF00784; MYTH4; 2.

DR SEQUENCE 2098 AA; 239782 MW; 3A668091 CRC32;

SO Query Match 74.2%; Score 49; DB 5; Length 2270; Best Local Similarity 62.5%; Pred. No. 4.77e+00; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 2182 QRTSEPT 2189

OY 1 QRTSEPT 8

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RESULT 13
ID 015878 PRELIMINARY: PRT: 2312 AA.
AC 015878:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE VOLTAGE-OPERATED CALCIUM CHANNEL, ALPHA-1 SUBUNIT.
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95236033.
RA SCHNEIDER T., WEI X., OLCESE R., COSTANTIN J.L., NEELY A., PALADE P.,
RA PEREZ-REYES E., QIN N., ZHOU J., CRAWFORD G.D.:
RT "Molecular analysis and functional expression of the human type E
RT neuronal Ca2+ channel alpha 1 subunit."
RT RECEPT. CHANNELS 2:255-270(1994).
EMBL: L27745: G443761: -.
PFRM: PF00520: ion_trans: 4.
SQ SEQUENCE 2312 AA; 261727 MW; C04D476D CRC32;

Query Match 74.2%; Score 49; DB 4; Length 2312;
Best Local Similarity 62.5%; Pred. No. 4.77e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 2224 QRYISEPY 2231
OY 1 QKYNSDPY 8

RESULT 14
ID 025981 PRELIMINARY: PRT: 259 AA.
AC 025981:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 29.4 KD PROTEIN.
GN HP140.
OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
OC HELICOBACTER.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-26695;
RX MEDLINE: 97394467.
RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA NELSON K., QUACKENBUSH J., ZHOU L., KIRNESS E.F., PETERSON S.,
RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODER A.,
RA MCKENNEY K., FITZGERALD L.M., LEE N.H., ADAMS M.D., HICKEY E.K.,
RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATHEY L., WALLIN E.,
RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
RA VENTER J.C.:
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori(published erratum appears in Nature 1997 Sep
RT 25:389(6649):412)."
RL NATURE 388:539-547(1997).
DR EMBL: AE000644: G2314621: -.
DR TIGR: HP1440: -.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 259 AA; 29361 MW; 59460701 CRC32;

Query Match 72.7%; Score 48; DB 2; Length 259;
Best Local Similarity 55.6%; Pred. No. 7.83e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 148 QTFHSNPT 156
OY 1 QKYNSDPY 9

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RESULT 15
ID 029360 PRELIMINARY: PRT: 270 AA.
AC 029360:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN AF0902.
OS ARCHAEoglobus fulgidus.
OC ARCHAEA; EURYARCHAEOTA; ARCHAEoglobales; ARCHAEoglobaceae;
OC ARCHAEoglobus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE: 98049343.
RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L.,
RA OVERBEER R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTIACH P., KAYNE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.:
RT "The complete genome sequence of the hyperthermophilic,
RT sulphate-reducing archaeon Archaeoglobus fulgidus."
RL NATURE 390:364-370(1997).
DR EMBL: AF01041: G2649696: -.
DR TIGR: AF0902: -.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 270 AA; 30971 MW; 195DB20D CRC32;

Query Match 71.2%; Score 47; DB 1; Length 270;
Best Local Similarity 55.6%; Pred. No. 1.28e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 19 EKYSPNPT 27
OY 1 QKYNSDPY 9

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Search completed: Thu Sep 2 12:10:23 1999
Job time : 23 secs.

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(TM)

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protein database search, using Smith-Waterman algorithm

t generated.

1 OKYISAPYT 9

PAM 150

179066 seqs, 54579741 residues

Listing first 45 summaries

sptrembl 9

13:sp_vertebrate 14:sp_virus

Mean 22.518; Variance 27.925; scale 0.806

ved by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description	Pred. No.
1	8	2370	4	014581	DIHYDROPIRIDINE-SENSIT	8.37e-01
1	8	2312	4	015878	VOLTAGE-OPERATED CALCI	8.37e-01
2	5	413	2	P96740	SIMILAR TO E.	5.90e+00
3	5	5	2	059193	THERMOLYSIN PRECURSOR	5.90e+00
3	5	8	2	059223	THERMOLYSIN PRECURSOR	5.90e+00
3	5	8	2	043880	THERMOLYSIN PRECURSOR	5.90e+00
4	2	92	4	012810	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	92	4	015461	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	236	4	014538	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	292	4	014538	MACROPHAGE LECTIN 2	9.47e+00
4	2	326	4	013048	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	337	2	034232	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	337	2	081136	ORF40X1 PROTEIN.	9.47e+00
4	2	351	4	015225	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	378	4	015236	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	402	4	015227	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	411	4	015228	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	419	4	015234	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	419	4	013047	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	419	4	015240	PREGNANCY-SPECIFIC BET	9.47e+00
4	2	424	4	075244	PSG9 PREGNANCY SPECIFI	9.47e+00
4	2	424	4	075244	PSG9-12.	9.47e+00

45	66.2	1683	13	Q91741	FOURTH COMPONENT OF CO	5.88e+010
44	68.2	993	4	Q48915	REPTIDE SYNTHETASE MOD	5.88e+010
43	65.2	533	4	Q16518	RETINAL PIGMENT EPTHE	5.88e+010
42	65.2	533	4	Q48915	REPTIDE SYNTHETASE MOD	5.88e+010
41	68.2	434	2	Q52963	CHEMOTAXIS MOTC PROTEI	5.88e+010
40	68.2	308	10	Q28261	ALPHA SUBUNIT OF F-ACTI	5.88e+010
39	68.2	252	2	Q52932	REPLICATION SYNTHETASE (F	5.88e+010
38	68.2	190	14	Q84303	REPLICATION PROTEIN (F	5.88e+010
37	69.7	4848	2	Q07944	PRISTINAYNCIN SYNTHASA	3.76e+010
36	69.7	3588	2	Q66070	LIChENISYNCIN SYNTHETASE	3.76e+010
35	69.7	1087	5	Q22450	SMILAIR TO DOPAMINE RE	3.76e+010
34	69.7	903	4	Q75159	KIAO684 PROTEIN (FRAG	3.76e+010
33	69.7	722	3	Q13839	PUTATIVE G2-SPECIFIC P	3.76e+010
32	69.7	691	8	P22831	NAHD DEHYDROGENASE (FR	3.76e+010
31	69.7	659	1	Q28894	HEMERODISULFIDE REDUCT	3.76e+010
30	69.7	560	5	Q46626	KIAD1.1 PROTEIN.	3.76e+010
29	71.2	495	9	P79678	SHEATH PROTEIN GPL.	2.39e+010
28	71.2	332	10	Q65485	HYPOTHEICAL 37.7 KD P	2.39e+010
27	71.2	154	13	Q91759	HYPOTHEICAL 37.7 KD P	2.39e+010
26	72.7	198	8	P73972	HYPOTHEICAL 63.9 KD P	1.51e+010
25	72.7	228	5	Q27918	P53 TUMOR SUPPRESSOR H	1.51e+010
24	72.7	228	5	Q27918	P53 TUMOR SUPPRESSOR H	1.51e+010
23	74.2	426	4	Q15237	PSG11 PRECURSOR.	9.47e+000
22	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
21	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
20	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
19	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
18	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
17	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
16	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
15	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
14	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
13	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
12	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
11	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
10	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
9	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
8	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
7	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
6	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
5	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
4	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
3	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
2	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000
1	74.2	424	4	Q15224	PREGNANCY-SPECIFIC-BET	9.47e+000

ALIGNMENTS

ID	Q14581	PRELIMINARY;	PRT;	2270 AA
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ID	RESULT	1	PRELIMINARY;	PRT;	2270	AA.
AC	014581	014580;				
DT	01-JAN-1998	(TREMBLEREL. 05, CREATED)				
DT	01-JAN-1998	(TREMBLEREL. 05, LAST SEQUENCE UPDATE)				
DT	01-NOV-1998	(TREMBLEREL. 06, LAST ANNOTATION UPDATE)				
DE	DIBYDROPIRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-1D SUBUNIT					
DE	(ALPHA-1E).					
GN	CACNA1D.					
OS	HOMO SAPIENS (HUMAN).					
OC	EXTRACOT.; METAEOA.; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMAT					
OC	CATARRHINI; HOMINIDAE; HOMO.					
RA	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HIPPOCAMPUS;					
RC	MEDLINE; 94350992.					
RA	WILLIAMS M.E., MARBIO L.M., DEAL C.R., HANS M., BRST P.F.,					
RA	PHILLIPSON L.H., MILLER R.J., JOHNSON E.C., HARPOID M.M., ELLIS S.B.;					
RT	"Structure and functional characterization of neuronal alpha 1e					
RT	calcium channel subtypes.;					
RL	J. BIOL. CHEM. 269:22347-22357(1994).					
CC	-1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE					
CC	IN EXCITATION-CONTRACTION COUPLING.					
CC	THE ALPHA-1 SUBUNIT BINDS DIHYDROPIRIDINE					
CC	(DHP). A CALCIUM CHANNEL BLOCKER.					
CC	-1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS					
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA.					
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.					
CC	-1- TISSUE SPECIFICITY: BRAIN, RETINA AND SPLEEN.					
CC	-1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN					
CC	(ALPHA-1E-1 AND ALPHA-1E-3) ARE PRODUCED BY ALTERNATIVE SPLICING					
CC	OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ALPHA-1E-3.					
CC	-1- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.					
DR	EMBL; L29385; G495870; -					
DR	EMBL; L29384; G495868; -					
DR	MM; 114206; -					
DR	PEPM; PF00520; 10n_trans; 4.					
RV	IONIC CHANNEL, TRANSMEMBRANE; ION TRANSPORT; VOLTAGE-GATED CHANNEL;					
RV	CALCIUM CHANNEL, GLYCOPROTEIN, REPEAT; PHOSPHORYLATION;					
RV	ALTERNATIVE SPLICING.					
FT	TRANSEM	90	108	S1 OF REPEAT 1 (POTENTIAL).		
FT	TRANSEM	128	146	S2 OF REPEAT 1 (POTENTIAL).		
FT	TRANSEM	159	173	S3 OF REPEAT 1 (POTENTIAL).		
FT	TRANSEM	186	205	S4 OF REPEAT 1 (POTENTIAL).		

FT TRANSMEM 224 244 S5 OF REPEAT I (POTENTIAL).
 FT TRANSMEM 327 350 S6 OF REPEAT I (POTENTIAL).
 FT TRANSMEM 447 496 S1 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 510 529 S2 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 539 557 S3 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 568 586 S4 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 606 625 S5 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 679 703 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 716 721 POLY-GLU.
 FT DOMAIN 748 753 POLY-ARG.
 FT DOMAIN 767 772 POLY-GLU.
 FT DOMAIN 1106 1112 POLY-GLU.
 FT TRANSMEM 1149 1165 S1 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1190 1208 S2 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1218 1240 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1228 1231 POLY-VAL.
 FT TRANSMEM 1255 1270 S4 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1290 1311 S5 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1399 1422 S6 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1480 1498 S1 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1514 1533 S2 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1542 1560 S3 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1572 1590 S4 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1610 1629 S5 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1699 1724 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 2241 2245 POLY-ARG.
 FT REPEAT 54 354 I.
 FT REPEAT 462 706 II.
 FT REPEAT 1140 1426 III.
 FT REPEAT 1463 1726 IV.
 FT CARBOHYD 66 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 1090 1090 POTENTIAL.
 FT CARBOHYD 1566 1566 POTENTIAL.
 FT CARBOHYD 1571 1571 POTENTIAL.
 FT CARBOHYD 1987 1987 POTENTIAL.
 FT VARSPLIC 748 MISSING (IN ALPHA-1E-1).
 SQ SEQUENCE 2270 AA; 257348 MW; 5464AF92 CRC32;

Query Match 81.8%; Score 54; DB 4; Length 2270;
 Best Local Similarity 75.0%; Pred. No. 8.37e-01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2182 QRYISEPY 2189
 QY 1 QRYISAPY 8
 RESULT 2
 AC 015878; PRELIMINARY; PRT; 2312 AA.
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE VOLTAGE-OPERATED CALCIUM CHANNEL, ALPHA-1 SUBUNIT.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95236033.
 RA SCHNEIDER T., WEI X., OLCESE R., COSTANTIN J.L., NEELY A., PALADE P.,
 RA PEREZ-REYES E., QIN N., ZHOU J., CRAWFORD G.D.;
 RT "Molecular analysis and functional expression of the human type E
 RT neuronal Ca2+ channel alpha 1 subunit."
 RL RECEPT. CHANNELS 2:255-270(1994).
 DR EMBL: L27745; G443761; -;
 DR PFM: PF00520; Ion-trans; -;
 SQ SEQUENCE 2312 AA; 261727 MW; C04D476D CRC32;

Query Match 81.8%; Score 54; DB 4; Length 2312;
 Best Local Similarity 75.0%; Pred. No. 8.37e-01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2224 QRYISEPY 2231
 QY 1 QRYISAPY 8
 RESULT 3
 ID P96740 PRELIMINARY; PRT; 413 AA.
 AC P96740;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SIMILAR TO E.
 GN COLI NLPC PROTEIN AND TO LISTERIA SPECIES P60-RELATED PROTEINS.
 OS BACILLUS SUBTILIS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RL LELONG C., GLASER P., PRESECAN E., DANCHIN A.;
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE: 98044033.
 RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
 RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTINI A., BORCHERT S.,
 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELL S.C., BRON S.,
 RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 RA DENIZOT F., DEVINE K.M., DOSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
 RA ENLITAN K.D., ERRINGTON J., FABBET C., FERRARI E., FOUGIER D.,
 RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
 RA CHIM S.T., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
 RA GUISEPTI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A.,
 RA HILBERT H., HOLSAPPEL S., HOSONO S., HUULO M.F., ITAYA M., JONES L.,
 RA JORIS B., KARAWATA D., KASAHARA Y., KLAERER-BLANCHARD M., KLEIN C.,
 RA KOHAYASHI Y., KOETTER P., KONINGSSTEIN G., KROGH S., KUMANO M.,
 RA KURITA K., LAPIDOS A., LARDINOS S., LABER J., LAZAREVIC V.,
 RA LEE S.M., LEVINE A., LIT H., MASUDA S., MAUEL C., MEDIGUE C.,
 RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 RA NOONE D., O'REILLY M., OGAWA K., OGIMAWA A., ODEGA B., PARK S.H.,
 RA PARRO V., POHL T.M., PORTELELL D., POROMOLIK S., PRESCOTT A.M.,
 RA PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
 RA RIEGER M., RIYOUTA C., ROCHA E., ROCHE B., ROSE M., SDALE Y.,
 RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
 RA SEKIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S.,
 RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEKAWA K.,
 RA TAKEUCHI M., TAKAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
 RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
 RA VIARI A., WANDUT R., WEDLER E., WEDLER H., WEITZENERGER T.,
 RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUOTO K., YATA K.,
 RA YOSHIDA K., YOSHIKAWA H.F., ZIMSTEIN E., YOSHIKAWA H., DANCHIN A.;
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 RT subtilis."
 RL NATURE 390:249-256(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL: 292954; E308092; -;
 DR EMBL: 293122; E1184482; -;
 DR PFM: PF00877; NLPC_P60; 3.
 SQ SEQUENCE 413 AA; 45247 MW; 82C5259A CRC32;

Query Match 75.8%; Score 50; DB 2; Length 413;
 Best Local Similarity 62.5%; Pred. No. 5.90e-00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KXISAPY 8

RESULT 4
ID 059193 PRELIMINARY: PRT: 546 AA.

AC 059193:

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE THERMOLYSIN PRECURSOR (EC 3.4.24.27)

DE (THERMOSTABLE NEUTRAL PROTEINASE).

GN NPR.

OS BACILLUS CALDOLYTICUS.

OC BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;

OC BACILLUS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Y-T;

ME: 96328267.

SAUL D.J., WILLIAMS L.C., TOOGOOD H.S., DANIEL R.M., BERGQUIST P.L.:

"Sequence of the gene encoding a highly thermostable neutral

protease from *Bacillus* sp. strain EAI: expression in *Escherichia*

coli and characterization."

RT BIOCHIM. BIOPHYS. ACTA 1308:74-80(1996).

RL FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.

-1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: XAA-|-LEU > XAA-|-PHE.

-1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR

PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4

(ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.

EMBL: U25629; G995782; -

DR PROSITE: PS00142; ZINC_PROTEASE; 1.

KM HYDROLASE: METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL;

KM METAL-BINDING.

FT SIGNAL

FT PROPEP

FT CHAIN

FT METAL

FT ACT_SITE

FT METAL

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RL BIOCHIM. BIOPHYS. ACTA 1308:74-80(1996).

CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.

CC HAS COLLAGENASE ACTIVITY

CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: XAA-|-LEU > XAA-|-PHE.

CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR

PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4

(ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.

EMBL: U25630; G995784; -

DR PROSITE: PS00142; ZINC_PROTEASE; 1.

KM HYDROLASE: METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL;

KM METAL-BINDING.

FT SIGNAL

FT PROPEP

FT CHAIN

FT METAL

FT ACT_SITE

FT METAL

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Query Match

Best Local Similarity 75.8%; Score 50; DB 2; Length 546;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 244 OKYINTTS 252

OY 1 KXISAPY 9

RESULT 6

ID 043880 PRELIMINARY: PRT: 546 AA.

AC 043880:

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE THERMOLYSIN PRECURSOR (EC 3.4.24.27)

DE (THERMOSTABLE NEUTRAL PROTEINASE).

OS ALICYCLOBACILLUS ACIDOCALDARIUS (BACILLUS ACIDOCALDARIUS).

OC BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;

OC ALICYCLOBACILLUS GROUP; ALICYCLOBACILLUS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BT1;

ME: 95309716.

RA VECERER B., RYSLIK P.:

"Cloning and sequencing of the neutral protease-encoding gene from a

thermophilic strain of *Bacillus* sp."

RT GENE 158:147-148(1995).

RL -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.

-1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: XAA-|-LEU > XAA-|-PHE.

-1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR

PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4

(ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.

EMBL: U07824; G563121; -

DR PROSITE: PS00142; ZINC_PROTEASE; 1.

KM HYDROLASE: METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL;

KM METAL-BINDING.

FT SIGNAL

FT PROPEP

FT CHAIN

FT METAL

FT ACT_SITE

FT METAL

FT ACT_SITE

FT ACT_SITE

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FT ACT_SITE

FT ACT_SITE

FT ACT_SITE

FT ACT_SITE

Db 244 OKYINTTYS 252
 |||::||
 QY 1 OKYISAPYT 9

RESULT 7
 ID 012810 PRELIMINARY; PRT; 92 AA.
 AC 012810;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN (FRAGMENT).
 GN PSGL1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95104846.
 RA MCLEACHAN P.A.; RUTHERFURD K.J.; BEGGS K.T.; SIMS S.E.;
 RT MANSFIELD B.C.;
 RT "Characterization of the PSGL1 gene."
 RL GENOMICS 22:356-363(1994).
 DR EMBL; U04323; G443729; -.
 KW PREGNANCY.
 FT NON_TER 1 1
 FT NON_TER 92 92
 SQ SEQUENCE 92 AA; 10443 MW; ADD694D3 CRC32;

Query Match 74.2%; Score 49; DB 4; Length 92;
 Best Local Similarity 71.4%; Pred. No. 9.47e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 65 KYIAGPY 71
 |||::||
 QY 2 KYISAPY 8

RESULT 8
 ID 015461 PRELIMINARY; PRT; 236 AA.
 AC 015461;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN-11 (FRAGMENT).
 GN PSGL1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-BLOOD;
 RX MEDLINE; 95104846.
 RA MCLEACHAN P.A.; RUTHERFURD K.J.; BEGGS K.T.; SIMS S.E.;
 RT MANSFIELD B.C.;
 RT "Characterization of the PSGL1 gene."
 RL GENOMICS 22:356-363(1994).
 DR EMBL; U08196; G493743; -.
 DR EMBL; U08194; G493743; JOINED.
 DR EMBL; U08195; G493743; JOINED.
 DR PFAM; PF00047; 19; 1.
 KW PREGNANCY.
 FT NON_TER 236 236
 FT NON_TER 236 236
 SQ SEQUENCE 236 AA; 26816 MW; 9E47AD86 CRC32;

Query Match 74.2%; Score 49; DB 4; Length 236;
 Best Local Similarity 71.4%; Pred. No. 9.47e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYIAGPY 215
 |||::||
 QY 2 KYISAPY 8

RESULT 9
 ID 014538 PRELIMINARY; PRT; 292 AA.
 AC 014538;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MACROPHAGE LECTIN 2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96108853.
 RA SUZUKI N.; YAMAMOTO K.; TOYOSHIMA S.; OSAMA T.; IRIKURA T.;
 RT "Molecular cloning and expression of cdna encoding human macrophage
 C-type lectin. Its unique carbohydrate binding specificity for Tn
 antigen."
 RT J. IMMUNOL. 156:128-135(1996).
 DR EMBL; D50532; D1009736; -.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PFAM; PF00059; Lectin_c; 1.
 KW LECTIN.
 FT NON_TER 292 292
 FT NON_TER 32937 MW; 7319BC29 CRC32;

Query Match 74.2%; Score 49; DB 4; Length 292;
 Best Local Similarity 55.6%; Pred. No. 9.47e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 205 OKYISAPYT 213
 |||::||
 QY 1 OKYISAPYT 9

RESULT 10
 ID 013048 PRELIMINARY; PRT; 326 AA.
 AC 013048;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC BETA 1-GLYCOPROTEIN 4 PRECURSOR.
 GN PSGL4.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-LIVER;
 RX MEDLINE; 95314639.
 RA TEGJUND S.; ZHOU G.O.; HAMMARSTRÖM S.;
 RT "Characterization of cdna encoding novel pregnancy-specific
 glycoprotein variants."
 RT BIOCHEM. BIOPHYS. RES. COMMUN. 211:656-664(1995).
 DR EMBL; U18469; G609318; -.
 DR PFAM; PF00047; 19; 2.
 KW SIGNAL; PREGNANCY.
 FT SIGNAL 1 34
 FT CHAIN 35 326
 FT POTENTIAL.
 FT PREGNANCY-SPECIFIC BETA 1-GLYCOPROTEIN
 SQ SEQUENCE 326 AA; 36229 MW; 3632C5AD CRC32;

Query Match 74.2%; Score 49; DB 4; Length 326;
 Best Local Similarity 71.4%; Pred. No. 9.47e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYIAGPY 215
 |||::||
 QY 2 KYISAPY 8

RESULT 11
 ID 034232 PRELIMINARY; PRT; 337 AA.

AC 034232;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE 0R40X1 PROTEIN.
OS VIBRIO CHOLERAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AT-1837;
RX MEDLINE: 97252505.
RT STROEHER U.H., PARASIVAN G., DREDGE B.K., MANNING P.A.;
RT "Novel Vibrio cholerae 0139 genes involved in lipopolysaccharide biosynthesis."
RL J. BACTERIOL. 179:2740-2747(1997).
DR EMBL: Y07786; E274690; -;
SQ SEQUENCE 337 AA; 40132 MW; 2DA47939 CRC32;
Query Match 74.2%; Score 49; DB 2; Length 337;
Best Local Similarity 87.5%; Pred. No. 9.47e+00;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 147 OKYISAPY 154
OY 1 OKYISAPY 8
RESULT 12
ID 087136 PRELIMINARY; PRT; 337 AA.
AC 087136;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ORF139-17 PROTEIN.
OS VIBRIO CHOLERAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MO45;
RA YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,
RA TAREDA Y.;
RT "The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are closely related to those of Vibrio cholerae 022.";
RT SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AB012956; D1034567; -;
SQ SEQUENCE 337 AA; 40147 MW; 176B46EB CRC32;
Query Match 74.2%; Score 49; DB 2; Length 337;
Best Local Similarity 87.5%; Pred. No. 9.47e+00;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 147 OKYISAPY 154
OY 1 OKYISAPY 8
RESULT 13
ID 015225 PRELIMINARY; PRT; 351 AA.
AC 015225;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN (SP1) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90268037.
RT ZHENG Q.X., TEASE L.A., SHUPERT W.L., CHAN W.Y.;
RT "Characterization of cDNAs of the human pregnancy-specific beta 1-glycoprotein family, a new subfamily of the immunoglobulin gene superfamily.";

RL BIOCHEMISTRY 29:2845-2890(1990).
DR EMBL: M31126; G190551; -;
DR PFAM: PF00047; 19; 2.
KW PREGNANCY.
FT NON_TER
SQ SEQUENCE 351 AA; 39874 MW; 51423514 CRC32;
Query Match 74.2%; Score 49; DB 4; Length 351;
Best Local Similarity 71.4%; Pred. No. 9.47e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 158 KYIAGPY 164
OY 2 KYIAGPY 8
RESULT 14
ID 015236 PRELIMINARY; PRT; 378 AA.
AC 015236;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 11 (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA MCDONALD R.E., MCLENACHAN P.A., MANSFIELD B.C.;
RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: M38046; G190610; -;
DR PFAM: PF00047; 19; 3.
RT PREGNANCY.
FT NON_TER
SQ SEQUENCE 378 AA; 43126 MW; 64A4E137 CRC32;
Query Match 74.2%; Score 49; DB 4; Length 378;
Best Local Similarity 71.4%; Pred. No. 9.47e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 161 KYIAGPY 167
OY 2 KYIAGPY 8
RESULT 15
ID 015227 PRELIMINARY; PRT; 402 AA.
AC 015227;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN PRECURSOR.
GN PSG11.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE: 92017749.
RA CHAN W.Y., ZHENG Q.X., MCMAHON J., TEASE L.A.;
RT "Characterization of new members of the pregnancy-specific beta 1-glycoprotein family.";
RT MOL. CELL. BIOCHEM. 106:161-170(1991).
RL EMBL: M94890; G190568; -;
DR PFAM: PF00047; 19; 2.
DR SIGNAL
FT CHAIN 36 402 POTENTIAL.
FT CHAIN 36 402 PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN.
SQ SEQUENCE 402 AA; 45336 MW; CF3E4568 CRC32;
Query Match 74.2%; Score 49; DB 4; Length 402;
Best Local Similarity 71.4%; Pred. No. 9.47e+00;

Matches	5;	Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;
Db	209	KYIAGPY	215						
		:							
QY	2	KYISAPY	8						

Search completed: Thu Sep 2 12:13:53 1999
Job time : 24 secs.

FT TRANSMEM 186 204 S4 OF REPEAT I.
FT TRANSMEM 224 243 S5 OF REPEAT I.
FT TRANSMEM 327 351 S6 OF REPEAT I.
FT TRANSMEM 477 495 S1 OF REPEAT II.
FT TRANSMEM 511 530 S2 OF REPEAT II.
FT TRANSMEM 539 557 S3 OF REPEAT II.
FT TRANSMEM 568 586 S4 OF REPEAT II.
FT TRANSMEM 606 625 S5 OF REPEAT II.
FT TRANSMEM 679 703 S6 OF REPEAT II.
FT TRANSMEM 1144 1162 S1 OF REPEAT III.
FT TRANSMEM 1179 1198 S2 OF REPEAT III.
FT TRANSMEM 1211 1229 S3 OF REPEAT III.
FT TRANSMEM 1244 1262 S4 OF REPEAT III.
FT TRANSMEM 1282 1301 S5 OF REPEAT III.
FT TRANSMEM 1389 1413 S6 OF REPEAT III.
FT TRANSMEM 1469 1487 S1 OF REPEAT IV.
FT TRANSMEM 1503 1522 S2 OF REPEAT IV.
FT TRANSMEM 1531 1549 S3 OF REPEAT IV.
FT TRANSMEM 1562 1580 S4 OF REPEAT IV.
FT TRANSMEM 1600 1619 S5 OF REPEAT IV.
FT TRANSMEM 1689 1713 S6 OF REPEAT IV.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 1556 1556 POTENTIAL.
FT CARBOHYD 1561 1561 POTENTIAL.
SQ SEQUENCE 2259 AA; 254250 MW; 3466267E CRC32;

Query Match 81.8%; Score 54; DB 1; Length 2259;
Best Local Similarity 75.0%; Pred. No. 2,11e-01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2172 QRYISEPY 2179

OY 1 QRYISAPY 8

RESULT 2 STANDARD: PRT: 309 AA.
ID YAOB_SCHPO
AC Q10111;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 35.3 KD PROTEIN C1866.11C IN CHROMOSOME I.
GN SPAC1866.11C.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.
[1]
SEQUENCE FROM N.A.
STRAIN-972;
RA CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDEAN M.A., WALSH S.V.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDbJ DATA BANKS.
CC -1- SIMILARITY: TO S. POMBE SPAC1464.04.
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CC -----
CC EMBL; 268198; E213816; -
DR HYPOTHETICAL PROTEIN.
KM
SQ SEQUENCE 309 AA; 35297 MW; 639221F7 CRC32;

Query Match 75.8%; Score 50; DB 1; Length 309;
Best Local Similarity 62.5%; Pred. No. 1,80e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 241 QRYVSGPY 248
OY 1 QRYISAPY 8

RESULT 3 STANDARD: PRT: 544 AA.
ID NPRE_BACCL
AC P23384;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 32, LAST ANNOTATION UPDATE)
DE BACILLOLYSIN PRECURSOR (EC 3.4.24.28) (THERMOSTABLE NEUTRAL PROTEASE).
OS BACILLUS CALDOLYTICUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC BACILLUS.
[1]
SEQUENCE FROM N.A.
RX MEDLINE; 91286196.
RA VAN DEN BERG B., ENEQUIST H.G., VAN DE HAAR M.E., EIJNSINK V.G.H.,
RA STOLP B.K., VENEMA G.;
RT "A highly thermostable neutral protease from *Bacillus caldolyticus*:
RT cloning and expression of the gene in *Bacillus subtilis* and
RT characterization of the gene product."
RT J. BACTERIOL. 173:4107-4115(1991).
CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.
CC -1- CATALYTIC ACTIVITY: SIMILAR, BUT NOT IDENTICAL, TO THAT OF
CC THERMOLYSIN.
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
CC PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4 (ZINC METALLOPROTEASE);
CC ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.

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DR EMBL; M63575; G143251; -
DR PIR; A42464; A42464.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR HSSP; P00800; 1TLP.
KM HYDROLASE; METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 225 ACTIVATION PEPTIDE.
FT CHAIN 226 544 BACILLOLYSIN.
FT METAL 370 370 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 371 371 BY SIMILARITY.
FT METAL 374 374 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 394 394 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 459 459 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 544 AA; 59413 MW; 2079A17D CRC32;

Query Match 75.8%; Score 50; DB 1; Length 544;
Best Local Similarity 55.6%; Pred. No. 1,80e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 242 QRYITVTS 250
OY 1 QRYISAPY 9

RESULT 4 STANDARD: PRT: 548 AA.
ID THER_BACST
AC P06874;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE THERMOLYSIN PRECURSOR (EC 3.4.24.27) (THERMOSTABLE NEUTRAL
DE PROTEINASE).
GN NPRT.
OS BACILLUS STEAROTHERMOPHILUS.

CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 230-243.
RX MEDLINE: 85289021.
RA TAKAGI M., IMANAGA T., AIBA S.;
RT "Nucleotide sequence and promoter region for the neutral protease
gene from *Bacillus stearothermophilus*.";
RL J. BACTERIOL. 163:824-831(1985).
CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: XAA-I-LEU > XAA-I-PHE.
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
CC PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4 (ZINC METALLOPROTEASE);
CC ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.
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CC -----
DR EMBL: M1446; G143247; .
DR PIR: A24924; HYBS
DR PROSITE: PS00442; ZINC_PROTEASE; 1.
DR HSSP: P00800; 1TLP.
KW HYDROLASE; METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL.
FT SIGNAL 1 25
FT PROPEP 26 229 ACTIVATION PEPTIDE.
FT CHAIN 230 548 THERMOLYSIN.
FT METAL 374 374 ZINC (CATALYTIC).
FT ACT_SITE 375 375
FT METAL 378 378 ZINC (CATALYTIC).
FT METAL 398 398 ZINC (CATALYTIC).
FT ACT_SITE 463 463 PROTON DONOR.
SQ SEQUENCE 548 AA: D9E072E2 CRC32;
Query Match 75.8%; Score 50; DB 1; Length 548;
Best Local Similarity 55.6%; Pred. No. 1.80e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DB 246 OKIINTYS 254
OY 1 OKIISAPY 9
SULP 5
ID VEL_HPV54 STANDARD; PRT; 633 AA.
AC 081020;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE REPLICATION PROTEIN EL.
GN EL.
OS HUMAN PAPILLOMAVIRUS TYPE 54.
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPAPOVIRIDAE; PAPILLOMAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RL DELIUS H.;
RA SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
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CC -----
DR EMBL: U37488; G1017785; .
DR PFAM: PF00519; EL; 1.
DR PFAM: PF00524; EL; 1.
KW EARLY PROTEIN; DNA REPLICATION; HELICASE; ATP-BINDING; DNA-BINDING;
KW NUCLEAR PROTEIN.
FT NP_BIND 460 467 ATP (POTENTIAL).
SQ SEQUENCE 633 AA: 71835 MW; 233A9251 CRC32;
Query Match 75.8%; Score 50; DB 1; Length 633;
Best Local Similarity 62.5%; Pred. No. 1.80e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 85 RYIGSPY 92
OY 1 OKIISAPY 8
RESULT 6
ID YL86_CAEEL STANDARD; PRT; 306 AA.
AC P34444;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 34.6 KD PROTEIN F54C8.6 IN CHROMOSOME III.
GN F54C8.6.
OS CAENORHABDITIS ELEGANS.
OC EURARYOTA; METAZOA; NEMATODA; SECCERNTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERS M.,
RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSYER N.,
RA LAFREILLE P., LIGHTING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SINGH M., SMALDON N., SMITH A., SMITH M., SONNHAMER E., STADEN R.,
RA SUSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans".
RL NATURE 368:32-38(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z22178; E1347201; .
DR WORMPEP: F54C8.6; CE00192.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 306 AA: 34610 MW; EE04BE68 CRC32;
Query Match 74.2%; Score 49; DB 1; Length 306;
Best Local Similarity 71.4%; Pred. No. 3.03e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 110 RYIGTPY 116
OY 2 RYISAPY 8

RESULT 7
ID PSGB_HUMAN STANDARD: PRT: 426 AA.
AC 000887:
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 11 PRECURSOR (PSBG-11)
DE (PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 11)
DE GLYCOPROTEIN B) (PS34) (PSG7).
GN PSBG11.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CAVIARIINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA:
RX MEDLINE: 90212666.
RA ARAKAWA F., KUROKI M., MISUMI Y., MATSUO Y., MATSUOKA Y.;
RT "The nucleotide and deduced amino acid sequences of a cDNA encoding a
RT new species of pregnancy-specific beta 1-glycoprotein (PS beta G).";
RT BIOCHIM. BIOPHYS. ACTA 1048:303-305(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA:
RX MEDLINE: 90256167.
RA STREYDIO C., SWISSELS S., GEORGES M., SZPIRER C., VASSART G.;
RT "Structure, evolution and chromosomal localization of the human
RT pregnancy-specific beta 1 glycoprotein gene family.";
RT GENOMICS 6:578-592(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER:
RX MEDLINE: 90226362.
RA KHAN W.N., HAMMARSTROM S.;
RT "Identification of a new carcinoembryonic antigen (CEA) family member
RT in human fetal liver -- cloning and sequence determination of
RT pregnancy-specific glycoprotein 7.";
RT BIOCHEM. BIOPHYS. RES. COMMUN. 168:214-225(1990).
RN [4]
RP SEQUENCE OF 23-143 FROM N.A.
RC TISSUE-BLOOD:
RX BEGGS K.T., MCLENACHAN T., MANSFIELD B.;
RT SUBMITTED (AUG-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE OF 416-426 FROM N.A.
RX MEDLINE: 95104846.
RA MCLENACHAN P.A., RUTHERFORD K.J., BEGGS K.T., SIMS S.E.,
RA MANSFIELD B.C.;
RT "Characterization of the PSBG gene";
RT GENOMICS 22:356-363(1994).
RN -1- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING
RN PREGNANCY.
RN -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 3
RN C2-LIKE AND ONE V-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC
RN ANTIGEN SUBFAMILY.
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CC -----
CC EMBL: X17610; G35745; -
CC EMBL: M34421; G306800; -
CC EMBL: M34481; G33767; -
CC EMBL: M38243; G553627; -
CC EMBL: U04325; G443734; -
CC MIM: 176398; -
CC PEAM: PRO0047; 19; 3
CC IMMUNOGLOBULIN FOLD; GLYCOPROTEIN; SIGNAL; MULTIGENE FAMILY.
CC SIGNAL 1 34 POTENTIAL.

FT CHAIN 35 426 PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN
FT DOMAIN 35 144 11.
FT DOMAIN 162 224 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 255 317 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 347 401 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 169 217 PROBABLE.
FT DISULFID 262 310 PROBABLE.
FT CARBOHYD 104 104 PROBABLE.
FT CARBOHYD 111 111 POTENTIAL.
FT CARBOHYD 199 199 POTENTIAL.
FT CARBOHYD 268 268 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
FT CARBOHYD 387 387 POTENTIAL.
FT CONFLICT 203 203 C -> Y (IN REF. 2 AND 3).
SQ SEQUENCE 426 AA; 48212 MW; B7809EE CRC32;

Query Match 74.2%; Score 49; DB 1; Length 426;
Best Local Similarity 71.4%; Pred. No. 3.03e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYIAGPY 215
Oy 2 KYISAPY 8
|||:|
|||:|

RESULT 8
ID PSGB_HUMAN STANDARD: PRT: 435 AA.
AC 000889:
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 6 PRECURSOR (PSBG-6).
GN PSBG OR HSCG3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CAVIARIINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER:
RX MEDLINE: 89392023.
RA ZIMMERMAN W., WEISS M., THOMPSON J.A.;
RT "cDNA cloning demonstrates the expression of pregnancy-specific
RT glycoprotein genes, a subgroup of the carcinoembryonic antigen gene
RT family, in fetal liver.";
RT BIOCHEM. BIOPHYS. RES. COMMUN. 163:1197-1209(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA THOMPSON J.A., KODMARI R., WAGNER K., BARNERT S., SCHLEUSSNER C.,
RA SCHREWE H., ZIMMERMAN W., MUELLER G., SCHEMP W., ZANINETTA D.,
RA AMATURO D., HARDMAN N.;
RT SUBMITTED (MAR-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE OF 23-142 FROM N.A.
RX MEDLINE: 89149826.
RA THOMPSON J.A., MAUCH E.M., CHEN F.S., HINODA Y., SCHREWE H.,
RA BERNIER B., BARNERT S., VON KLEIST S., SHIYEL J.E., ZIMMERMAN W.;
RT "Analysis of the size of the carcinoembryonic antigen (CEA) gene
RT family: isolation and sequencing of N-terminal domain exons.";
RT BIOCHEM. BIOPHYS. RES. COMMUN. 158:996-1004(1989).
RN [4]
RP SEQUENCE OF 1-142 FROM N.A.
RX MEDLINE: 90332674.
RA LESLIE K.K., WAINMAN S., LEI K.-J., CHOU D.Y., PLOUZEC C.A.,
RA DENG H.-C., TORRES J., CHOU J.Y.;
RT "Linkage of two human pregnancy-specific beta 1-glycoprotein genes:
RT one is associated with hydatidiform mole.";
RT PROC. NATL. ACADE. SCI. U.S.A. 87:5822-5826(1990).
CC -1- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING
CC PREGNANCY.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 3
CC C2-LIKE AND ONE V-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC

ANTIGEN SUBFAMILY.

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DR EMBL M33666; G190640; .
 DR EMBL M32621; G553626; .
 DR EMBL M32620; G553626; JOINED.
 DR EMBL M37757; G190607; .
 DR EMBL M37756; G190607; JOINED.
 DR MIM: 176395; .

DR PFAM: PF00047; 1g; 3. GLYCOPROTEIN; SIGNAL; MULTIGENE FAMILY.
 KW IMMUNOGLOBULIN FOLD; GLYCOPROTEIN 6.

FT SIGNAL 1 34
 FT CHAIN 35 435
 FT DOMAIN 161 223
 FT DOMAIN 254 316
 FT DOMAIN 346 400
 FT DISULFID 168 216
 FT DISULFID 261 309
 FT DISULFID 353 393
 FT CARBOHYD 61 61
 FT CARBOHYD 103 103
 FT CARBOHYD 110 110
 FT CARBOHYD 198 198
 FT CARBOHYD 267 267
 FT CARBOHYD 302 302
 FT CARBOHYD 386 386
 FT SEQUENCE 435 AA; 48813 MW; 48A3CA7B CRC32;

Query Match 74.2%; Score 49; DB 1; Length 435;
 Best Local Similarity 71.4%; Pred. No. 3.03e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 208 KTIAGPY 214

QY 2 KTIASAPY 8

RESULT 9
 ID PSG4_HUMAN STANDARD; PRT; 498 AA.

01-OCT-1996 (REL. 34, CREATED)
 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).
 PSG4 OR HSCGM4.

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RA THOMPSON J.A., KOUKARI R., WAGNER K., BARNEST S., SCHUESSNER C.,
 RA SCHUEHE H., ZIMMERMANN W., MUELLER G., SCHEMP W., ZANINETTA D.,
 RA AMATURO D., HARDMAN N.;
 RL SUBMITTED (MAR-1990) TO EMBL/GENBANK/DBJ DATA BANKS.

RP SEQUENCE OF 23-143 FROM N.A.
 RX MEDLINE: 89149826.

RA THOMPSON J.A., MAUCH E.M., CHEN F.S., HINODA Y., SCHREME H.,
 RA BERLING B., BARNEST S., SHIVELY J.E., ZIMMERMANN W.;
 RT "Analysis of the size of the carcinoembryonic antigen (CEA) gene
 RT family: Isolation and sequencing of N-terminal domain exons."
 RL BIOCHEM. BIOPHYS. RES. COMMON. 158:996-1004(1989).

RP SEQUENCE OF 208-498 FROM N.A.
 RC TISSUE-LIVER;

RX MEDLINE: 89392023.
 RA ZIMMERMANN W., WEISS M., THOMPSON J.A.;
 RT "cDNA cloning demonstrates the expression of pregnancy-specific
 RT glycoprotein genes, a subgroup of the carcinoembryonic antigen gene
 RT family, in fetal liver."
 RL BIOCHEM. BIOPHYS. RES. COMMON. 163:1197-1209(1989).

RP SEQUENCE OF 1-143 FROM N.A.

RA CHAN W.-Y., BORJIGIN J., ZHENG Q.-X., SHUPERT W.L.;
 RT "Characterization of cDNA encoding human pregnancy-specific beta 1-
 RT glycoprotein from placenta and extraplacental tissues and their
 RT comparison with carcinoembryonic antigen."
 RL DNA 7:545-555(1988).

CC -1- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING
 CC PREGNANCY.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 3
 CC C2-LIKE AND ONE V-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC
 CC ANTIGEN SUBFAMILY.

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DR EMBL M32627; G440315; ALT-SEQ.
 DR EMBL M32622; G440315; JOINED.
 DR EMBL M32623; G440315; JOINED.
 DR EMBL M32624; G440315; JOINED.
 DR EMBL M32625; G440315; JOINED.
 DR EMBL M32626; G440315; JOINED.
 DR EMBL M32655; G190651; .
 DR MIM: 176393; .

DR PFAM: PF00047; 1g; 3.
 KW IMMUNOGLOBULIN FOLD; GLYCOPROTEIN; SIGNAL; MULTIGENE FAMILY.

FT SIGNAL 1 34
 FT CHAIN 35 498
 FT DOMAIN 161 224
 FT DOMAIN 254 307
 FT DOMAIN 431 485
 FT DISULFID 169 217
 FT DISULFID 261 300
 FT DISULFID 438 478
 FT CARBOHYD 104 104
 FT CARBOHYD 111 111
 FT CARBOHYD 199 199
 FT CARBOHYD 258 258
 FT CARBOHYD 352 352
 FT CARBOHYD 383 383
 FT CARBOHYD 387 387
 FT CONFLICT 18 18
 FT CONFLICT 208 209
 FT CONFLICT 237 320
 FT CONFLICT 321 321
 FT CONFLICT 351 351
 FT SEQUENCE 498 AA; 55801 MW; 48A4536B CRC32;

Query Match 74.2%; Score 49; DB 1; Length 498;
 Best Local Similarity 71.4%; Pred. No. 3.03e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KTIAGPY 215

QY 2 KTIASAPY 8

RESULT 10
 ID G6PD_MEDSA STANDARD; PRT; 515 AA.
 AC 042919;

FT TRANSMEM 428 447 S1 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 461 480 S2 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 490 508 S3 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 519 537 S4 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 557 576 S5 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 630 654 S6 OF REPEAT II (POTENTIAL).
 FT TRANSMEM 1101 1117 S1 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1142 1161 S2 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1170 1192 S3 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1207 1224 S4 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1244 1263 S5 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1351 1374 S6 OF REPEAT III (POTENTIAL).
 FT TRANSMEM 1432 1450 S1 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1466 1485 S2 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1494 1512 S3 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1524 1542 S4 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1562 1581 S5 OF REPEAT IV (POTENTIAL).
 FT TRANSMEM 1651 1676 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 667 704 POLY-GLU.
 FT DOMAIN 718 723 POLY-ARG.
 FT DOMAIN 1058 1064 POLY-GLU.
 FT DOMAIN 1180 1183 POLY-VAL.
 FT DOMAIN 2193 2196 POLY-ARG.
 FT CARBOHYD 17 17 POTENTIAL.
 FT CARBOHYD 205 205 POTENTIAL.
 FT CARBOHYD 1039 1039 POTENTIAL.
 FT CARBOHYD 1042 1042 POTENTIAL.
 FT CARBOHYD 1518 1518 POTENTIAL.
 FT CARBOHYD 1523 1523 POTENTIAL.
 FT CARBOHYD 1641 1641 POTENTIAL.
 FT CARBOHYD 1939 1939 POTENTIAL.
 SQ SEQUENCE 2222 AA; 252114 MW; 9CCAB868 CRC32;

Query Match 74.2%; Score 49; DB 1; Length 2222;
 Best Local Similarity 75.0%; Pred. No. 3.03e+00;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2134 OHYISEPY 2141

Oy 1 OKYISAPY 8

RESULT 13
 ID YG64_HAEIN STANDARD; PRT: 251 AA.
 AC P45305;
 DT 01-NOV-1995 (REL. 32, CREATED)
 RT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 RL 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 CC HYPOTHETICAL PROTEIN H11664.
 CC H11664.
 CC HAEMOPHILUS INFLUENZAE.
 CC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURILLACEAE;
 CC HAEMOPHILUS.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-RD / RM20;
 CC MEDLINE; 95350630.
 CC FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 CC KERELAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 CC MCKENNEY K., SUTTON G., FITZHUGH R., FIELDS C.A., GOCAYNE J.D.,
 CC SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELEY J.M.,
 CC WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
 CC UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUNDER D.M., BRANDON R.C.,
 CC FINE L.D., FITCHMAN J.L., FUHRMAN J.L., GEOGAGAN N.S.M.,
 CC GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 CC VENTER J.C.;
 CC "Whole-genome random sequencing and assembly of Haemophilus
 CC influenzae Rd.";
 CC SCIENCE 269:496-512(1995).
 CC -1- SIMILARITY: BELONGS TO THE UPF0006 FAMILY.
 CC -----
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 CC -----
 CC EMBL: U32839; G1574514; ALT_INIT.
 CC TIGR: H11664;
 CC PROSITE; PS01137; UPF0006_1; 1.
 CC PROSITE; PS01090; UPF0006_2; FALSE_NEG.
 CC PROSITE; PS01091; UPF0006_3; 1.
 CC PFAM; PF01026; UPF0006; 1.
 CC HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 251 AA; 29334 MW; B07778CC CRC32;

Query Match 72.7%; Score 48; DB 1; Length 251;
 Best Local Similarity 62.5%; Pred. No. 5.04e+00;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 164 OKFESTPY 171

Oy 1 OKYISAPY 8

RESULT 14
 ID YG1E_SVVD STANDARD; PRT: 604 AA.
 AC Q04548;
 DT 01-JUN-1994 (REL. 29, CREATED)
 RT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 RL 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 CC GLYCOPROTEIN E PRECURSOR (MEMBRANE GLYCOPROTEIN 2).
 CC GE OR US4
 CC SIMIAN VARICELLA VIRUS (STRAIN DHV) (CERCOPITHECINE HERPESVIRUS 9).
 CC VIRUSES; DSDNA VIRUSES; NO RNA STAGE; HERPESVIRIDAE;
 CC ALPHAHERPESVIRINAE; VARICELLOVIRUS.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE; 93212509.
 CC FLETCHER T.M. III, GRAY W.L.;
 CC "DNA sequence and genetic organization of the unique short (US)
 CC region of the simian varicella virus genome.";
 CC VIROLOGY 193:762-773(1993).
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN E.
 CC -----

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 CC -----

CC EMBL; L07067; G310719; -
 CC PIR; D46113; D46113.
 CC GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL.
 CC SIGNAL
 CC CHAIN 1 24
 CC TRANSMEM 25 604
 CC CARBOHYD 527 544
 CC CARBOHYD 117 117
 CC CARBOHYD 249 249
 CC CARBOHYD 303 303
 CC CARBOHYD 419 419
 CC CARBOHYD 505 505
 CC SEQUENCE 604 AA; 67583 MW; 01400A6F CRC32;

Query Match 72.7%; Score 48; DB 1; Length 604;
 Best Local Similarity 66.7%; Pred. No. 5.04e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 52 ODYINAAVT 60

Oy 1 OKYISAPY 9

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RESULT 15
ID PGCV CHICK STANDARD: PRT: 3562 AA.
AC 090953: 090945: (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN)
GN (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M).
OS CP562.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-LIMB BUD;
RX MEDLINE: 93300846.
RA SHINOMURA T., NISHIDA Y., ITO K., KIMATA K.;
CDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
expressed during chondrogenesis in chick limb buds. Alternative
spliced multiforms of PG-M and their relationships to versican.*;
J. BIOL. CHEM. 268:14461-14469(1993).
CC -1- FUNCTION: MAY PLAY A ROLE IN INTERCELLULAR SIGNALING AND IN
CONNECTING CELLS WITH THE EXTRACELLULAR MATRIX. MAY TAKE PART IN
THE REGULATION OF CELL MOTILITY, GROWTH AND DIFFERENTIATION. BINDS
HYALURONIC ACID.
CC -1- TISSUE SPECIFICITY: PRECHONDROGENIC CONDENSATION AREA OF
DEVELOPING LIMB BUDS.
CC -1- DEVELOPMENTAL STAGE: DISAPPEARS AFTER THE CARTILAGE DEVELOPMENT
(BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO FORMS OF VERSICAN (V0
AND V1) GENERATED BY ALTERNATIVE EXON USAGE.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN V-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC -----
EMBL: X60226; G505285; -;
EMBL: D13542; G391644; -;
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 2.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS01241; LINK; 2.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
DR PFAM: PF00008; EGF; 2.
DR PFAM: PF00047; Ig; 1.
DR PFAM: PF00059; lectin_C; 1.
DR PFAM: PF00084; sush1; 1.
DR PFAM: PF00193; link; 2.
DR HSP: P00740; IIXA.
DR GLYCOPROTEIN: PROTEOGLYCAN; LECTIN; EXTRACELLULAR MATRIX; SUSHI;
KW SIGNAL: REPEAT: EGF-LIKE DOMAIN; IMMUNOGLOBULIN FOLD; HYALURONIC ACID;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 3562 VERSICAN CORE PROTEIN, V0 FORM.
FT DOMAIN 37 136 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 166 243 LINK 1.
FT DOMAIN 264 345 LINK 2.
FT DOMAIN 3254 3290 EGF-LIKE 1.
FT DOMAIN 3292 3328 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

FT	DOMAIN	3330	3459	C-TYPE LECTIN.
FT	REPEAT	3460	3518	SUSHI.
FT	DISULFID	44	129	BY SIMILARITY.
FT	DISULFID	171	242	BY SIMILARITY.
FT	DISULFID	195	216	BY SIMILARITY.
FT	DISULFID	269	344	BY SIMILARITY.
FT	DISULFID	293	314	BY SIMILARITY.
FT	DISULFID	3258	3269	BY SIMILARITY.
FT	DISULFID	3263	3278	BY SIMILARITY.
FT	DISULFID	3280	3289	BY SIMILARITY.
FT	DISULFID	3286	3307	BY SIMILARITY.
FT	DISULFID	3301	3316	BY SIMILARITY.
FT	DISULFID	3318	3327	BY SIMILARITY.
FT	DISULFID	3334	3345	BY SIMILARITY.
FT	DISULFID	3362	3454	BY SIMILARITY.
FT	DISULFID	3430	3446	BY SIMILARITY.
FT	DISULFID	3461	3504	BY SIMILARITY.
FT	DISULFID	3450	3517	BY SIMILARITY.
FT	CARBOHYD	163	163	POTENTIAL.
FT	CARBOHYD	235	235	POTENTIAL.
FT	CARBOHYD	329	329	POTENTIAL.
FT	CARBOHYD	529	529	POTENTIAL.
FT	CARBOHYD	709	709	POTENTIAL.
FT	CARBOHYD	948	948	POTENTIAL.
FT	CARBOHYD	1409	1409	POTENTIAL.
FT	CARBOHYD	1479	1479	POTENTIAL.
FT	CARBOHYD	1523	1523	POTENTIAL.
FT	CARBOHYD	1530	1530	POTENTIAL.
FT	CARBOHYD	1625	1625	POTENTIAL.
FT	CARBOHYD	1751	1751	POTENTIAL.
FT	CARBOHYD	1988	1988	POTENTIAL.
FT	CARBOHYD	2088	2088	POTENTIAL.
FT	CARBOHYD	2089	2089	POTENTIAL.
FT	CARBOHYD	2507	2507	POTENTIAL.
FT	CARBOHYD	2642	2642	POTENTIAL.
FT	CARBOHYD	2679	2679	POTENTIAL.
FT	CARBOHYD	2748	2748	POTENTIAL.
FT	CARBOHYD	2762	2762	POTENTIAL.
FT	CARBOHYD	3069	3069	POTENTIAL.
FT	CARBOHYD	3194	3194	POTENTIAL.
FT	CARBOHYD	3232	3232	POTENTIAL.
FT	CARBOHYD	3545	3545	POTENTIAL.
FT	CARBOHYD	485	1411	MISSING (IN V1).
SO	SEQUENCE	3562 AA;	388078 MW;	6C04125A CRC32;

Query Match 72.7% Score 48; DB 1: length 3562;
Best Local Similarity 55.6% Pred. No. 5.04e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 2336 RYLSPT 2344
QY 1 QRTSAPY 9

Search completed: Thu Sep 2 12:13:12 1999
Job time : 8 secs.

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 100.0%; Score 66; DB 27; Length 9;
Best Local Similarity 100.0%; Pred. No. 9,35e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 QKYSAPYT 9
| | | | |
OY 1 QKYSAPYT 9

RESULT 2
ID W27578 standard; peptide: 9 AA.
AC W27578:

DE 19-MAR-1998 (first entry)
KW Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PM W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
PI Manfouh JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
Claim 20; Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 89.4%; Score 59; DB 27; Length 9;
Best Local Similarity 88.9%; Pred. No. 6,23e+00;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 QKYSAPYT 9
| | | | |
OY 1 QKYSAPYT 9

RESULT 3
ID W27573 standard; peptide: 9 AA.
AC W27573:

DE 19-MAR-1998 (first entry)
KW Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PM W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
PI Manfouh JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
Claim 20; Page 68; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 84.8%; Score 56; DB 27; Length 9;
Best Local Similarity 88.9%; Pred. No. 1,38e+01;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 QKYSAPYT 9
| | | | |
OY 1 QKYSAPYT 9

RESULT 4
ID W27574 standard; peptide: 9 AA.
AC W27574:

DE 19-MAR-1998 (first entry)
KW Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; HIV; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; DMN;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U022219.
 PR 25-NOV-1996: US-031476.
 PA 09-FEB-1996: US-559226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 69; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC sporidylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical cell
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:
 Query Match 84.8%: Score 56; DB 27; Length 9;
 Best Local Similarity 88.9%: Pred. No. 1.38e+01;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 gkynsapyt 9
 | | | | | | |
 1 QKTSAPY 9
 QY 1 QKTSAPY 9

PT obtaining agonists and antagonists
 PS Claim 34: Page 201-211; 285pp: English.
 CC DNA encoding alpha 1E human calcium channel subunits have
 CC been isolated from an oligo dT-primed human hippocampus
 CC library. The resulting clones, which are splice variants,
 CC were designated alpha 1E-1 and alpha 1E-3. These splice variants
 CC differ by virtue of a 57 bp insert in 1E-3. Alpha 1E-1 has
 CC a calculated mol. wt. of 254,836 and alpha 1E-3 has a calculated
 CC mol. wt. of 257,348. Alpha 1E-3 has a 19 AA insert relative to
 CC alpha 1E-1 in the region that appears to be the cytoplasmic loop
 CC between transmembrane domains II56 and II151.
 SQ Sequence 2270 AA:
 Query Match 81.8%: Score 54; DB 14; Length 2270;
 Best Local Similarity 75.0%: Pred. No. 2.34e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 2182 gxyisepy 2189
 | : | | | | |
 1 QKTSAPY 8
 QY 1 QKTSAPY 8

RESULT 7
 ID R69604 standard; Protein: 2270 AA.
 AC R69604;
 DT 30-AUG-1995 (first entry)
 DE Calcium channel alpha-1E subunit.
 KM Calcium channel alpha-1E; h-alpha-1E; neuron; NX-HB1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 2106
 FT /note="not known"

PN W09504144-A.
 PD 09-FEB-1995.
 PR 29-JUL-1994: US-100589.
 PR 30-JUL-1993: US-100740.
 PA (NEUR-) NEUREX CORP.
 PI Bell JR, Cong R, Hashimoto C, Horne WA, Palma A;
 PI Philip M, Zhou M;
 DR WPI: 95-082228/11.
 DR N-PSDB: 083735.
 PT New DNA encoding new alpha-1E subunit of neuronal calcium channel
 PT and related vectors and transformed eukaryotic cells, useful
 PT for screening cpds. for ability to block calcium uptake in
 PT neurons
 PS Claim 2: Fig.1: 43pp; English.
 CC Overlapping partial cDNA clones H24, H6, I2 and 3-69A were isolated
 CC from a human hippocampus library using probes based on rat calcium
 CC channel sequences. These overlapping clones were ligated to generate
 CC a full-length cDNA, designated NX-HE1 (given in Q83735), encoding a
 CC 5th neuronal calcium channel alpha subunit, termed 1E or h-alpha-1E
 CC (R69604). 1E was expressed in Xenopus oocytes and human embryonic
 CC kidney HEK 293 cells.
 SO Sequence 2270 AA;

Query Match 81.8%; Score 54; DB 13; Length 2270;
 Best Local Similarity 75.0%; Pred. No. 2.34e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 2182 gylsely 2189
 1 QKYSAPY 8

RESULT 8
 ID W27570 standard; peptide: 9 AA.
 AC W27570:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 67; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC scleriosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 80.3%; Score 53; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3.03e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 gylsely 9
 1 QKYSAPY 9

RESULT 9
 ID W27582 standard; peptide: 9 AA.
 AC W27582:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 78.8%; Score 52; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3.93e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkynsdpyt 9
| | | | |
OY 1 OKTISAPYT 9

RESULT 10
ID W27575 standard; peptide; 9 AA.

AC W27575;
DE 19-MAR-1998 (first entry)
KW Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HIVEC;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
PI Mankevich JA, McGuiness BR, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity; e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 69; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HVEC).
SO Sequence 9 AA:

Query Match 77.3%; Score 51; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 5.08e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkynsdpyt 9
| | | | |
OY 1 OKTISAPYT 9

RESULT 11
ID W27577 standard; peptide; 9 AA.

AC W27577;
DE 19-MAR-1998 (first entry)
KW Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HIVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
PI Mankevich JA, McGuiness BR, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity; e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HVEC).
SO Sequence 9 AA:

Query Match 77.3%; Score 51; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.08e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsdpyt 8
| | | | |
OY 1 OKTISAPYT 8

RESULT 12
ID W27576 standard; peptide; 9 AA.

AC W27576;
DE 19-MAR-1998 (first entry)
KW Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HIVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.

PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Markovitch JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 77.3%; Score 51; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 5.08e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapy 8
 ||| ||||
 QY 1 OKYISAPY 8

RESULT 13

W27572 standard; peptide: 9 AA.

AC W27572;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 PT light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Markovitch JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 75.8%; Score 50; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 6.56e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkygrapyt 9
 ||| ||||
 QY 1 OKYISAPY 9

RESULT 14

W77308 standard; protein: 316 AA.

AC W77308;
 DT 02-DEC-1998 (first entry)
 DE Thermolysin protein sequence.
 KW Metallo-endopeptidase; thermolysin-like protease; TLP-site;
 KW thermolysin; thermal stability; production; protein hydrolysate;
 KW aspartame; unhairing; leather manufacture; detergent.
 OS Undefined.
 PN EP-867512-A1.
 PD 30-SEP-1998.
 PF 27-MAR-1997; 200931.
 PR 27-MAR-1997; EP-200931.
 PA (UYGR-) RUTSUNT V GRONINGEN.
 PI Van Den Burg L, Veltman OR, Venema G;
 DR WPI: 98-497863/43.
 PT New recombinant DNA encoding mutant metallo-endo-peptidase with
 PT improved thermal stability - used to produce protein hydrolysates
 PT and aspartame, for unhairing in leather manufacture and in
 PT detergents
 PS Disclosure; Page 11; 22pp; English.
 CC The present sequence represents a thermolysin. The specification
 CC describes a metallo-endopeptidase derived from Bacillus
 CC stearotheophilus CU21. The protein is a thermolysin-like
 CC protease designated TLP-site, which differs from thermolysin by
 CC a 3 amino acid insertion of Ser-Tyr-Tyr between positions 25-26 of
 CC the thermolysin sequence. The specification also describes
 CC recombinant DNA coding for a metallo-endopeptidase in which at
 CC least one codon is mutated to code for cysteine to generate a
 CC stabilising disulphide bridge. Other mutants are described in which
 CC at least one codon is mutated to code for an amino acid providing
 CC reduced capacity to bind with calcium. The mutations improve the
 CC thermal stability of the enzyme. The enzymes can be used to produce
 CC protein hydrolysates, in the production of aspartame, for unhairing
 CC in leather manufacture, or in detergents.
 SQ Sequence 316 AA;

Query Match 75.8%; Score 50; DB 35; Length 316;
 Best Local Similarity 55.6%; Pred. No. 6.56e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 17 qkynntys 25
 ||||:|:
 QY 1 OKYISAPY 9


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RESULT 15
ID R76564 standard; Protein; 319 AA.
AC R76564;
DT 08-DEC-1995 (first entry)
DE Neutral protease NP-ste.
KW Protease; metallo-endopeptidase; stabilization; enzyme engineering;
KW thermostability; aspartame; sweetener; leather; dewooling; brewing;
KW NP-ste.
OS Bacillus stearothermophilus.
PN W09520663-A.
PD 03-AUG-1995.
PF 26-JAN-1995; NL0037.
PR 27-JAN-1994; EP-200182.
RA (UGR-) RIJKSUNIV GRONINGEN.
PI Eljstink VGH, Venema G;
PI WPI; 95-275448/36.
DR N-PSDB: 093164.
PT Thermostable neutral protease variants from Bacillus stearothermophilus
PT and B. thermoproteolyticus - useful for aspartame production, reverse
PT hydrolysis in leather production, etc.
PT Claim 1; Fig.1; 44pp; English.
CC The nprt gene of B. stearothermophilus CU-21 encodes neutral protease
CC NP-ste. Alignment of the enzyme sequence with that of thermolysin
CC was used to design stabilization mutations in NP-ste. Preferred
CC mutants are T64F, A72P, T59A, G61A, A4T and S68D/P. Some mutants
CC are more thermostable than thermolysin.
SQ Sequence 319 AA;

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 WIRE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:12:33 1999; Maspar time 3.08 Seconds
 Tabular output not generated. 117.107 Million cell updates/sec

Title: >US-08-599-226-24
 Description: (1-9) from US08599226.pep
 Perfect Score: 66
 Sequence: 1 QKXISAPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: BL60
 1:plrl 2:plrl2 3:plrl3 4:plrl4

Statistics: Mean 22.925; Variance 28.716; scale 0.798

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	54	81.8	2251	2	B54972	voltage-dependent cal	8.58e-01
2	54	81.8	2259	2	S29236	calcium channel prote	8.58e-01
3	54	81.8	2270	2	A54972	voltage-dependent cal	8.58e-01
4	50	75.8	413	2	B70070	muirein hydrolase homo	5.80e+00
5	50	75.8	544	2	A42464	microbial metalloprot	5.80e+00
6	50	75.8	546	2	S72176	thermolysin (EC 3.4.2	5.80e+00
7	50	75.8	546	2	JC4113	neutrol proteinase (E	5.80e+00
8	50	75.8	546	2	S72175	thermolysin (EC 3.4.2	5.80e+00
9	50	75.8	548	1	HYBS	bacillolysin (EC 3.4.	5.80e+00
10	49	74.2	326	2	JC4124	pregnancy-specific g1	9.21e+00
11	49	74.2	332	2	B71606	probable integral mem	9.21e+00
12	49	74.2	351	2	B34595	pregnancy-specific be	9.21e+00
13	49	74.2	402	2	A54312	pregnancy-specific be	9.21e+00
14	49	74.2	419	2	A36109	pregnancy-specific be	9.21e+00
15	49	74.2	419	2	B54312	pregnancy-specific be	9.21e+00
16	49	74.2	424	2	B36109	pregnancy-specific be	9.21e+00
17	49	74.2	424	2	A34595	pregnancy-specific be	9.21e+00
18	49	74.2	426	2	C55181	pregnancy-specific be	9.21e+00
19	49	74.2	426	2	S09016	pregnancy-specific g1	9.21e+00
20	49	74.2	426	2	B35334	pregnancy-specific be	9.21e+00
21	49	74.2	435	2	D33258	pregnancy-specific be	9.21e+00
22	49	74.2	436	2	B55181	pregnancy-specific be	9.21e+00
23	49	74.2	495	2	A55181	pregnancy-specific be	9.21e+00

24	49	74.2	507	2	S05542	hypothetical protein,	9.21e+00
25	49	74.2	515	2	S57785	glucose-6-phosphate 1	9.21e+00
26	49	74.2	2222	2	A37490	voltage-dependent cal	9.21e+00
27	49	74.2	2272	2	C54972	voltage-dependent cal	9.21e+00
28	48	72.7	259	2	E64174	hypothetical protein	1.45e+01
29	48	72.7	558	2	S75104	hypothetical protein	1.45e+01
30	48	72.7	604	1	D46113	glycoprotein E precu	1.45e+01
31	48	72.7	3562	2	A47171	chondroitin sulfate P	1.45e+01
32	47	71.2	106	2	A49138	Iga kappa rheumatoid	2.28e+01
33	47	71.2	196	2	A30484	histone HSB - African	2.28e+01
34	47	71.2	217	2	A26721	histone H1-gamma, emb	2.28e+01
35	47	71.2	544	2	G69072	conserved hypothetical	2.28e+01
36	46	69.7	249	2	S21935	histone H1 - fruit fl	3.54e+01
37	46	69.7	549	2	S09654	histone H1 - fruit fl	3.54e+01
38	46	69.7	552	2	S45886	hypothetical protein	3.54e+01
39	46	69.7	659	2	H69421	heterodisulfide reduc	3.54e+01
40	46	69.7	903	2	T00358	hypothetical protein	3.54e+01
41	46	69.7	1673	2	I50806	complement C5 precu	3.54e+01
42	46	69.7	1680	1	C5MS	complement C5 precu	3.54e+01
43	45	68.2	649	1	M1WU11	El protein - human pa	5.47e+01
44	45	68.2	845	2	H73317	probable methyl-acep	5.47e+01
45	45	68.2	988	2	S37078	chloride channel prot	5.47e+01

ALIGNMENTS

RESULT 1
 ENTRY B54972 #type complete
 TITLE voltage-dependent calcium channel alpha 1E-1 - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 17-Mar-1999

ACCESSIONS
 REFERENCE
 #authors Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Ellis, S.B.
 Harpold, M.M.; Miller, R.J.; Johnson, E.C.;
 J. Biol. Chem. (1994) 269:22347-22357
 Structure and functional characterization of neuronal
 alpha-1E calcium channel subtypes.
 #cross-references WUID:94350992
 #accession B54972
 #status preliminary; nucleic acid sequence not shown;
 translation not shown

SUMMARY
 #molecule_type mRNA
 #residues 1-2251 #label WIL
 #cross-references GB:I29384; NID:q495867; PID:q495868
 CLASSIFICATION
 #superfamily voltage-dependent calcium channel protein
 #length 2251 #molecular_weight 254836 #checksum 4202

Query Match 81.8%; Score 54; DB 2; Length 2251;
 Best Local Similarity 75.0%; Pred. No. 8.58e-01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 2163 ORYISEPY 2170
 QY 1 QKXISAPYT 8

RESULT 2
 ENTRY S29236 #type complete
 TITLE calcium channel protein B1T-1, brain - rabbit
 ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic
 DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Sep-1998
 ACCESSIONS
 REFERENCE S29236
 #authors Nildome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
 FEBS Lett. (1992) 308:7-13
 Molecular cloning and characterization of a novel calcium
 channel from rabbit brain.

#cross-references MUID:92354772
#accession S29236
#status Preliminary
#molecule_type mRNA
#residues 1-2259 #label NIT
#cross-references EMBL:X67855; NID:g1472; PID:g1473
CLASSIFICATION #superfamily voltage-dependent calcium channel protein
#alpha-1 chain
KEYWORDS transmembrane protein
SUMMARY #length 2259 #molecular-weight 254250 #checksum 5523

Query Match 81.8%; Score 54; DB 2; Length 2259;
Best Local Similarity 75.0%; Pred. No. 8,58e-01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2172 ORYISEPY 2179
QY 1 OKYISAPY 8

RESULT 3
ENTRY A54972 #type complete
TITLE voltage-dependent calcium channel alpha 1c-3 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 17-Mar-1999

ACCESSIONS A54972
REFERENCE A54972
#authors Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Miller, R.J.; Johnson, E.C.; Harpold, M.M.; Ellis, S.B.
#journal J. Biol. Chem. (1994) 269:2247-22357
#title Structure and functional characterization of neuronal alpha-1c calcium channel subtypes.
#cross-references MUID:94350992
#accession A54972
#status preliminary
#molecule_type mRNA
#residues 1-2270 #label WIL
#cross-references GB:L29385; NID:9495869; PID:9495870
CLASSIFICATION #superfamily voltage-dependent calcium channel protein
#alpha-1 chain
SUMMARY #length 2270 #molecular-weight 257348 #checksum 387

Query Match 81.8%; Score 54; DB 2; Length 2270;
Best Local Similarity 75.0%; Pred. No. 8,58e-01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2182 OKYISEPY 2189
QY 1 OKYISAPY 8

RESULT 4
ENTRY B70070 #type complete
TITLE murein hydrolase homolog ywtd - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
ACCESSIONS B70070
REFERENCE A69580
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bortero, M.G.; Bessieres, P.; Boloitin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devigne, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galazzi, A.; Galleron, N.; Ghim, S.Y.; Glaeser, P.; Goffeau, A.; Glightly, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,

C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klier, B.; Klier, C.; Kobyash, Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarovic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Meliello, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Nobeck, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogihara, A.; Oudga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetalle, D.; Potvilk, S.; Prescott, A.M.; Pressecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serrier, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Yamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, E.; Vassarotti, A.; Viari, A.; Wandurt, R.; Wedler, E.; Wedler, H.; Welteneeger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

#journal Nature (1997) 390:249-256
#title The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
#cross-references MUID:98044033
#accession B70070
#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA
#residues 1-413 #label KUN
#cross-references GB:299122; GB:AL009126; NID:g2636029; PID:el184492;
#experimental_source strain 168

GENETICS
SUMMARY #gene ywtd #length 413 #molecular-weight 45247 #checksum 1968

Query Match 75.8%; Score 50; DB 2; Length 413;
Best Local Similarity 62.5%; Pred. No. 5,80e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 174 ERYIGVY 181
QY 1 OKYISAPY 8

RESULT 5
ENTRY A42464 #type complete
TITLE microbial metalloproteinase (EC 3.4.24.-) precursor - Bacillus caldolyticus
ORGANISM #formal_name Bacillus caldolyticus
DATE 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 22-May-1998
ACCESSIONS A42464
REFERENCE A42464
#authors van den Burg, B.; Enequist, H.G.; van der Haar, M.E.; Eljstink, V.G.H.; Stulp, B.K.; Venema, G.
#journal J. Bacteriol. (1991) 173:4107-4115
#title A highly thermostable neutral protease from Bacillus caldolyticus: cloning and expression of the gene in Bacillus subtilis and characterization of the gene product.
#cross-references MUID:91286196
#accession A42464
#status preliminary
#molecule_type DNA
#residues 1-544 #label VAN
#cross-references GB:W63575; NID:g143250; PID:g143251
CLASSIFICATION #superfamily thermolysin
KEYWORDS hydrolase; metalloproteinase; zinc
FEATURE 370,374,394 #binding_site zinc (His, His, Glu) #status predicted\

371,459 #active_site Glu, His #status predicted
SUMMARY #length 544 #molecular-weight 59413 #checksum 8971

Query Match 75.8%; Score 50; DB 2; Length 544;
Best Local Similarity 55.6%; Pred. No. 5,80e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 244 OKIINTYS 250
1 OKIISAPY 9

RESULT 6
ENTRY 572176 #type complete
TITLE thermolysin (EC 3.4.24.27) precursor - *Bacillus caldolyticus*
(strain YP-7)
ALTERNATE_NAMES thermolysin neutral protease
ORGANISM #formal_name *Bacillus caldolyticus*
#strain YP-7
#variety
DATE 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change
ACCESSIONS 572176
REFERENCE 572175
#authors Saul, D.J.; Williams, L.C.; Toogood, H.S.; Daniel, R.M.;
Bergquist, P.L.
#journal Biochim. Biophys. Acta (1996) 1308:74-80
#title Sequence of the gene encoding a highly thermostable neutral
protease from *Bacillus* sp. strain EAI: expression in
Escherichia coli and characterisation.
#cross-references MUID:96328267
#accession 572176
#status nucleic acid sequence not shown
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#residues 1-546 #label SAV
#cross-references EMBL:U25629; NID:9995781; PID:9995782

GENETICS
#gene npr
CLASSIFICATION #superfamily thermolysin
KEYWORDS calcium; hydrolase; metalloprotease; zinc
FEATURE
1-25 #domain signal sequence #status predicted #label SIG\
26-228 #domain propeptide #status predicted #label PRO\
229-546 #product thermolysin #status predicted #label MAT\
287,289,291 #binding_site calcium (Asp, Asp, Glu) #status predicted\
368,407,415,417, #binding_site calcium (Asp, Glu, Asp, Glu, Glu) #status
predicted\
372,376,396 #binding_site zinc (His, His, Glu) #status predicted\
373,461 #active_site Glu, His #status predicted\
423,424,427,430 #binding_site calcium (Tyr, Thr, Ile, Asp) #status
predicted
SUMMARY #length 546 #molecular-weight 59770 #checksum 8106

Query Match 75.8%; Score 50; DB 2; Length 546;
Best Local Similarity 55.6%; Pred. No. 5,80e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 244 OKIINTYS 252
1 OKIISAPY 9

RESULT 7
ENTRY JC4113 #type complete
TITLE neutral protease (EC 3.4.24.-) - *Bacillus* sp.
ORGANISM #formal_name *Bacillus* sp.
DATE 26-Jul-1995 #sequence_revision 19-Oct-1995 #text_change
08-Sep-1997
ACCESSIONS JC4113
REFERENCE JC4113
#authors Vecerek, B.; Kyslik, P.
#journal Gene (1995) 158:147-148
#title Cloning and sequencing of the neutral protease-encoding gene

from a thermophilic strain of *Bacillus* sp.
#cross-references MUID:95309716
#accession JC4113
#molecule_type DNA
#residues 1-546 #label VEC
#cross-references GB:U07824; NID:9563120; PID:9563121
#note The authors translated the codon TGG for residue 285 as
Val and ACG for residue 462 as Pro
COMMENT The optimum temperature for this enzyme activity is 82 degrees
centigrade.

GENETICS
#gene npr
CLASSIFICATION #superfamily thermolysin
KEYWORDS hydrolase; metalloprotease; zinc
FEATURE
372,376,396 #binding_site zinc (His, His, Glu) #status predicted\
373,461 #active_site Glu, His #status predicted
SUMMARY #length 546 #molecular-weight 59769 #checksum 8126

Query Match 75.8%; Score 50; DB 2; Length 546;
Best Local Similarity 55.6%; Pred. No. 5,80e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 244 OKIINTYS 252
1 OKIISAPY 9

RESULT 8
ENTRY 572175 #type complete
TITLE thermolysin (EC 3.4.24.27) precursor - *Bacillus* sp. (strain
EAI)
ALTERNATE_NAMES thermolysin neutral protease
ORGANISM #formal_name *Bacillus* sp.
#variety
DATE 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change
26-Feb-1998
ACCESSIONS 572175
REFERENCE 572175
#authors Saul, D.J.; Williams, L.C.; Toogood, H.S.; Daniel, R.M.;
Bergquist, P.L.
#journal Biochim. Biophys. Acta (1996) 1308:74-80
#title Sequence of the gene encoding a highly thermostable neutral
protease from *Bacillus* sp. strain EAI: expression in
Escherichia coli and characterisation.
#cross-references MUID:96328267
#accession 572175
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-546 #label SAV
#cross-references EMBL:U25630; NID:9995783; PID:9995784
#experimental_source strain EAI

GENETICS
#gene npr
CLASSIFICATION #superfamily thermolysin
KEYWORDS calcium; hydrolase; metalloprotease; zinc
FEATURE
1-25 #domain signal sequence #status predicted #label SIG\
26-228 #domain propeptide #status predicted #label PRO\
229-546 #product thermolysin #status predicted #label MAT\
287,289,291 #binding_site calcium (Asp, Asp, Glu) #status predicted\
368,407,415,417, #binding_site calcium (Asp, Glu, Asp, Glu, Glu) #status
predicted\
372,376,396 #binding_site zinc (His, His, Glu) #status predicted\
373,461 #active_site Glu, His #status predicted\
423,424,427,430 #binding_site calcium (Tyr, Thr, Ile, Asp) #status
predicted
SUMMARY #length 546 #molecular-weight 59812 #checksum 8151

Query Match 75.8%; Score 50; DB 2; Length 546;
Best Local Similarity 55.6%; Pred. No. 5,80e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 244 OKYINTVS 252
||||:|:
QY 1 OKYISAPY 9

RESULT 9
ENTRY HYBS #type complete
TITLE bacillolysin (EC 3.4.24.28) precursor - Bacillus
#organism steatothermophilus
#protein_name Bacillus metalloprotease:
#formal_name Bacillus steatothermophilus
#product pregnancy-specific glycoprotein 4a' #status
30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change
05-Sep-1997

ACCESSIONS
#authors A24924; B24924; A25253
#journal Takagi, M.; Imanaka, T.; Alba, S.
#title J. Bacteriol. (1985) 163:824-831
#cross-references MIM:85289021
#accession A24924

GENETICS
#molecule_type DNA
#residues 1-548 #label TAK
#cross-references GB:M1446; NID:g143246; PID:g143247
#accession B24924

FEATURES
#molecule_type protein
#residues 230-243 #label TAK2

CLASSIFICATION
#gene nprt
#superfamily thermolysin
#keywords calcium; extracellular protein; hydrolase; metalloprotease;
zinc

FEATURES
1-25 #domain signal sequence #status predicted #label SIG\
26-229 #domain propeptide #status predicted #label PRO\
230-548 #product bacillolysin #status experimental #label MAT\
370,378,398 #binding_site zinc (His, His, Glu) #status predicted\
379,463 #active_site Glu, His #status predicted
SUMMARY #length 548 #molecular-weight 59580 #checksum 2930

Query Match 75.8%; Score 50; DB 1; Length 548;
Best Local Similarity 55.6%; Pred. No. 5,80e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 246 OKYINTVS 254
||||:|:
QY 1 OKYISAPY 9

RESULT 10
ENTRY JC4124 #type complete
TITLE pregnancy-specific glycoprotein 4a' precursor - human
#organism #formal_name Homo sapiens #common_name man
DATE 26-Jul-1995 #sequence_revision 19-Oct-1995 #text_change
17-Mar-1999

ACCESSIONS
#authors JC4124
#journal Teglund, S.; Zhou, G.Q.; Hammarstrom, S.
#title Biochem. Biophys. Res. Commun. (1995) 211:656-664
#cross-references MIM:95314639
#accession JC4124

GENETICS
#molecule_type mRNA
#residues 1-326 #label TEG
#cross-references GB:O18469; NID:g609317; PID:g609318
#experimental_source fetal liver
#protein_name This protein belongs to the carcinoembryonic antigen family. This
#organism syncytiotrophoblasts and released to the maternal circulation
#title during pregnancy.

GENETICS
#gene GDB:128240; OMIM:176393
#cross-references GDB:128240; OMIM:176393
#map_position 19q13.2-19q13.2
#classification #superfamily carcinoembryonic antigen; carcinoembryonic
#protein_name antigen precursor amino-terminal homology; immunoglobulin
#organism homology
glycoprotein

FEATURES
1-138 #domain carcinoembryonic antigen precursor
amino-terminal homology #label CEAN\
1-34 #domain signal sequence #status predicted #label SIG\
35-326 #product pregnancy-specific glycoprotein 4a' #status
predicted #label MAT\
162-219 #domain immunoglobulin homology #label IMM1\
254-303 #domain immunoglobulin homology #label IMM2\
104,111,199 #binding_site carbohydrate (asn) (covalent) #status
predicted

SUMMARY #length 326 #molecular-weight 36229 #checksum 9518

Query Match 74.2%; Score 49; DB 2; Length 326;
Best Local Similarity 71.4%; Pred. No. 9,21e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 209 KYIASPY 215
||||:|:
QY 2 KYISAPY 8

RESULT 11
ENTRY B71606 #type complete
TITLE probable integral membrane protein PFB0790C - malaria
#organism parasite (Plasmodium falciparum)
#formal_name Plasmodium falciparum
DATE 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change
13-Nov-1998

ACCESSIONS
#authors B71606
#journal Gardner, M.J.; Tettelin, H.; Carnucci, D.J.; Cummings, L.M.;
#title Argund, L.; Koonin, E.V.; Shallom, S.; Mason, T.; Yu, K.;
Fuji, C.; Pederson, J.; Shen, K.; Jing, J.; Aston, C.;
Lai, Z.; Schwartz, D.C.; Perera, M.; Salzberg, S.; Zhou,
L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Fraser, C.M.; Adams, M.D.; Venter, J.C.; Hoffman, S.L.
#journal Science (1998) 282:1126-1132
#title chromosome 2 sequence of the human malaria parasite
#organism Plasmodium falciparum.
#accession B71606
#status preliminary; nucleic acid sequence not shown;
translation not shown

GENETICS
#molecule_type DNA
#residues 1-332 #label GAR
#cross-references GB:AE001418; GB:AE001362; NID:g3845275; PID:g3845278;
#experimental_source clone 3D7
TIGR:PFB0790C

SUMMARY #length 332 #molecular-weight 39208 #checksum 3654

Query Match 74.2%; Score 49; DB 2; Length 332;
Best Local Similarity 71.4%; Pred. No. 9,21e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 257 KYIASPY 263
||||:|:
QY 2 KYISAPY 8

RESULT 12
ENTRY B34595 #type fragment
TITLE pregnancy-specific beta-1 glycoprotein 2 - human (fragment)
#organism #formal_name Homo sapiens #common_name man
DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change

31-Oct-1997
ACCESSIONS B34595
REFERENCE A94644
#authors Zheng, Q.X.; Tease, L.A.; Shupert, W.L.; Chan, W.Y.
#journal Biochemistry (1990) 29:2845-2852
#title Characterization of cDNAs of the human pregnancy-specific beta-1-glycoprotein family, a new subfamily of the immunoglobulin gene superfamily.
#cross-references GB:M31126; NID:q190550; PID:q190551; GB:J02893;
#accession B34595
#molecule_type mRNA
#residues 1-351 #label ZHE
#cross-references GB:M31126; NID:q190550; PID:q190551; GB:J02893;
GB:X15102
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology
glycoprotein
KEYWORDS
FEATURE
1-92 #domain carcinoembryonic antigen precursor
111-168 #amino-terminal homology (fragment) #label CEAN\
203-252 #domain immunoglobulin homology #label IMM2\
53,60,148,243,319 #binding_site carbohydrate (Asn) (covalent) #status predicted
#length 351 #checksum 8643
SUMMARY
Query Match 74.2%; Score 49; DB 2; Length 351;
Best Local Similarity 71.4%; Pred. No. 9.21e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 158 KYIAGPY 164
QY 2 KYISAPY 8
RESULT 13
ENTRY A54312 #type complete
TITLE pregnancy-specific beta-1 glycoprotein 2 precursor, placental (clone hPS91) - human
ALTERNATE_NAMES PSG2
ORGANISM #formal_name Homo sapiens #common_name man
DATE 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
ACCESSIONS A54312
REFERENCE A54312
#authors Chan, W.Y.; Zheng, Q.X.; McMahon, J.; Tease, L.A.
#journal Mol. Cell. Biochem. (1991) 106:161-170
#title Characterization of new members of the pregnancy-specific beta-1-glycoprotein family.
#cross-references MUID:92017749
#accession A54312
#molecule_type mRNA
#status preliminary
#residues 1-402 #label CHA
#cross-references GB:M94890; GB:M37102; NID:q190567; PID:q190568
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology
duplication; glycoprotein
KEYWORDS
FEATURE
1-138 #domain carcinoembryonic antigen precursor
1-34 #amino-terminal homology #label CEAN\
35-402 #domain signal sequence #status predicted #label SIG\
#product pregnancy-specific beta-1 glycoprotein 2
#status predicted #label MAT\
162-219 #domain immunoglobulin homology #label IMM1\
254-303 #domain immunoglobulin homology #label IMM2\
SUMMARY
#length 402 #molecular-weight 45336 #checksum 4851
Query Match 74.2%; Score 49; DB 2; Length 402;
Best Local Similarity 71.4%; Pred. No. 9.21e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 209 KYIAGPY 215
QY 2 KYISAPY 8
RESULT 14
ENTRY A36109 #type complete
TITLE pregnancy-specific beta-1 glycoprotein 9 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 31-Oct-1997
ACCESSIONS A36109; S08052
REFERENCE A36109
#authors Barnett, T.R.; Pickle II, W.; Elling, J.J.
#journal Biochemistry (1990) 29:10213-10218
#title Characterization of two new members of the pregnancy-specific beta-1-glycoprotein family from the myeloid cell line KG-1 and suggestion of two distinct classes of transcription unit.
#cross-references MUID:91104939
#accession A36109
#molecule_type mRNA
#residues 1-419 #label BA2
#cross-references GB:X17097; NID:q35753; PID:q35754
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology
glycoprotein; plasma; tandem repeat
KEYWORDS
FEATURE
1-138 #domain carcinoembryonic antigen precursor
1-34 #amino-terminal homology #label CEAN\
35-419 #domain signal sequence #status predicted #label SIG\
#product pregnancy-specific glycoprotein 9 #status predicted #label MAT\
162-219 #domain immunoglobulin homology #label IMM1\
255-312 #domain immunoglobulin homology #label IMM2\
347-396 #domain immunoglobulin homology #label IMM3\
SUMMARY
#length 419 #molecular-weight 47085 #checksum 9487
Query Match 74.2%; Score 49; DB 2; Length 419;
Best Local Similarity 71.4%; Pred. No. 9.21e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 209 KYIAGPY 215
QY 2 KYISAPY 8
RESULT 15
ENTRY B54312 #type complete
TITLE pregnancy-specific beta-1 glycoprotein 4 precursor, placental (clone hPS133) - human
ALTERNATE_NAMES PSG4
ORGANISM #formal_name Homo sapiens #common_name man
DATE 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
ACCESSIONS B54312
REFERENCE B54312
#authors Chan, W.Y.; Zheng, Q.X.; McMahon, J.; Tease, L.A.
#journal Mol. Cell. Biochem. (1991) 106:161-170
#title Characterization of new members of the pregnancy-specific beta-1-glycoprotein family.
#cross-references MUID:92017749
#accession B54312
#molecule_type mRNA
#status preliminary
#residues 1-419 #label CHA
#cross-references GB:M94891; GB:M37103; NID:q190569; PID:q190570
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology
duplication; glycoprotein
KEYWORDS

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FEATURE
1-138      #domain carcinoembryonic antigen precursor
           amino-terminal homology #label CEAN\
1-34      #domain signal sequence #status predicted #label SIG\
35-419     #product pregnancy-specific beta-1 glycoprotein 4
162-219    #status predicted #label MAR\
255-312    #domain immunoglobulin homology #label IMM1\
347-396    #domain immunoglobulin homology #label IMM2\
SUMMARY    #domain immunoglobulin homology #label IMM3
           #length 419 #molecular-weight 47079 #checksum 9283

Query Match 74.2%; Score 49; DB 2; Length 419;
Best Local Similarity 71.4%; Pred. No. 9.21e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 209 KYIAGPY 215
QY 2 KITSAPY 8

Arch completed: Thu Sep 2 12:12:47 1999
Job time : 14 secs.

```


WATERMAN

(TM)

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MSrch:pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Sep 2 12:14:10 1999; MasPar time 1.33 Seconds
68.459 Million cell updates/sec
Tabular output not generated.

Title: >US-08-599-226-24
Description: (1-9) from US08599226.pep
Perfect Score: 66
Sequence: 1 OKYISAPYR 9

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-15aused
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 15.299; Variance 46.593; scale 0.328

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	49	74.2	248	4	5169835-15	4.05e+01
2	49	74.2	292	2	US-08-688-	4.05e+01
3	49	74.2	354	4	5169835-4	4.05e+01
4	49	74.2	424	4	5169835-6	4.05e+01
5	45	68.2	107	2	US-08-899-	1.10e+02
6	45	68.2	107	2	US-08-276-	1.10e+02
7	45	68.2	107	2	US-08-899-	1.10e+02
8	45	68.2	107	2	US-08-899-	1.10e+02
9	45	68.2	107	2	US-08-899-	1.10e+02
10	44	66.7	376	2	US-08-758-	1.10e+02
11	44	66.7	533	1	US-08-488-	1.40e+02
12	44	66.7	1025	2	US-08-304-	1.40e+02
13	44	66.7	1025	2	US-08-304-	1.40e+02
14	44	66.7	376	2	US-08-222-	1.40e+02
15	44	66.7	376	2	US-08-222-	1.40e+02
16	44	66.7	376	2	US-08-222-	1.40e+02
17	43	65.2	108	1	US-08-899-	1.79e+02
18	43	65.2	108	1	US-08-899-	1.79e+02
19	43	65.2	108	1	US-08-899-	1.79e+02
20	43	65.2	108	1	US-08-899-	1.79e+02
21	43	65.2	108	1	US-08-899-	1.79e+02
22	42	63.6	53	2	US-08-162-	2.27e+02
23	42	63.6	92	2	US-08-273-	2.27e+02

24	42	63.6	92	2	US-08-273-	Sequence 45, Applicati	2.27e+02
25	42	63.6 <td>93</td> <td>4</td> <td>5169835-26</td> <td>Patent No. 5169835.</td> <td>2.27e+02</td>	93	4	5169835-26	Patent No. 5169835.	2.27e+02
26	42	63.6 <td>109</td> <td>2</td> <td>US-08-162-</td> <td>Sequence 24, Applicati</td> <td>2.27e+02</td>	109	2	US-08-162-	Sequence 24, Applicati	2.27e+02
27	42	63.6 <td>109</td> <td>3</td> <td>PCT-US93-0</td> <td>Sequence 3, Applicatio</td> <td>2.27e+02</td>	109	3	PCT-US93-0	Sequence 3, Applicatio	2.27e+02
28	42	63.6 <td>109</td> <td>2</td> <td>US-07-934-</td> <td>Sequence 3, Applicatio</td> <td>2.27e+02</td>	109	2	US-07-934-	Sequence 3, Applicatio	2.27e+02
29	42	63.6 <td>109</td> <td>3</td> <td>PCT-US93-0</td> <td>Sequence 24, Applicati</td> <td>2.27e+02</td>	109	3	PCT-US93-0	Sequence 24, Applicati	2.27e+02
30	42	63.6 <td>144</td> <td>4</td> <td>5169835-8</td> <td>Patent No. 5169835.</td> <td>2.27e+02</td>	144	4	5169835-8	Patent No. 5169835.	2.27e+02
31	42	63.6 <td>230</td> <td>4</td> <td>5169835-13</td> <td>Patent No. 5169835.</td> <td>2.27e+02</td>	230	4	5169835-13	Patent No. 5169835.	2.27e+02
32	42	63.6 <td>419</td> <td>4</td> <td>5169835-2</td> <td>Patent No. 5169835.</td> <td>2.27e+02</td>	419	4	5169835-2	Patent No. 5169835.	2.27e+02
33	42	63.6 <td>2482</td> <td>1</td> <td>US-08-328-</td> <td>Sequence 6, Applicatio</td> <td>2.27e+02</td>	2482	1	US-08-328-	Sequence 6, Applicatio	2.27e+02
34	42	63.6 <td>3248</td> <td>3</td> <td>PCT-US95-1</td> <td>Sequence 1, Applicatio</td> <td>2.27e+02</td>	3248	3	PCT-US95-1	Sequence 1, Applicatio	2.27e+02
35	42	63.6 <td>3248</td> <td>1</td> <td>US-08-353-</td> <td>Sequence 1, Applicatio</td> <td>2.27e+02</td>	3248	1	US-08-353-	Sequence 1, Applicatio	2.27e+02
36	41	62.1	107	3	PCT-US95-0	Sequence 6, Applicatio	2.89e+02
37	41	62.1	108	2	US-08-070-	Sequence 7, Applicatio	2.89e+02
38	41	62.1	210	2	US-08-781-	Sequence 4, Applicatio	2.89e+02
39	41	62.1	390	2	US-08-477-	Sequence 6, Applicatio	2.89e+02
40	41	62.1	390	1	US-08-121-	Sequence 6, Applicatio	2.89e+02
41	41	62.1	492	1	US-08-315-	Sequence 7, Applicatio	2.89e+02
42	41	62.1	510	1	US-08-489-	Sequence 1, Applicatio	2.89e+02
43	41	62.1	812	2	US-08-750-	Sequence 3, Applicatio	2.89e+02
44	41	62.1	812	1	US-08-446-	Sequence 2, Applicatio	2.89e+02
45	41	62.1	822	2	US-08-222-	Sequence 7, Applicatio	2.89e+02

ALIGNMENTS

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XX	xxxxxx			
AC	xxxxxx			
DT	01-JAN-1900			
XX	Patent No. 5169835.			
DE				
XX				
CC	Patent No. 5169835			
CC	APPLICANT: WAI-YEE, CHAN			
CC	TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS			
CC	CURRENT APPLICATION DATA:			
CC	NUMBER OF SEQUENCES: 48			
CC	APPLICATION NUMBER: US/07/390,409			
CC	FILING DATE: 07-AUG-1989			
CC	SEQ ID NO:15:			
CC	LENGTH: 248			
SO	SEQUENCE 268 AA; 29952 MW; 427605 CN;			
Query Match 74.2%; Score 49; DB 4; Length 248;				
Best Local Similarity 71.4%; Pred. No. 4.05e+01;				
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;				
DB	206 KYIAGPY 212			
QY	2 KYISAPY 8			
RESULT	2	STANDARD:	PRT:	292 AA.
ID	US-08-688-342-4			
XX	xxxxxx			
AC	xxxxxx			
DT				
XX				
DE	Sequence 4, Application US/08688342			
CC	Sequence 4, Application US/08688342			
CC	Patent No. 5871964			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Au-Young, Janice			
CC	APPLICANT: Cocks, Benjamin G.			
CC	APPLICANT: Goll, Surya K.			
CC	APPLICANT: Hillman, Jennifer L.			
CC	TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN			
CC	NUMBER OF SEQUENCES: 5			

CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC STREET: 3174 Porter Drive
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: US
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/688,342
CC FILING DATE: Filed Herewith
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Billings, Lucy J.
CC REGISTRATION NUMBER: 36,749
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-855-0555
CC TELEFAX: 415-845-4166
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 292 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC LIBRARY: GenBank
CC CLONE: 1235724
SQ SEQUENCE 292 AA; 32937 MW; 431088 CN;

Query Match 74.2%; Score 49; DB 2; Length 292;
Best Local Similarity 55.6%; Pred. No. 4.05e+01;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 205 QKYLGSAYT 213
OY 1 QKYLGSAYT 9

RESULT 3
ID 5169835-4 STANDARD; PRT; 384 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Patent No. 5169835.
XX
CC Patent No. 5169835
CC APPLICANT: MAI-YEE, CHAN
CC TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
CC NUMBER OF SEQUENCES: 48
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/390,409
CC FILING DATE: 07-AUG-1989
CC SEQ ID NO: 4:
CC LENGTH: 354
CC SEQUENCE 384 AA; 43378 MW; 901456 CN;

Query Match 74.2%; Score 49; DB 4; Length 354;
Best Local Similarity 71.4%; Pred. No. 4.05e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 161 KYIAGPY 167
OY 2 KYIAGPY 8

RESULT 4

ID 5169835-6 STANDARD; PRT; 459 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Patent No. 5169835.
XX
CC Patent No. 5169835
CC APPLICANT: MAI-YEE, CHAN
CC TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
CC NUMBER OF SEQUENCES: 48
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/390,409
CC FILING DATE: 07-AUG-1989
CC SEQ ID NO: 6:
CC LENGTH: 424
CC SEQUENCE 459 AA; 51394 MW; 1257782 CN;

Query Match 74.2%; Score 49; DB 4; Length 424;
Best Local Similarity 71.4%; Pred. No. 4.05e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 208 KYIAGPY 214
OY 2 KYIAGPY 8

RESULT 5
ID US-08-699-575-87 STANDARD; PRT; 107 AA.
XX
AC xxxxxx
XX
DT
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DE Sequence 87, Application US/08899575
XX
CC Sequence 87, Application US/08899575
CC Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbes, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ

Query Match 68.2%; Score 45; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.10e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYHSSPYT 96
| | | | |
QY 1 QYISAPYT 9

RESULT 6
ID US-08-276-852-87 STANDARD: PRT; 107 AA.
XX xxxxxx
AC
XX
DT
XX
DE Sequence 87, Application US/08276852
CC
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Bardas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ

Query Match 68.2%; Score 45; DB 1; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.10e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYHSSPYT 96
| | | | |
QY 1 QYISAPYT 9

RESULT 7
ID US-08-899-575-87 STANDARD: PRT; 107 AA.
XX xxxxxx
AC
XX
DT
XX
DE Sequence 87, Application US/08899575
CC
CC Patent No. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Bardas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein

SO SEQUENCE 107 AA; 11654 MW; 62438 CN;
Query Match 68.2%; Score 45; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.10e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYHSSPYT 96
| | | | |
1 QKYSAPYT 9

RESULT 8
ID PCT-US95-08743-87 STANDARD; PRT; 107 AA.
AC xxxxxx
XX
XX
DT
XX
DE Sequence 87, Application PC/TUS9508743
XX
CC Sequence 87, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;

Query Match 68.2%; Score 45; DB 3; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.10e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYHSSPYT 96
| | | | |
1 QKYSAPYT 9

RESULT 9
ID US-08-304-076A-2 STANDARD; PRT; 375 AA.
AC xxxxxx
XX
XX
DT
XX
DE Sequence 2, Application US/08304076A
XX
CC Sequence 2, Application US/08304076A
CC Patent No. 5618692
CC GENERAL INFORMATION:
CC APPLICANT: Handelsman, Jo
CC APPLICANT: Malner, Jocelyn L.
CC APPLICANT: Sohl, Elizabeth A.
CC APPLICANT: Stewart, Sandra J.
CC APPLICANT: Stabb, Eric
CC TITLE OF INVENTION: Zwitterion Resistance Gene and
CC TITLE OF INVENTION: Biocontrol Bacteria with the Gene

CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Quarles & Brady
CC STREET: 1 South Pinckney St.
CC CITY: Madison
CC STATE: WI
CC COUNTRY: US
CC ZIP: 53703
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/304,076A
CC FILING DATE: 12-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seay, Nicholas J
CC REGISTRATION NUMBER: 27,386
CC REFERENCE/DOCKET NUMBER: 96-296-9293-0
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 608-251-5000
CC TELEFAX: 608-251-9166
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 375 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 375 AA; 4348 MW; 730341 CN;

Query Match 68.2%; Score 45; DB 1; Length 375;
Best Local Similarity 55.6%; Pred. No. 1.10e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 113 QMEIPKPYT 121
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1 QKYSAPYT 9

RESULT 10
ID US-08-758-621-10 STANDARD; PRT; 376 AA.
AC xxxxxx
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DT
XX
DE Sequence 10, Application US/08758621
XX
CC Sequence 10, Application US/08758621
CC Patent No. 5846821
CC GENERAL INFORMATION:
CC APPLICANT: Gueriot, Mary Lou, and Elde, David J.
CC TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: LAHIVE & COCKFIELD
CC STREET: 60 State Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: USA
CC ZIP: 02109-1875
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/758,621
CC FILING DATE:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 60/018,578

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CC      FILING DATE: 29-MAY-1996
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Silverl, Jean M.
CC      REGISTRATION NUMBER: 39,030
CC      REFERENCE/DOCKET NUMBER: DCI-099CP
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (617)227-7400
CC      TELEFAX: (617)227-5941
CC      INFORMATION FOR SEQ ID NO: 10:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 376 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SO      SEQUENCE 376 AA; 41581 MW; 770726 CN;

Query Match      66.7%; Score 44; DB 2; Length 376;
Best Local Similarity 50.0%; Pred.No. 1.40e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0.

306 RYVSGSYT 313
      :|:|:|
OY      2 KYISAPYT 9

RESULT 11
ID      US-08-488-305A-6      STANDARD:      PRT;      533 AA.
XX      xxxxxx
XX
XX
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DE      Sequence 6, Application US/08488305A
CC
CC      Sequence 6, Application US/08488305A
CC      Patent No. 5679772
CC      GENERAL INFORMATION:
CC      APPLICANT: B v/k, Claes Olaf; Eriksson, Ulf; Peterson, Per A.
CC      TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which
CC      TITLE OF INVENTION: bind Thereeto, Nucleic Acid Sequence Coding
CC      Patent No. 5679772
CC      TITLE OF INVENTION: Therefore, And Uses Thereof
CC      NUMBER OF SEQUENCES: 6
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Felfe & Lynch
CC      STREET: 805 Third Avenue
CC      CITY: New York City
CC      STATE: New York
CC      COUNTRY: USA
CC      ZIP: 10022
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 kb storage
CC      COMPUTER: IBM PS/2
CC      OPERATING SYSTEM: PC-DOS
CC      SOFTWARE: Wordperfect
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/488,305A
CC      FILING DATE: 7-JUNE-1995
CC      CLASSIFICATION: 530
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Kohl1, Vlnet
CC      REGISTRATION NUMBER: 37,003
CC      REFERENCE/DOCKET NUMBER: LUD 5280.3
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (212) 688-9200
CC      TELEFAX: (212) 838-3884
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 533 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      SEQUENCE 533 AA; 60970 MW; 1558915 CN;

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	Query Match	66.7%	Score 44;	DB 1;	Length 533;
	Best Local Similarity	66.7%	Pred. No.	1.40e+02;	
	Matches	6;	Conservative	1;	Mismatches 2; Indels 0; Gaps 0;
Db	424 ORYGKPYT 432				
Oy	1 OKYISAPYT 9				
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RESULT 12					
ID	US-08-304-309-4	STANDARD;	PRT;	1025 AA.	
AC	xxxxxx				
Dt					
Sequence 4,	Application US/08304309				
CC	Sequence 4, Application US/08304309				
CC	Patent No. 5856454				
CC	GENERAL INFORMATION:				
CC	APPLICANT: GONZALEZ, Frank J.				
CC	TITLE OF INVENTION: FERNANDEZ-SALGUERO, Pedro				
CC	TITLE OF INVENTION: CLONING AND EXPRESSION OF cDNA FOR HUMAN				
CC	TITLE OF INVENTION: DIHYDROXYRIMIDINE DEHYDROGENASE				
CC	NUMBER OF SEQUENCES: 13				
CC	CORRESPONDENCE ADDRESSES:				
CC	ADDRESS: Townsend and Townsend Kourile and Crew				
CC	STREET: Stewart Street Tower, One Market Plaza				
CC	City: San Francisco				
CC	STATE: California				
CC	COUNTRY: US				
CC	ZIP: 94105-1493				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/304,309				
CC	FILING DATE: 09-SEP-1994				
CC	CLASSIFICATION: 435				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Smith, Timothy L.				
CC	REGISTRATION NUMBER: 35,367				
CC	REFERENCE/DOCKET NUMBER: 15280-210				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: (415) 543-9600				
CC	TELEFAX: (415) 543-5043				
CC	INFORMATION FOR SEQ ID NO: 4:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 1025 amino acids				
CC	TYPE: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
CC	SEQUENCE 1025 AA; 111423 MW; 5408679 CN;				
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Query Match	66.7%; Score 44; DB 2; Length 1025;				
Best Local Similarity	62.5%; Pred. No. 1.40e+02;				
Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;				
Db	504 HKYIOAOY 511				
Oy	1 OKYISAPY 8				
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RESULT 13					
ID	US-08-222-617A-13	STANDARD;	PRT;	3665 AA.	
AC	xxxxxxx				
Dt					
XX					
XX					

DE Sequence 13, Application US/08222617A
XX
CC Sequence 13, Application US/08222617A
CC Patent No. 5882879
CC GENERAL INFORMATION:
CC APPLICANT: Veenstra, Annemarie E.
CC APPLICANT: Martin, Juan F.
CC APPLICANT: Garcia, Bruno D.
CC APPLICANT: Gutierrez, Santiago
CC APPLICANT: Barredo, Jose L.
CC APPLICANT: Von Doehren, Hans
CC APPLICANT: Palissa, Harriet
CC APPLICANT: Van Liempt, Henk
CC TITLE OF INVENTION: A Method for Influencing Beta-Lactam
CC TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
CC TITLE OF INVENTION: Quantities of ACV Synthetase
CC NUMBER OF SEQUENCES: 27
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
CC STREET: 300 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/222,617A
CC FILING DATE: 04-APR-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC REFERENCE/DOCKET NUMBER: 97,157
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3665 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Acremonium chrysogenum
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..3665
CC OTHER INFORMATION: /label= ACVS
CC OTHER INFORMATION: /note= "ACV Synthetase from Acremonium
CC OTHER INFORMATION: chrysogenum; aa 1-3665"
SQ SEQUENCE 3665 AA: 409362 MW: 69161875 CN;

Query Match 66.7%; Score 44; DB 2; Length 3665;
Best Local Similarity 50.0%; Pred. No. 1.40e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DB 632 OKFLPNPY 639
QY 1 OKYISAPY 8

RESULT 14
ID US-08-222-617A-4 STANDARD: PRT: 3712 AA.
XX
XX xxxxxx
DT
XX
XX Sequence 4, Application US/08222617A
XX

CC Sequence 4, Application US/08222617A
CC Patent No. 5882879
CC GENERAL INFORMATION:
CC APPLICANT: Veenstra, Annemarie E.
CC APPLICANT: Martin, Juan F.
CC APPLICANT: Garcia, Bruno D.
CC APPLICANT: Gutierrez, Santiago
CC APPLICANT: Barredo, Jose L.
CC APPLICANT: Von Doehren, Hans
CC APPLICANT: Palissa, Harriet
CC APPLICANT: Van Liempt, Henk
CC APPLICANT: Montenegro, Eduardo P.
CC TITLE OF INVENTION: A Method for Influencing Beta-Lactam
CC TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
CC TITLE OF INVENTION: Quantities of ACV Synthetase
CC NUMBER OF SEQUENCES: 27
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
CC STREET: 300 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/222,617A
CC FILING DATE: 04-APR-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC REFERENCE/DOCKET NUMBER: 97,157
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3712 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Modified-site
CC LOCATION: 2555
CC OTHER INFORMATION:
CC OTHER INFORMATION: /note= "Xaa-Ala or Ser"
SQ SEQUENCE 3712 AA: 414762 MW: 71091070 CN;

Query Match 66.7%; Score 44; DB 2; Length 3712;
Best Local Similarity 50.0%; Pred. No. 1.40e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DB 632 OKFLPNPY 639
QY 1 OKYISAPY 8

RESULT 15
ID US-08-222-617A-25 STANDARD: PRT: 3712 AA.
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DT
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XX Sequence 25, Application US/08222617A
XX
XX Patent No. 5882879
XX GENERAL INFORMATION:
XX APPLICANT: Veenstra, Annemarie E.
XX APPLICANT: Martin, Juan F.
XX APPLICANT: Garcia, Bruno D.
XX APPLICANT: Gutierrez, Santiago
XX APPLICANT: Barredo, Jose L.
XX

CC APPLICANT: Von Doehren, Hans
 CC APPLICANT: Palissa, Harriet
 CC APPLICANT: Van Liempt, Henk
 CC APPLICANT: Montenegro, Eduardo P.
 CC TITLE OF INVENTION: A Method for Influencing Beta-Lactam
 CC TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
 CC TITLE OF INVENTION: Quantities of ACV Synthetase
 CC NUMBER OF SEQUENCES: 27
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 CC STREET: 300 South Wacker Drive
 CC CITY: Chicago
 CC STATE: Illinois
 CC COUNTRY: USA
 CC ZIP: 60606
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/222,617A
 CC FILING DATE: 04-APR-1994
 CC CLASSIFICATION: 435
 CC ATTORNEY/AGENT INFORMATION:
 CC REFERENCE/DOCKET NUMBER: 97,157
 CC INFORMATION FOR SEQ ID NO: 25:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 3712 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: Protein
 CC SEQUENCE 3712 AA; 414739 MW; 71073185 CN;
 CC
 CC Query Match 66.7%; Score 44; DB 2; Length 3712;
 CC Best Local Similarity 50.0%; Pred. No. 1.40e+02;
 CC Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Db 632 OKFLPNPY 639
 CC ||::: ||
 CC QY 1 OKYISAPY 8

Search completed: Thu Sep 2 12:14:18 1999
 Job time : 8 secs.

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 W E S E R E H (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:16:25 1999; Maspar time 2.13 Seconds
 119.711 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-599-226-25
 Description: (1-9) from US08599226.pep
 Perfect Score: 73
 Sequence: 1 QXNRPPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: .swiss-prot37
 1:swissprot

Statistics: Mean 23.709; Variance 27.935; scale 0.849

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	57	78.1	689	1	YBP3_YEAST	HYPOTHETICAL 77.3 KD P	1.16e+01
2	54	74.0	279	1	PRC2_DROME	PROTEASOME 29 KD SUBO	5.42e+01
3	53	72.6	626	1	BGAL_LEULA	BETA-GALACTOSIDASE IAR	8.97e+01
4	52	71.2	1262	1	GNRP_MOUSE	GUANINE NUCLEOTIDE REL	1.47e+00
5	51	69.9	263	1	PRC2_RAT	PROTEASOME COMPONENT C	2.41e+00
6	51	69.9	263	1	PRC2_HUMAN	PROTEASOME COMPONENT C	2.41e+00
7	51	69.9	301	1	CDK2_YEAST	CHITIN DEACETYLASE 2 P	2.41e+00
8	50	68.5	148	1	Y452_METJA	HYPOTHETICAL PROTEIN M	3.91e+00
9	50	68.5	360	1	DCAM_SOLTU	S-ADENOSYL METHIONINE D	3.91e+00
10	50	68.5	544	1	H15_DROME	T-BOX PROTEIN H15	3.91e+00
11	50	68.5	673	1	TAGE_BACSU	PROBABLE POLY(GLYCEROL	3.91e+00
12	49	67.1	387	1	OIN_AVTIS3	TRANSFORMING PROTEIN B	6.30e+00
13	49	67.1	451	1	BFL_CHICK	TRANSFORMATION FACTOR B	6.30e+00
14	49	67.1	469	1	BFL_HUMAN	TRANSFORMATION FACTOR B	6.30e+00
15	49	67.1	477	1	BFL_HUMAN	TRANSFORMATION FACTOR B	6.30e+00
16	49	67.1	480	1	BFL_HUMAN	TRANSFORMATION FACTOR B	6.30e+00
17	49	67.1	481	1	BFL_MOUSE	TRANSFORMATION FACTOR B	6.30e+00
18	49	67.1	536	1	ZPB_PIG	ZONA PELLUCIDA SPM-B	6.30e+00
19	49	67.1	560	1	DTX_COROM	DIPHHERIA TOXIN PRECU	6.30e+00
20	49	67.1	567	1	DTX_CORB	DIPHHERIA TOXIN PRECU	6.30e+00
21	49	67.1	1015	1	BGAL_ARPSP	BETA-GALACTOSIDASE (EC	1.01e+01
22	48	65.8	314	1	IF2A_RAT	EUKARYOTIC TRANSLATION	1.01e+01
23	48	65.8	314	1	IF2A_HUMAN	EUKARYOTIC TRANSLATION	1.01e+01

24	48	65.8	1156	1	CRVU_BACTR	131 KD CRYSTAL PROTEIN	1.01e+01
25	47	64.4	107	1	COTT_BACSU	SPORE COAT PROTEIN T P	1.60e+01
26	47	64.4	219	1	NUTM_NEUCR	NADH-UBIQUINONE OXIDOR	1.60e+01
27	47	64.4	287	1	PCAR_HUMAN	IMMUNOGLOBULIN ALPHA F	1.60e+01
28	47	64.4	481	1	KRL_HSV11	SERINE/THREONINE-PROTE	1.60e+01
29	47	64.4	758	1	YJ06_YEAST	POTATIVE 86.7 KD TRANS	1.60e+01
30	47	64.4	1134	1	TIEL_MOUSE	TYROSINE-PROTEIN KINAS	1.60e+01
31	47	64.4	1136	1	TIEL_BOVIN	TYROSINE-PROTEIN KINAS	1.60e+01
32	47	64.4	1138	1	TIEL_HUMAN	TYROSINE-PROTEIN KINAS	1.60e+01
33	46	63.0	288	1	Y026_HUMAN	HYPOTHETICAL PROTEIN K	2.52e+01
34	46	63.0	359	1	YF22_METTH	HYPOTHETICAL PROTEIN M	2.52e+01
35	46	63.0	406	1	BHMT_HUMAN	BETAINE--HOMOCYSTEINE	2.52e+01
36	46	63.0	421	1	CHDE_MICRO	CHITIN DEACETYLASE PRE	2.52e+01
37	46	63.0	427	1	FIXC_AKOVI	FIXC PROTEIN	2.52e+01
38	46	63.0	491	1	CG2A_DROME	G2/MITOTIC-SPECIFIC CY	2.52e+01
39	46	63.0	519	1	TYR2_HUMAN	DOPACHROME TAUTOMERASE	2.52e+01
40	46	63.0	521	1	NPRE_BACAM	BACILLOLYSIN PRECURSOR	2.52e+01
41	46	63.0	615	1	ALBU_CHICK	SERUM ALBUMIN PRECURSO	2.52e+01
42	46	63.0	628	1	YEH5_YEAST	HYPOTHETICAL 70.6 KD P	2.52e+01
43	46	63.0	734	1	PSAB_PORPU	PHOTOSYSTEM I P700 CHL	2.52e+01
44	46	63.0	742	1	PSAB_MASIA	PHOTOSYSTEM I P700 CHL	2.52e+01
45	46	63.0	1087	1	KA23_SCHPO	PROBABLE SERINE/THREON	2.52e+01

ALIGNMENTS

RESULT 1
 ID YBP3_YEAST STANDARD: PRT: 689 AA.

AC P38227;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 77.3 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.
 GN YBR043C OR YBR0413.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCHAROMYCETALES;
 NC SACCHAROMYCETACEAE; SACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA ANDRE B., CZIEPLOCH C., HEIN C., JAUNIAUX J.C., URRESTARAZU A.,
 RA VISSERS S.;
 RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBI DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
 AS THE DRUG RESISTANCE TRANSLUCASE FAMILY). BELONGS TO THE
 CAR1/CYR1 SUBFAMILY.
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 or send an email to license@sib-sib.ch).
 CC EMBL: Z35912; G536268; -.
 DR PIR: S45901; S45901.
 KW HYPOTHETICAL PROTEIN; TRANSPORT; TRANSMEMBRANE.
 FT TRANSMEM 109 131 POTENTIAL.
 FT TRANSMEM 140 163 POTENTIAL.
 FT TRANSMEM 176 193 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT TRANSMEM 266 283 POTENTIAL.
 FT TRANSMEM 476 493 POTENTIAL.
 FT TRANSMEM 511 532 POTENTIAL.
 FT TRANSMEM 559 577 POTENTIAL.
 FT TRANSMEM 587 609 POTENTIAL.
 FT TRANSMEM 625 642 POTENTIAL.
 FT TRANSMEM 649 668 POTENTIAL.
 FT TRANSMEM 77300 MM; 3616EDAE CRC32;
 SQ SEQUENCE 689 AA;
 Query Match 78.1%; Score 57; DB 1; Length 689;

Best Local Similarity 85.7%; Pred. No. 1.16e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 500 KYSRPPY 506
11:11111
QY 2 KYNRPY 8

RESULT 2
ID PRC2.DROME STANDARD; PRT: 279 AA.
AC P12881;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROTEASOME 29 KD SUBUNIT (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE
DE COMPLEX 35 KD SUBUNIT).
GN PROS35 OR PROS-35
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-18 AND 194-206.
RC STRAIN-OREGON-R;
RX MEDLINE: 90005444.
RA HAASZ C., PESOLD-HURT B., MÜLTHAUP G., BEYREUTHER K.,
RA KLOETZEL P.-M.;
RT "THE PROS-35 GENE ENCODES THE 35 KD PROTEIN SUBUNIT OF DROSOPHILA
RT "leucopostoc proteasome";
RL EMBO J. 8:2373-2379(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R;
RX MEDLINE: 92249308.
RA FRENTZEL S., TROXELL M., HAASZ C., PESOLD-HURT B., GLATZER K.H.,
RA KLOETZEL P.-M.;
RT Molecular characterization of the genomic regions of the Drosophila
RT alpha-type subunit proteasome genes PROS-Dm28.1 and PROS-Dm35.";
RL EUR. J. BIOCHEM. 205:1043-1051(1992).
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC ARG. PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC NEUTRAL OR SLIGHTLY BASIC PH. THE 35 KD SUBUNIT IS PROBABLY A
CC REGULATORY SUBUNIT. THE PROTEASOME HAS AN ATP-DEPENDENT
CC PROTEOLYTIC ACTIVITY.
CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
CC PROTEOLYTIC PATHWAY.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC ALSO IN THE NUCLEUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 11A; ALSO KNOWN AS THE
CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
CC
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CC
CC EMBL: X15497; G8382; -
DR EMBL: X62285; G8388; -
DR PIR: S05507; SNEFSK.
DR PIR: S23450; S23450.
DR FLIBASE: FB90003151; PROS35.
DR PROSITE: PS00388; PROTEASOME_A; 1.
DR PFAM: PF00227; Proteasome; 1.
DR HSSP: P25156; 1PMA.
KM PROTEASOME: HYDROLASE; PROTEASE; PHOSPHORYLATION
FT MOD_RES 103 103 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 279 AA; 31058 MW; AA16BBD6 CRC32;

Query Match 74.0%; Score 54; DB 1; Length 279;
Best Local Similarity 62.5%; Pred. No. 5.42e-01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 121 ORDRPPY 128
1:11111
QY 1 ORYNRPY 8

RESULT 3
ID BGAL.LEVIA STANDARD; PRT: 626 AA.
AC Q02603;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE BETA-GALACTOSIDASE LARGE SUBUNIT (EC 3.2.1.23) (LACTASE).
GN LACT.
OS LECONOSTOC LACTIS.
OC PLASMID P263.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; LACTOBACILLACEAE;
OC LECONOSTOC.
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-6.
RC STRAIN-NZ6009;
RX MEDLINE: 92325034.
RA DAVID S., STEVENS H., VAN RIEL M., SIMONS G., DE VOS W.M.;
RA "leucopostoc lactis beta-galactosidase is encoded by two overlapping
RT genes";
RL J. BACTERIOL. 174:4475-4481(1992).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL: M92281; G149635; -
DR PIR: A42891; A42891.
DR PROSITE: PS00719; GLYCOSYL_HYDROL_F2_1; 1.
DR PROSITE: PS00608; GLYCOSYL_HYDROL_F2_2; 1.
DR PFAM: PF00703; glycosyl_hydrof; 1.
DR HSSP: P00722; 1BGL.
KM HYDROLASE; GLYCOSIDASE; PLASMID.
FT ACT_SITE 318 318 HAS AN EFFECT ON THERMOSTABILITY
FT ACT_SITE 466 466 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 534 534 NOCTEOPHILE (BY SIMILARITY).
SQ SEQUENCE 626 AA; 72113 MW; 802C903C CRC32;
Query Match 72.6%; Score 53; DB 1; Length 626;
Best Local Similarity 85.7%; Pred. No. 8.97e-01;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 104 YNRPPY 110
111111
QY 3 YNRPPY 9

OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE: 93010996.
 RA CEN H., LOWY D.D.;
 RT "Isolation of multiple mouse cDNAs with coding homology to
 RT Saccharomyces cerevisiae CDC25: identification of a region related to
 RT Bcr, Vav, Dbl and CDC24.";
 RL EMO J. 11:4007-4015(1992).
 RN [2]
 RP SEQUENCE OF 791-1262 FROM N.A.
 RC STRAIN-SWISS; TISSUE-BRAIN;
 RX MEDLINE: 92289680.
 RA MARGARI E., VANONI M., ZIPPEL R., COCCETTI P., BRAMBILLA R.,
 RA FERRARI C., STURANI E.P., ALBERGHINA L.;
 RT "Cloning by functional complementation of a mouse cDNA encoding a
 RT homologue of CDC25, a Saccharomyces cerevisiae RAS activator.";
 RL EMO J. 11:2151-2157(1992).
 RN [3]
 RP SEQUENCE OF 1031-1226 FROM N.A.
 RC MEDLINE: 92357779.
 RA WEI W., MOSTELLER R.D., SANTAL P., GONZALES E., MCKINNEY D.,
 RA DASGUPTA C., LI P., LIU B.X., BROEK D.;
 RT "Identification of a mammalian gene structurally and functionally
 RT related to the CDC25 gene of Saccharomyces cerevisiae.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 89:7100-7104(1992).
 CC -1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: TO OTHER GUANINE-NUCLEOTIDE RELEASING FACTORS OF THE
 CC CDC25 FAMILY.
 CC -1- SIMILARITY: CONAINS 2 PH DOMAINS.
 CC -----
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 CC -----
 DR EMBL: L20899; G388247; -;
 DR EMBL: X59868; G50358; -;
 DR PIR: S20730; S20730.
 DR PIR: S22693; S22693.
 DR MGI: 99694; RASGRF1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR PROSITE: PS00741; GDS_CDC24; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PFAM: PF00169; PH; 2.
 DR PFAM: PF00612; IQ; 1.
 DR PFAM: PF00617; RASGEF; 1.
 DR PFAM: PF00618; RASGEF; 1.
 DR PFAM: PF00621; RASGEF; 1.
 DR GUANINE-NUCLEOTIDE RELEASING FACTOR.
 FT DOMAIN 22 130 PH.
 FT DOMAIN 460 588 PH.
 FT CONFLICT 1033 1033 E -> D (IN REF. 3).
 SO SEQUENCE 1262 AA; 144101 MW; 021C787F CRC32;
 Query Match 71.28; Score 52; DB 1; Length 1262;
 Best Local Similarity 62.58; Pred. No. 1,47e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 1060 EXERTPY 1067
 :11:111
 1 OKTNRPPY 8
 RESULT 5 STANDARD; PRT; 263 AA.
 ID PRG2_RAT

AC P18420;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE (PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
 DE (PROTEASOME CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT
 DE C2).
 GN PSM1.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-LIVER;
 RX MEDLINE: 90057428.
 RA FUJIMURA T., TANAKA K., KUMATORI A., SHIN S., YOSHIMURA T.,
 RA ICHIHARA A., TOKUNAGA F., ARUGA R., IWANAGA S., KAKIYUKA A.,
 RA NAKANISHI S.;
 RT "Molecular cloning of cDNA for proteasomes (multicatalytic proteinase
 RT complexes) from rat liver: primary structure of the largest component
 RT (C2)."
 RL BIOCHEMISTRY 28:7332-7340(1989).
 RN [2]
 RP SEQUENCE OF 1-30.
 RC TISSUE-LIVER;
 RX MEDLINE: 90243011.
 RA TOKUNAGA F., ARUGA R., IWANAGA S., TANAKA K., ICHIHARA A., TAKAO T.,
 RA SHIMONISHI Y.;
 RT "The NH2-terminal residues of rat liver proteasome (multicatalytic
 RT proteinase complex) subunits, C2, C3 and C8, are N
 RT alpha-acetylated.";
 RL FEBS LETT. 263:373-375(1990).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
 CC PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL RAT TISSUES.
 CC -1- PIM: ITS C-TERMINAL EXTENSION IS PARTIALLY CLEAVED OFF BY LIMITED
 CC PROTEOLYSIS LEADING TO A CONVERSION OF THE PROTEASOME FROM ITS
 CC LATENT INTO ITS ACTIVE FORM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
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 CC -----
 DR EMBL: M29859; G206382; -;
 DR EMBL: D90265; G220877; -;
 DR PIR: A32968; SNRRC2
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PFAM: PF00227; Proteasome; 1.
 DR HSSP: P25156; 1PMA.
 DR PROTEASOME; HYDROLASE; PROTEASE; ACETYLATION.
 FT MOD.RES 1 ACETYLATION.
 SO SEQUENCE 263 AA; 29517 MW; 01D55620 CRC32;
 Query Match 69.98; Score 51; DB 1; Length 263;
 Best Local Similarity 62.58; Pred. No. 2,41e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 121 ORYGRPY 128

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QY      1 OKXRRPPY 8
      1:11111
RESULT  6
ID      PRC2_HUMAN      STANDARD:      PRT;      263 AA.
AC      P25786;
DT      01-MAY-1992 (REL. 22, CREATED)
DT      01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT      15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE      PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
DE      (PROTEASOME NU CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT
DE      C2) (30 KD PROSOMAL PROTEIN) (PROS-30).
GN      HOMO SAPIENS (HUMAN).
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 93013039.
RA      SILVA-PEREIRA I., BEY F., COUX O., SCHERRER K.;
RT      "Two MRNAs exist for the Hs PROS-30 gene encoding a component of
RT      human prosomes";
RT      GENE 120:235-242(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 91223105.
RA      TAMURA T., LEE D.H., OSAKA F., FUJIMURA T., SHIN S., CHUNG C.H.,
RA      TANAKA K., ICHIHARA A.;
RT      "Molecular cloning and sequence analysis of cDNAs for five major
RT      subunits of human proteasomes (multi-catalytic proteinase
RT      complex)";
RT      BIOCHIM. BIOPHYS. ACTA 1089:95-102(1991).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 91363412.
RA      DEMARTINO G.N., ORTH K., MCCULLOUGH M.L., LEE L.W., MUNN T.2.,
RA      MOOMAN C.R., DAMSON P.A., SLAUGHTER C.A.;
RT      "The primary structures of four subunits of the human,
RT      high-molecular-weight proteinase, macropain (proteasome), are
RT      distinct but homologous";
RT      BIOCHEMA. BIOPHYS. ACTA 1079:29-38(1991).
RN      [4]
RP      FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
RP      WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
RP      ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
RP      NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
RP      PROTEOLYTIC ACTIVITY.
CC      -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
CC      PROTEOLYTIC PATHWAY.
CC      -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC      SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC      -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC      ALSO IN THE NUCLEUS.
CC      -1- ALTERNATIVE PRODUCTS: TWO FORMS (SHORT AND LONG) ARE PRODUCED BY
CC      ALTERNATIVE SPLICING OF THE GENE FOR THIS PROTEIN.
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
CC      PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M64992; G190447; ALT-SEQ.
DR      EMBL: D00759; G220022; -.
DR      EMBL: X61969; G296738; -.
DR      PIR: S15897; S15897.
DR      PIR: JCI445; JCI445.
DR      AARHUS/GENE-2DPAGE: 2223; IEF.
DR      MIM: 602854; -.

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DR      PROSITE: P500388; PROTEASOME_A; 1.
DR      PFAM: PF00227; proteasome; 1.
DR      HSSP: P25156; 1PMA.
DR      PROTEASOME: HYDROLASE; PROTEASE; ACETYLATION; ALTERNATIVE SPLICING.
FT      MOD_RES      1      1      ACETYLATION (BY SIMILARITY).
FT      VARSPIC      1      1      M -> MQLSKV (IN LONG FORM).
SQ      SEQUENCE      263 AA; 29555 MW; 6CD09A93 CRC32;
Query Match      69.9%; Score 51; DB 1; Length 263;
Best local Similarity 62.5%; Pred. No. 2.41e+00;
Matches      5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db      121 OKXRRPPY 128
QY      1 OKXRRPPY 8
      1:11111
RESULT  7
ID      CDA2_YEAST      STANDARD:      PRT;      301 AA.
AC      Q06702;
DT      01-NOV-1997 (REL. 35, CREATED)
DT      01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      CHITIN DEACETYLASE 2, PRECURSOR (EC 3.5.1.41).
DE      CDA2 OR YLR307W OR I2142.2.
GN      SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
OC      EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCAROMYCETALES;
OC      SACCAROMYCETACEAE; SACCAROMYCES.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN-S288C / AB972;
RA      JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
RA      FAVELLO A., FULTON L., GATTUNG S., GRACO T., KIRSTEN J.,
RA      KUGARA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,
RA      JOHNSON D., JOHNSTON L., LANGSTON Y., LARREILLE P., LE T.,
RA      MARDIS E., MENZIES S., MILLER N., NHAN M., PAULEY A., PELUSO D.,
RA      RIFKEN L., RILES L., TAICH A., TREVASIS E., VIGNANI D.,
RA      WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.;
RL      SUBMITTED (NOV-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN      [2]
RP      CHARACTERIZATION.
RX      MEDLINE: 97279228.
RA      MISHRA C., SEMINO C.E., MCCREATH R.J., DE LA VEGA H., JONES B.J.,
RA      SPECHT C.A., ROBBINS P.W.;
RT      "Cloning and expression of two chitin deacetylase genes of
RT      Saccharomyces cerevisiae";
RT      YEAST 13:327-336(1997).
RN      [3]
RP      FUNCTION: HYDROLYZES THE N-ACETAMIDO GROUPS OF N-ACETYL-D-
RP      GLUCOSAMINE RESIDUES IN CHITIN.
CC      -1- CATALYTIC ACTIVITY: CHITIN + H(2)O = CHITOSAN + ACETATE.
CC      -1- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY DURING SPOULATION.
CC      -1- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: U17247; G577218; -.
DR      SGD: L0003113; CDA2.
KW      HYDROLASE; CHITIN DEGRADATION; SIGNAL; GLYCOPROTEIN; SPOULATION.
FT      SGNL      1      2      POTENTIAL.
FT      CHAIN      2      301      CHITIN DEACETYLASE 2.
FT      CARBOHYD      26      26      POTENTIAL.
FT      CARBOHYD      50      50      POTENTIAL.
FT      CARBOHYD      68      68      POTENTIAL.
FT      CARBOHYD      189      189      POTENTIAL.
SQ      SEQUENCE      301 AA; 34642 MW; 1759E4C7 CRC32;
Query Match      69.9%; Score 51; DB 1; Length 301;

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DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE T-BOX PROTEIN H15.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EYE;
RA BROOK W.J., COHEN S.M.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: CONTAINS A T-BOX DOMAIN.
-----
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-----
CC EMBL: X98766; E255227; -.
DR FLYBASE: FBgn016660; H15.
DR PROSITE: PS01264; TBOX_2; FALSE_NEG.
DR PROSITE: PS01283; TBOX_1; 1.
DR PFM: PF00907; T-box; 1.
DR HSP: P24781; 1XB.
KM DNA-BINDING; NUCLEAR PROTEIN.
FT DOMAIN 56 59 POLY-ALA.
FT DOMAIN 83 91 POLY-GLN.
FT DOMAIN 118 125 POLY-PRO.
FT DNA_BIND 170 356 T-BOX.
FT DOMAIN 242 245 POLY-PRO.
FT DOMAIN 436 443 POLY-PRO.
SQ SEQUENCE 544 AA; 60010 MW; 701FD98D CRC32;

Query Match
Best Local Similarity 55.8%; Score 50; DB 1; Length 544;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 414 OMGRSPYT 422
QY 1 OKYNRPYT 9

RESULT 11
ID TAGC_BACSU STANDARD; PRT; 673 AA.
AC P13484;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PROBABLE POLY(GLYCEROL-PHOSPHATE) ALPHA-GLYCOSYLTRANSFERASE
DE (EC 2.4.1.52) (TEICHOIC ACID BIOSYNTHESIS PROTEIN E).
GN TAGC OR RODD OR GTAA.
OS BACILLUS SUBTILIS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE: 90014186.
RA HONEYMAN A.L., STEWART G.C.;
RL "The nucleotide sequence of the rodC operon of Bacillus subtilis.";
MO. MICROBIO. 3:1257-1268(1989).
CC -1- CATALYTIC ACTIVITY: UDP-GLUCOSE + POLY(GLYCEROL PHOSPHATE) -> UDP +
CC -1- ALPHA-D-GLUCOSYLPOLY(GLYCEROL PHOSPHATE).
CC -1- PATHWAY: POLY(GLYCEROL PHOSPHATE) TEICHOIC ACID BIOSYNTHESIS, AN
CC ESSENTIAL CELL WALL POLYMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

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CC -----
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-----
CC EMBL: X15200; G580920; -.
DR EMBL: 299122; E1184479; -.
DR PIR: S06048; S06048.
DR SUBTILIST; BG10724; TAGC.
DR PFM: PF00534; Glycos.transf.1; 1.
KM TEICHOIC ACID BIOSYNTHESIS; TRANSFERASE; GLYCOSYLTRANSFERASE.
SQ SEQUENCE 673 AA; 78303 MW; 2A398F64 CRC32;

Query Match
Best Local Similarity 62.5%; Score 50; DB 1; Length 673;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 504 EKYSRPNY 511
QY 1 OKYNRPYT 8

RESULT 12
ID QIN_AVT33 STANDARD; PRT; 387 AA.
AC P56260;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE TRANSFORMING PROTEIN QIN (ONCOGENE QIN).
GN V-QIN
OS AVIAN SARCOMA VIRUS (STRAIN 31) (ASV31).
OC VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
OC [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE: 93261605.
RA LI J., VOGT P.K.;
RL "The retroviral oncogene qin belongs to the transcription factor
RT family that includes the homeotic gene fork head.";
RL PROC. NATL. ACAD. SCI. U.S.A. 90:4490-4494(1993).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- THIS PROTEIN IS SYNTHESIZED AS A GAG-QIN POLYPROTEIN.
CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
-----
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-----
CC EMBL: L10719; -; NOT ANNOTATED CDS.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS00659; FORK_HEAD_3; 1.
KM DNA-BINDING; NUCLEAR PROTEIN; TRANSFORMING PROTEIN; ONCOGENE.
FT DOMAIN 42 54 POLY-HIS.
FT DOMAIN 55 58 POLY-PRO.
FT DOMAIN 64 67 POLY-ALA.
FT DNA_BIND 101 106 POLY-ALA.
FT DNA_BIND 142 233 FORK-HEAD.
SQ SEQUENCE 387 AA; 42283 MW; F34EB3C2 CRC32;

Query Match
Best Local Similarity 50.0%; Score 49; DB 1; Length 387;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 140 KYKRPFS 147
QY 1 OKYNRPYT 8

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OY 2 KYNRPPT 9

RESULT 13
ID BFLCHICK STANDARD: PRT: 451 AA.
AC 090964;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE TRANSCRIPTION FACTOR BF-1 (BRAIN FACTOR 1) (BFL1) (CBF-1) (PROTO-ONCOGENE C-QIN) (N-62-5) (CBQ 3-1).
GN FKHL1 OR QIN.
OS GALUS GALUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES; NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASININAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95132616.
RA CHANG H.W., LI J., KRETZSCHMAR D., VOGT P.K.;
RT "Avian cellular homolog of the qin oncogene."
PROC. NATL. ACAD. SCI. U.S.A. 92:447-451(1995).
[2]
RP SEQUENCE FROM N.A.
RX STRAIN-WHITE LEGHORN; TISSUE-RETINA;
RA MEDLINE: 96338226.
RA YUASA J., HIRANO S., YAMAGATA M., NODA M.;
RT "Visual projection map specified by topographic expression of transcription factors in the retina."
NATURE 382:632-635(1996).
-1- FUNCTION: MAY DETERMINE THE NASOTEMPORAL AXIS OF THE RETINA, AND CONSEQUENTLY SPECIFY THE TOPOGRAPHICAL PROJECTION OF THE RETINAL GANGLION-CELL AXONS TO THE TECTUM BY CONTROLLING EXPRESSION OF THEIR TARGET GENES.
-1- DEVELOPMENTAL STAGE: CAN BE DETECTED IN REGIONS INCLUDING PRIMITIVE RETINA AND NEUROEPITHELIUM BY EMBRYONIC DAY 2 (E2). AT E3, EXPRESSED IN THE NASAL RETINA AND PIGMENT EPITHELIUM AS WELL AS IN THE TELENCEPHALON, AND AT E7 IS EXPRESSED IN RETINAL GANGLION CELLS. LEVELS BEGIN TO DECLINE FROM E4 AND ALMOST DISAPPEAR BY E10.
-1- TISSUE SPECIFICITY: RETINA AND BRAIN.
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
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CC
DR EMBL: J36814; G642603; -
DR EMBL: U47275; G1546782; -
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS00659; FORK_HEAD_3; 1.
DR PFAM: PF00250; Fork_head; 1.
KM TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; PROTO-ONCOGENE.
FT DOMAIN 45 54
FT DOMAIN 55 58
FT DOMAIN 64 67
FT DOMAIN 103 106
FT DNAS_BIND 142 233
FT DNAS_BIND 451 AA; 48856 MW; 698F3964 CRC32;
SQ SEQUENCE

Query Match 67.1%; Score 49; DB 1; Length 451;
Best Local Similarity 50.0%; Pred. No. 6,30e+00;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 140 KYKPPFS 147
ID 11:11:11:
OY 2 KYNRPPT 9

RESULT 14
ID BFLHUMAN STANDARD: PRT: 469 AA.
AC P55315;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (HFK2).
GN FKHL2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-BRAIN;
RX MEDLINE: 95048332.
RA MURPHY D.B., WIESE S., BURFEIND P., SCHMUNDT D., MATTEI M.-G.,
RT SCHULZ-SCHAEFFER W., THIES U.;
RT "Human brain factor 1, a new member of the fork head gene family."
GENOMICS 21:551-557(1994).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95322450.
RA WIESE S., MURPHY D.B., SCHLUNG A., BURFEIND P., SCHMUNDT D.,
RA SCHNITZLE V., MATTEI M.-G., THIES U.;
RT "The genes for human brain factor 1 and 2, members of the fork head gene family, are clustered on chromosome 14q."
BIOCHIM. BIOPHYS. ACTA 1262:105-112(1995).
-1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ESTABLISHMENT OF THE REGIONAL SUBDIVISION OF THE DEVELOPING BRAIN AND IN THE DEVELOPMENT OF THE TELENCEPHALON. SEQUENCE-SPECIFIC DNA-BINDING PROTEIN WITH A DISTINCT BINDING SPECIFICITY (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
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CC
DR EMBL: X78202; G967048; -
DR EMBL: X74143; G516383; -
DR MIM: 600779; -
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS00659; FORK_HEAD_3; 1.
DR PFAM: PF00250; Fork_head; 1.
KM TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN.
FT DOMAIN 33 56
FT DOMAIN 57 59
FT DOMAIN 70 73
FT DOMAIN 83 88
FT DNAS_BIND 161 252
FT DNAS_BIND 469 AA; 50539 MW; 349275D5 CRC32;
SQ SEQUENCE

Query Match 67.1%; Score 49; DB 1; Length 469;
Best Local Similarity 50.0%; Pred. No. 6,30e+00;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 159 KYKPPFS 166
ID 11:11:11:
OY 2 KYNRPPT 9

RESULT 15
ID BFLHUMAN STANDARD: PRT: 477 AA.
AC P55315;

DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE TRANSCRIPTION FACTOR BF-1 (BRAIN FACTOR 1) (BF1) (HF1).
GN FKHL1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 95048332.
RA MURPHY D.B., WIESE S., BUREFIND P., SCHMUNDT D., MATTEI M.-G.,
RA SCHULZ-SCHAEFFER W., THIES U.;
RT "Human brain factor 1, a new member of the fork head gene family";
RL GENOMICS 21:551-557(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 95322450.
RA WIESE S., MURPHY D.B., SCHLUNG A., BUREFIND P., SCHMUNDT D.,
RA SCHMIDTLE V., MATTEI M.-G., THIES U.;
RT "The genes for human brain factor 1 and 2, members of the fork head
RL BIOCHIM. BIOPHYS. ACTA 1262:105-112(1995).
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ESTABLISHMENT OF THE
CC REGIONAL SUBDIVISION OF THE DEVELOPING BRAIN AND IN THE
CC DEVELOPMENT OF THE TELEENCEPHALON. SEQUENCE-SPECIFIC DNA-BINDING
CC PROTEIN WITH A DISTINCT BINDING SPECIFICITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC -----
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CC -----
DR EMBL: X74142; G516381; -
DR MIM: 164874; -
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00659; FORK_HEAD_3; 1.
DR PFAM; PF00250; Fork head; 1.
KW TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW DEVELOPMENTAL PROTEIN.
FT DOMAIN 33 57 HIS-RICH.
FT DOMAIN 58 80 PRO-RICH.
FT DOMAIN 72 75 POLY-GLN.
FT DOMAIN 99 102 POLY-LEU.
FT DNA_BIND 168 259 FORK-HEAD.
SQ SEQUENCE 477 AA; 51340 MW; A882DCDA CRC32;

Query Match 67.1%; Score 49; DB 1; Length 477;
Best Local Similarity 50.0%; Pred. No. 6.30e+00;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Db 166 KYKPPFS 173
QY 2 KYRPPYT 9

Search completed: Thu Sep 2 12:16:33 1999
Job time : 8 secs.

 WIRENET (TM)

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:15:56 1999; MasPar time 3.04 Seconds
 118.746 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-599-226-25
 Description: (1-9) from US08599226.pep
 Perfect Score: 73
 Sequence: 1 QKYNRPPT 9

Scoring table:
 PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: PIR60
 1:PIR1 2:PIR2 3:PIR3 4:PIR4

Statistics: Mean 23.064; Variance 30.875; scale 0.747

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	57	78.1	689	2	S45901	probable membrane pro	4.33e-01
2	54	74.0	279	1	SNF5K	multicatalytic endope	1.75e+00
3	53	72.6	626	2	A42891	beta-galactosidase (E	2.75e+00
4	52	71.2	215	2	JE0242	Ig kappa chain NIG26	4.32e+00
5	52	71.2	534	2	S71800	transcription factor	4.32e+00
6	52	71.2	1260	2	S28407	guanine nucleotide-ex	4.32e+00
7	51	69.9	212	2	B71974	hypothetical protein	6.73e+00
8	51	69.9	231	2	H64533	hypothetical protein	6.73e+00
9	51	69.9	263	1	SNR5C2	multicatalytic endope	6.73e+00
10	51	69.9	269	2	JC1445	multicatalytic endope	6.73e+00
11	51	69.9	301	2	SS1439	hypothetical protein	6.73e+00
12	51	69.9	521	2	I39956	neutral proteinase (E	6.73e+00
13	51	69.9	1009	2	C64483	hypothetical protein	6.73e+00
14	50	68.5	148	2	D64356	conserved hypothetical	1.04e+01
15	50	68.5	360	2	S28047	TUBJ3 protein - potat	1.04e+01
16	50	68.5	360	2	S52662	S-adenosylmethionine	1.04e+01
17	50	68.5	673	2	S06048	poly(glycerol-phospha	1.04e+01
18	49	67.1	109	2	B54743	transcription factor	1.61e+01
19	49	67.1	387	2	A47446	HNF-3/fork head fam11	1.61e+01
20	49	67.1	451	2	A55909	transforming protein	1.61e+01
21	49	67.1	469	2	I37451	HBF-G2 (HFK-2) protei	1.61e+01
22	49	67.1	476	2	A54743	transcription factor	1.61e+01
23	49	67.1	480	2	JH0672	brain factor 1 protel	1.61e+01

ENTRY	TITLE	ALIGNMENTS
24	49	67.1 536 2 S35712
25	49	67.1 560 1 DOGGA
26	49	67.1 560 1 DOGGA
27	49	67.1 1015 2 I39697
28	49	67.1 1041 2 PQ0442
29	49	67.1 1202 2 PQ0440
30	48	65.8 106 2 G02071
31	48	65.8 264 2 D71197
32	48	65.8 315 2 A25711
33	48	65.8 315 2 S18461
34	48	65.8 539 2 S67049
35	48	65.8 549 2 S49446
36	48	65.8 613 2 S55615
37	48	65.8 707 2 T01803
38	48	65.8 1013 2 S65195
39	48	65.8 1156 2 A29838
40	47	64.4 82 2 A41051
41	47	64.4 239 2 G02630
42	47	64.4 367 2 S49009
43	47	64.4 481 1 TYRE17
44	47	64.4 658 2 S23391
45	47	64.4 1134 1 JN0711

RESULT 1
 ENTRY TITLE S45901 #type complete
 probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae)
 ALTERNATE_NAMES
 ORGANISM #formal_name Saccharomyces cerevisiae
 DATE 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 04-Sep-1998
 ACCSSIONS
 REFERENCE S45901
 #authors Andre, B.; Czlepuch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
 #submision submitted to the Protein Sequence Database, August 1994
 #accession S45901
 #molecule_type DNA
 #residues 1-689 #label AND
 #cross-references EMBL:Z5912; NID:G536267; PID:G536268; MIPS:YBR043c
 #experimental_source strain S288C
 GENETICS
 #map_position 2R
 CLASSIFICATION #superfamily yeast probable membrane protein YBR043c
 KEYWORDS
 FEATURE
 108-124 #domain transmembrane #status predicted #label TM1
 140-161 #domain transmembrane #status predicted #label TM2
 177-193 #domain transmembrane #status predicted #label TM3
 239-256 #domain transmembrane #status predicted #label TM4
 255-287 #domain transmembrane #status predicted #label TM5
 476-493 #domain transmembrane #status predicted #label TM6
 513-529 #domain transmembrane #status predicted #label TM7
 535-579 #domain transmembrane #status predicted #label TM8
 587-603 #domain transmembrane #status predicted #label TM9
 629-645 #domain transmembrane #status predicted #label TM10
 648-670 #domain transmembrane #status predicted #label TM11
 SUMMARY #length 689 #molecular_weight 77300 #checksum 8706
 Query Match 78.1%; Score 57; DB 2; Length 689;
 Best Local Similarity 85.7%; Pred. No. 4.33e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 500 KSRPPY 506
 QY 2 KYNRPY 8
 RESULT 2
 ENTRY SNF5K #type complete

TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) 35k chain
ALTERNATE_NAMES - fruit fly (Drosophila melanogaster)
19S cylinder particle 35k chain; multicatalytic proteinase
ORGANISM 35k chain; prosome 35k chain; proteasome 35k chain
DATE #formal_name Drosophila melanogaster
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
ACCESSIONS S23450; S05507; A38761
REFERENCE S23450
#authors Frentzel, S.; Troxell, M.; Haass, C.; Pesold-Hurt, B.;
Glaetzer, K.H.; Klotzel, P.M.
#journal Eur. J. Biochem. (1992) 205:1043-1051
#title Molecular characterization of the genomic regions of the
Drosophila alpha-type subunit proteasome genes PROS-Dm28.1
and PROS-Dm35.
#cross-references MVID:92249308
#accession S23450
#molecule_type DNA
#residues 1-279 ##label FREN
#cross-references EMBL:X62285; NID:98387; PID:98388
#experimental_source strain Canton S
REFERENCE S05507
#authors Haass, C.; Pesold-Hurt, B.; Multhaup, G.; Beyreuther, K.;
Klotzel, P.M.
#journal EMBO J. (1989) 8:2373-2379
#title The PROS-35 gene encodes the 35 kd protein subunit of
Drosophila melanogaster proteasome.
#cross-references MVID:90005444
#accession S05507
#molecule_type mRNA
#residues 1-279 ##label HAA
#cross-references EMBL:X15497; NID:98381; PID:98382
#accession A38761
#molecule_type protein
#residues 4-18:194-206 ##label HAA2
GENETICS PROS-35
#gene
#cross-references FlyBase:FBgn0003151
#map_position 89F-90A
#introns 1/3; 211/3
CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9
KEYWORDS hydrolase; phosphoprotein; proteinase
SUMMARY #length 279 #molecular_weight 31058 #checksum 365
Query Match 74.0%; Score 54; DB 1; Length 279;
Best Local Similarity 62.5%; Pred. No. 1.75e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
121 QRYDRPPY 128
1:11111
QY 1 QKYNRPY 8

RESULT 3
ENTRY A42891 #type complete
TITLE beta-galactosidase (EC 3.2.1.23), 75k chain - Leuconostoc
lactis (strain NZ6009) plasmid pNZ63
ORGANISM #formal_name Leuconostoc lactis
DATE 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
ACCESSIONS A42891
REFERENCE A42891
#authors David, S.; Stevens, H.; Van Riel, M.; Simons, G.; de Vos,
W.M.
#journal J. Bacteriol. (1992) 174:4475-4481
#title Leuconostoc lactis beta-galactosidase is encoded by two
overlapping genes.
#cross-references MVID:9235034
#accession A42891
#status Preliminary
#molecule_type DNA
#residues 1-626 ##label DAV
#cross-references GB:M92281; NID:9149634; PID:9149635

#note authors translated the codon GAT for residue 569 as Gln,
and CAA for residue 570 as Asp
KEYWORDS glycosidase; hydrolase
SUMMARY #length 626 #molecular_weight 72113 #checksum 9411
Query Match 72.6%; Score 53; DB 2; Length 626;
Best Local Similarity 85.7%; Pred. No. 2.75e+00;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 104 YRRPPT 110
1:11111
QY 3 YNRPPY 9

RESULT 4
ENTRY JF0242 #type complete
TITLE Ig kappa chain NIC26 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
ACCESSIONS JF0242
REFERENCE JF0241
#authors Alim, M.A.; Yamaki, S.; Hossein, M.S.; Takeda, K.; Kojima,
M.; Takashi, I.; Shinoda, T.
#submission submitted to JIPID, November 1998
#description Structure relationship of kappa type light chains with AL
amyloidosis: Multiple deletions found in a VKIY protein.
#accession JF0242
#molecule_type protein
#residues 1-215 ##label ALI
SUMMARY #length 215 #molecular_weight 23518 #checksum 9963
Query Match 71.2%; Score 52; DB 2; Length 215;
Best Local Similarity 66.7%; Pred. No. 4.32e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 90 QOYDRPPWT 98
1:11111
QY 1 QKYNRPY 9

RESULT 5
ENTRY S71800 #type fragment
TITLE transcription factor FAS-1 - African clawed frog (fragment)
ALTERNATE_NAMES #formal_name Xenopus laevis #common_name African clawed frog
ORGANISM #formal_name Xenopus laevis #sequence_revision 25-Apr-1997 #text_change
DATE 05-Dec-1997
ACCESSIONS S71800
REFERENCE S71800
#authors Chen, X.; Rubock, M.J.; Whitman, M.
#journal Nature (1996) 383:691-696
#title A transcriptional partner for MAD proteins in TGF-beta
signaling.
#cross-references MVID:97032727
#accession S71800
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-534 ##label CHE
CLASSIFICATION #superfamily unassigned fork head proteins; fork head
DNA-binding domain homology
KEYWORDS DNA binding; transcription factor
FEATURE 117-209
SUMMARY #domain fork head DNA-binding domain homology #label FHD
#length 534 #checksum 6119
Query Match 71.2%; Score 52; DB 2; Length 534;
Best Local Similarity 44.4%; Pred. No. 4.32e+00;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
DB 113 HRYKPPYS 121
:::1111:

QY 1 OKYNRPYT 9

RESULT 6

ENTRY S28407 #type complete

TITLE guanine nucleotide-exchange activator CDC25 homolog - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 10-Sep-1997

ACCESSIONS S28407; S22693; B46199; S20730

REFERENCE S28407

#authors Cen, H.; Papageorge, A.G.; Zippel, R.; Lowy, D.R.; Zhang, K.

#journal EMBO J. (1992) 11:4007-4015

#title Isolation of multiple mouse cDNAs with coding homology to Saccharomyces cerevisiae CDC25: identification of a region related to Bcr, Vav, Dbl and CDC24.

#cross-references MIM:93010996

#accession S28407

#status not compared with conceptual translation

#molecule_type mRNA

REFERENCE S22693

#residues 1-1260 #label CEN

#authors Martegani, E.; Vanoni, M.; Zippel, R.; Cocchetti, P.; Brambilla, R.; Ferrari, C.; Sturani, E.; Alberghina, L.

#journal EMBO J. (1992) 11:2151-2157

#title Cloning by functional complementation of a mouse cDNA encoding a homologue of CDC25, a Saccharomyces cerevisiae RAS activator.

#cross-references MIM:92289680

#accession S22693

#molecule_type mRNA

REFERENCE S22693

#residues 789-1260 #label MAR

#cross-references EMBL:X59868; NID:g50357; PID:g50358

#authors Wei, W.; Mosteller, R.D.; Sanyal, P.; Gonzales, E.; McKinney, D.; Dasgupta, C.; Li, P.; Liu, B.X.; Broek, D.

#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104

#title Identification of a mammalian gene structurally and functionally related to the CDC25 gene of Saccharomyces cerevisiae.

#cross-references MIM:92357779

#accession B46199

#status preliminary

#molecule_type nucleic acid

#residues 1029-1030, 'D', 1032-1224 #label WEI

#experimental_source fetus

#note sequence extracted from NCBI backbone (NCBIN:111101, NCBIP:111102)

CLASSIFICATION #superfamily CDC25-type guanine nucleotide exchange activator homology; CDC24 homology; pleckstrin repeat homology

FEATURE

242-428 #domain CDC24 homology #label CD24\

1021-1257 #domain CDC25-type guanine nucleotide exchange activator homology #label SOS

SUMMARY #length 1260 #molecular-weight 143900 #checksum 9725

Query Match 71.2%; Score 52; DB 2; Length 1260;

Best Local Similarity 62.3%; Pred. No. 4.3e+00;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1058 EXERTPT 1065

QY 1 OKYNRPYT 8

RESULT 7

ENTRY B71974 #type complete

TITLE hypothetical protein jhp0104 - Helicobacter pylori (strain 199)

ORGANISM #formal_name Helicobacter pylori

DATE 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 12-Feb-1999

ACCESSIONS B71974

REFERENCE A71800

#authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Voyls, G.F.; Trust, T.J.

#journal Nature (1999) 397:176-180

#title Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.

#cross-references MIM:99120557

#accession B71974

#status preliminary

#molecule_type DNA

#residues 1-212 #label ARN

#cross-references GB:AE001449; GB:AE001439; NID:g4154604; PID:g4154611

#experimental_source strain J99

GENETICS

SUMMARY #gene jhp0104

#length 212 #molecular-weight 24741 #checksum 3051

Query Match 69.9%; Score 51; DB 2; Length 212;

Best Local Similarity 71.4%; Pred. No. 6.73e+00;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 101 YARNPYS 107

QY 3 YNRPYT 9

RESULT 8

ENTRY H64533 #type complete

TITLE hypothetical protein HP0112 - Helicobacter pylori (strain 2695)

ORGANISM #formal_name Helicobacter pylori

DATE 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 10-Oct-1997

ACCESSIONS H64533

REFERENCE A64520

#authors Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klein, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.R.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.

#journal Nature (1997) 388:519-547

#title The complete genome sequence of the gastric pathogen Helicobacter pylori.

#cross-references MIM:97394467

#accession H64533

#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-231 #label TOM

#cross-references GB:AE000533; GB:AE000511; NID:g2313196; PID:g2313200; TIGR:HP0112

GENETICS

SUMMARY #start_codon TTG

#length 231 #molecular-weight 27143 #checksum 4895

Query Match 69.9%; Score 51; DB 2; Length 231;

Best Local Similarity 71.4%; Pred. No. 6.73e+00;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 120 YARNPYS 126

QY 3 YNRPYT 9

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RESULT 9
ENTRY SNRNC2 #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2
ALTERNATE_NAMES multicatalytic proteinase component C2; proteasome chain C2
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 17-Oct-1997
ACCESSION A32968; A38799; S09741
REFERENCE A32968
#authors Fujimura, T.; Tanaka, K.; Kumatori, A.; Shin, S.; Yoshimura, T.; Ichihara, A.; Tokunaga, F.; Aruga, R.; Iwanaga, S.; Kakizuka, A.; Nakanishi, S.
#journal Biochemistry (1989) 28:7332-7340
#title Molecular cloning of cDNA for proteasomes (multicatalytic proteinase complexes) from rat liver: primary structure of the largest component (C2).
#cross-references MIM:90057428
#accession A32968
#molecule_type mRNA
#residues 1-263 #label FUJ1
#cross-references EMBL:M29659; NID:g206381; PID:g206382
#accession A38799
#molecule_type protein
#residues 2-25:42-58; 63-74, 'X', 76-79, 'X', 81; 116-135; 190-203; 218-226, 'XX', 229, 'X', 231; 244-246, 'X', 248-262 #label FUJ2
REFERENCE S09741
#authors Tokunaga, F.; Aruga, R.; Iwanaga, S.; Tanaka, K.; Ichihara, A.; Takao, T.; Shimonishi, Y.
#journal FEBS Lett. (1990) 263:373-375
#title The NH2-terminal residues of rat liver proteasome (multicatalytic proteinase complex) subunits, C2, C3 and C8, are N-alpha-acetylated.
#cross-references MIM:90243011
#accession S09741
#molecule_type protein
#residues 1-30 #label TOK
CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9
KEYWORDS acetylated amino end; hydrolase; proteinase
FEATURE 1-263
#product multicatalytic endopeptidase complex chain C2
#status experimental #label MAT\
#modified site acetylated amino end (Met) #status experimental
SUMMARY #length 263 #molecular-weight 29517 #checksum 9238
Query Match 69.9%; Score 51; DB 1; Length 263;
Best Local Similarity 62.5%; Pred. No. 6.73e+00;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 121 ORGYRPPY 128
QY 1 QKYNRPY 8
RESULT 10
ENTRY JC1445 #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2, long splice form - human
ALTERNATE_NAMES macropain nu chain; multicatalytic endopeptidase complex HC2 chain; multicatalytic endopeptidase complex nu chain; multicatalytic proteinase chain C2; prosome 30-33K chain; proteasome alpha 1 subunit; proteasome chain C2; proteasome nu chain
CONTAINS multicatalytic endopeptidase complex chain C2, short splice form
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997
ACCESSION JC1445; S15897; S17520; S25410; PC2321

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REFERENCE JC1445
#authors Pereira, I.S.; Bey, F.; Coux, O.; Scherrer, K.
#journal Gene (1992) 120:235-242
#title Two mRNAs exist for the Hs PROS-30 gene encoding a component of human prosome.
#accession JC1445
#molecule_type mRNA
#residues 1-269 #label PER
#cross-references GB:M64992
REFERENCE S15897
#authors Tamura, T.; Lee, D.H.; Osaka, F.; Fujimura, T.; Shin, S.; Chung, C.H.; Tanaka, K.; Ichihara, A.
#journal Biochim. Biophys. Acta (1991) 1089:95-102
#title Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multi-catalytic proteinase complexes).
#cross-references MIM:9123105
#accession S15897
#molecule_type mRNA
#residues 'M', 8-269 #label TAM
#cross-references EMBL:D00759; NID:g220021; PID:d1001114; PID:g220022
REFERENCE S17520
#authors Dewarino, G.N.; Orth, K.; McCullough, M.L.; Lee, L.W.; Munn, T.Z.; Mowbray, C.R.; Dawson, P.A.; Slaughter, C.A.
#journal Biochim. Biophys. Acta (1991) 1079:29-38
#title The primary structures of four subunits of the human, high-molecular-weight proteinase, macropain (prosome), are distinct but homologous.
#cross-references MIM:91363412
#accession S17520
#status not compared with conceptual translation
#molecule_type mRNA
#residues 'M', 8-269 #label DEM
#cross-references GB:X61969; NID:g236737; PID:g296738
#accession S25410
#molecule_type protein
#residues 10-40; 46-61; 68-75; 89-95; 103-128; 132-148; 164-168; 176-195; 203-223; 225-267 #label DE2
REFERENCE PC2315
#authors Kristensen, P.; Johnsen, A.H.; Uderwitz, W.; Tanaka, K.; Hendill, K.B.
#journal Biochem. Biophys. Res. Commun. (1994) 205:1785-1789
#title Human proteasome subunits from 2-dimensional gels identified by partial sequencing.
#cross-references MIM:95110324
#accession PC2321
#molecule_type protein
#residues 69-88 #label KRI
COMMENT #experimental_source placenta
#The proteasome consists of subunits of 21K-30K arranged in 4 stacked rings.
GENETICS
#gene GDB:PSMAL1; HSPROS-30
#cross-references GDB:134040
CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9
KEYWORDS hydrolase; phosphoprotein; proteinase
FEATURE 2-269
#product multicatalytic endopeptidase complex chain C2, long splice form #status predicted #label MAT\
#short splice form #status predicted #label MATS\
#binding site phosphate (Tyr) (covalent) #status predicted
SUMMARY #length 269 #molecular-weight 30239 #checksum 5946
Query Match 69.9%; Score 51; DB 2; Length 269;
Best Local Similarity 62.5%; Pred. No. 6.73e+00;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 127 ORGYRPPY 134
QY 1 QKYNRPY 8

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RESULT 11
ENTRY S51439 #type complete
TITLE hypothetical protein YLR307w - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein L2142.2
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Apr-1998

ACCESSIONS S51439
REFERENCE S51437
#authors Pauley, A.
#submission submitted to the EMBL Data Library, November 1994
#description The sequence of S. cerevisiae cosmid L2142.
#accession S51439
#molecule_type DNA
#residues 1-301 #label PAU
#cross-references EMBL:U17247; NID:g577216; PID:g577218; MIPS:YLR307w

GENETICS
#map_position 12R.
CLASSIFICATION #superfamily nodeB homology
FEATURE 113-264 #domain nodeB homology #label NOB
SUMMARY #length 301 #molecular-weight 34642 #checksum 1795

Query Match 69.9%; Score 51; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 6.73e+00;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 197 KXFRPPY 203
111111
QY 2 KXNRPPY 8

RESULT 12
ENTRY 139956 #type complete
TITLE neutral proteinase (EC 3.4.24.-) - Bacillus amyloliquefaciens
ORGANISM #formal_name Bacillus amyloliquefaciens
DATE 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 18-Mar-1997

ACCESSIONS 139956
REFERENCE 139956
#authors Shimada, H.; Honjo, M.; Mita, I.; Nakayama, A.; Akao, A.;
#journal J. Biotechnol. (1985) 2:75-85
#title The nucleotide sequence and some properties of the neutral
#accession 139956
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-521 #label RES
#cross-references GB:M5723; NID:g143352; PID:g143353

GENETICS
#start_codon GTG
CLASSIFICATION #superfamily thermolysin
KEYWORDS hydrolase; metalloproteinase
SUMMARY #length 521 #molecular-weight 56725 #checksum 6816

Query Match 69.9%; Score 51; DB 2; Length 521;
Best Local Similarity 75.0%; Pred. No. 6.73e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 308 OKNRMSY 315
111111
QY 1 OKYRPPY 8

RESULT 13
ENTRY C64483 #type complete
TITLE hypothetical protein MJ1468 - Methanococcus jannaschii
ORGANISM #formal_name Methanococcus jannaschii
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change

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ACCESSIONS C64483
REFERENCE A64300
#authors Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghegan, N.S.M.; Feldman, J.F.; Fuhrmann, J.D.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
#journal Science (1996) 273:1058-1073
#title Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
#cross-references M01D:96337999
#accession C64483
#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA
#residues 1-1009 #label BUL
#cross-references GB:U67587; GB:L77117; NID:g1592103; PID:g1592109; TIGR:MJ1468; PID:g1511480

GENETICS
#map_position FOR1437031-1440060
SUMMARY #length 1009 #molecular-weight 115119 #checksum 4486

Query Match 69.9%; Score 51; DB 2; Length 1009;
Best Local Similarity 62.5%; Pred. No. 6.73e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 776 HXFRPPY 783
111111
QY 1 OKYRPPY 8

RESULT 14
ENTRY D64356 #type complete
TITLE conserved hypothetical protein MJ0452 - Methanococcus jannaschii
ORGANISM #formal_name Methanococcus jannaschii
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Sep-1998

ACCESSIONS D64356
REFERENCE A64300
#authors Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghegan, N.S.M.; Feldman, J.F.; Fuhrmann, J.D.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
#journal Science (1996) 273:1058-1073
#title Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
#cross-references M01D:96337999
#accession D64356
#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA
#residues 1-148 #label BUL
#cross-references GB:U67496; GB:L77117; NID:g1591148; PID:g1591156; TIGR:MJ0452; PID:g1510527

GENETICS
#map_position REV404962-404516
CLASSIFICATION #superfamily Methanococcus jannaschii conserved hypothetical protein MJ0452
SUMMARY #length 148 #molecular-weight 16226 #checksum 7846

```

Query Match 68.5%; Score 50; DB 2; Length 148;
 Best Local Similarity 62.5%; Pred. No. 1.04e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 96 KYNKPTVA 103
 |||:| |:
 QY 2 KYNRPPT 9

RESULT 15

ENTRY S28047 #type complete
 TITLE TUB13 protein - potato

ORGANISM #formal_name Solanum tuberosum #common_name potato
 DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
 09-Sep-1997

ACCESSIONS S28047
 REFERENCE S28046
 #authors Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie,
 L.A.; Pearce, S.R.; Flavell, A.J.
 #journal Plant Mol. Biol. (1992) 20:641-651
 #title Expression and sequence analysis of cDNAs induced during the
 early stages of tuberisation in different organs of the
 potato plant (Solanum tuberosum L.).

#accession S28047
 #molecule_type mRNA
 #residues 1-360 #label TAY
 #cross-references EMBL:Z11680; NID:g21484; PID:g21485

GENETICS TUB13
 #gene
 SUMMARY #length 360 #molecular-weight 39726 #checksum 7941

Query Match 68.5%; Score 50; DB 2; Length 360;
 Best Local Similarity 62.5%; Pred. No. 1.04e+01;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 332 QKFTRTPY 339
 ||:| | |
 QY 1 QKYNRPPT 8

Search completed: Thu Sep 2 12:16:07 1999
 Job time : 11 secs.

(TM)

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generated.

ОКХНРРРПТ 5

2AM 150

179066 seqs, 54579741 residues

Listing first 45 summaries

sptremb19

13:sp_vertebrate 14:sp_virus

Mean 22.997; Variance 29.669; scale 0.775

ved by analysis of the total score distribution.

SUMMARIES

7.1	719 14	P87541	VIRAL POLYPROTEIN PREC	1.74e+01
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45	47	64.4	1117	5	077448	TELOMERASE REVERSE TRA	4.19e+01
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ALIGNMENTS

13	044626	PRELIMINARY;	PRT;	560	AA
ID	044626				
ID	044626				

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DE K11D12.1 PROTEIN

OS CAENORHABDITIS ELEGANS

OC RHABDITINA; RHABDITOID

RP SEQUENCE FROM N.A

RX MEDLINE; 94150718

RA BONEFIELD J., BURTON

RA GARDNER A., GREEN

RA LIGHTNING J., LLO

RA SMALDON N., SMITH

RA WATSON A., WEINST

RT *elegans*.²¹

RN [2]

RC STRAIN-BRISTOL N2

RL SUBMITTED (JAN-19

RP SEQUENCE FROM N.A.

RA WATERSTON R.;

DR EMBL; AF039047; G

ZINC-FINGER; META

Customer Match

Query Match

78.18; Score 57; DB 5; Length 560;

Best Local Similarity 75.08; Pred. No. 4.09e-01;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 81 OKYRRPY 88

OY 1 OKYRRPY 8

RESULT 2
ID P92024 PRELIMINARY; PRT; 494 AA.

AC P92024;

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE MEX-1.

OS MEX-1.

OC CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;

OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RC STRAIN-N2;

RT SEQUENCE FROM N.A.

RX MEDLINE: 97195715.

RT GUEDES S., PRIESS J.R.;

RT "The C. elegans MEX-1 protein is present in germline blastomeres and

is a P granule component."

RL DEVELOPMENT 124:731-739(1997).

DR EMBL: U81043; G1899062; -.

PR PAM: PF00642; zf-CCCH; 2.

SO SEQUENCE 494 AA; 56608 MW; 716506D2 CRC32;

Query Match 74.08; Score 54; DB 5; Length 494;
Best Local Similarity 62.58; Pred. No. 1.74e+00;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 263 QYRRRPPF 270

OY 1 QYRRRPPY 8

RESULT 3
ID 074958 PRELIMINARY; PRT; 400 AA.

AC 074958;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 44.6 KD PROTEIN.

OS SPC3736.12C.

OC SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;

OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;

OC SCHIZOSACCHAROMYCES.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-972H-;

RA WOOD V., RAJANDREAM M.A., BARRELL B.G., MURPHY L., HARRIS D.;

RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AL023705; E1294539; -.

KW HYPOTHETICAL PROTEIN.

SO SEQUENCE 400 AA; 44629 MW; 68320162 CRC32;

Query Match 72.68; Score 53; DB 3; Length 400;
Best Local Similarity 65.78; Pred. No. 2.79e+00;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 201 YRRPPYT 207

OY 3 YRRPPYT 9

RESULT 4
ID P70056 PRELIMINARY; PRT; 534 AA.

AC P70056;

DT 01-FEB-1997 (TREMBLREL. 02, CREATED)

DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE FORKHEAD ACTIVITY SIGNAL TRANSDUCER 1 (FRAGMENT).

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;

OC MESOBRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 97032727.

RA CHEN X., ROBOCK M.J., WHITMAN M.;

RT "A transcriptional partner for MAD proteins in TGF-beta signalling."

RL NATURE 383:691-696(1996).

DR EMBL: U70980; G1657774; -.

PR PAM: PF00250; Forkhead; 1.

FT NON_TER 534 534

SO SEQUENCE 534 AA; 59374 MW; 38762BCB CRC32;

Query Match 71.28; Score 52; DB 13; Length 534;
Best Local Similarity 44.48; Pred. No. 4.45e+00;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 113 HRYRRPPYS 121

OY 1 QYRRRPPYT 9

RESULT 5
ID 018508 PRELIMINARY; PRT; 1695 AA.

AC 018508;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)

DE C38D4.3 PROTEIN.

OS C38D4.3.

OC CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;

OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]

RP SEQUENCE FROM N.A.

RL SUBMITTED (OCT-1994) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE: 94150718.

RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BRKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHONKREIN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SUJSTON J.,

RA THIERRY-MIES J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPOAT J., WOHLMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

elegans."

RL NATURE 368:32-38(1994).

DR EMBL: Z46241; E1344466; -.

SO SEQUENCE 1695 AA; 191254 MW; 7425AB2B CRC32;

Query Match 71.28; Score 52; DB 5; Length 1695;
Best Local Similarity 44.48; Pred. No. 4.45e+00;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 315 EKYDRSFS 323

OY 1 OKYRRPPYT 9

RESULT 6
ID 036979 PRELIMINARY; PRT; 3082 AA.

AC 036979;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE POLYPROTEIN.
 OS ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV).
 OC VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
 OC POTYVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SINGAPORE.
 RA LEE K.C., WONG S.M.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF014811; G2462849;
 DR PFAM; PF00271; helicase_C; 1.
 DR PFAM; PF00680; RNA_dep_RNA_pol; 1.
 DR PFAM; PF00767; Poty-coat; 1.
 DR PFAM; PF00851; Peptidase_C6; 1.
 DR PFAM; PF00863; Peptidase_C4; 1.
 KW POLYPROTEIN.
 FT CHAIN 1 313 P1.
 FT CHAIN 314 769 HELPER COMPONENT-PROTEINASE.
 FT CHAIN 770 1115 P2.
 FT CHAIN 1116 1167 P3.
 FT CHAIN 1168 1801 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1802 1854 6K2.
 FT CHAIN 1855 2044 SMALL NUCLEAR INCLUSION-GENOME LINKED
 FT CHAIN 2045 2287 VPG.
 FT CHAIN 2288 2803 SMALL NUCLEAR INCLUSION-PROTEINASE.
 FT CHAIN 2804 3082 LARGE NUCLEAR INCLUSION.
 FT CHAIN 3082 350508 COAT PROTEIN.
 SQ SEQUENCE 3082 AA; 350508 MW; 43030AF1 CRC32;
 Query Match 71.2%; Score 52; DB 14; Length 3082;
 Best Local Similarity 75.0%; Pred. No. 4.45e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 279 OKXSRP 286
 QY 1 OKXSRP 8
 RESULT 7
 ID 042181; PRELIMINARY; PRT; 4578 AA.
 AC 042181;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PKD1. PROTEIN.
 OS FUGU RUBRIDES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIDES).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
 OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;
 OC TETRAODONTIFORMES; TETRAODONTIDEI; TETRAODONTIDAE; FUGU.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97449170.
 RA SANDFORD R., SCOTTO B., APARICIO S., BRENNER S., VAUDIN M., WILSON R.,
 RA CHISSE S., PERIN K., BATEMAN A., CHOTHA C., HUGHES J., HARRIS P.;
 RT Comparative analysis of the polycystic kidney disease 1 (PKD1) gene
 RT reveals an integral membrane glycoprotein with multiple evolutionary
 RT conserved domains.
 RT HUM. MOL. GENET. 6:1483-1489(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA VAUDIN M.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WASHU;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA WATERSTON R.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF013614; G2627436;
 DR PFAM; PF00059; lectin_c; 1.
 DR PFAM; PF00801; PKD; 14.
 SQ SEQUENCE 4578 AA; 504591 MW; DE8EE954 CRC32;
 Query Match 71.2%; Score 52; DB 13; Length 4578;
 Best Local Similarity 75.0%; Pred. No. 4.45e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 2824 OSTNDP 2831
 QY 1 OKXSRP 8
 RESULT 8
 ID 024934; PRELIMINARY; PRT; 231 AA.
 AC 024934;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 27.1 KD PROTEIN.
 OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
 OC BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
 OC HELICOBACTER.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-26695.
 RX MEDLINE; 97394467.
 RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
 RA FLEISCHMANN R.D., KENCHAM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
 RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
 RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODER A.,
 RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
 RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
 RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATHEY L., WALLIN E.,
 RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
 RA VENTER J.C.;
 RT The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori [published erratum appears in Nature 1997 Sep
 RT 25;389(6649):412].
 RL NATURE 388:539-547(1997).
 DR EMBL; AE000533; G2313200;
 DR TIGR; HP0112;
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 231 AA; 27143 MW; 0E7453D0 CRC32;
 Query Match 69.9%; Score 51; DB 2; Length 231;
 Best Local Similarity 71.4%; Pred. No. 7.05e+00;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 120 YARPPT 126
 QY 3 YNRPPY 9
 RESULT 9
 ID 027562; PRELIMINARY; PRT; 248 AA.
 AC 027562;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PRTC.
 OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 OC EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIID.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SHAULSKY G., ESCALANTE R., LOOMIS W.F.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S25A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY.

CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH.
 CC THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY.
 CC THE COMPONENT C3 MAY HAVE A POTENTIAL REGULATORY EFFECT ON
 CC ANOTHER COMPONENT(S) OF THE PROTEASOME COMPLEX THROUGH TYROSINE
 CC PHOSPHORYLATION.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 DR EMBL: U60168; G1405364; -.
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PFAM: PF00227; proteasome; 1.
 KW PROTEASOME; HYDROLASE; PROTEASE.
 QY SEQUENCE 248 AA; 27988 MW; BEE84ACC CRC32;
 RESULT 10
 ID 042265 PRELIMINARY; PRT; 260 AA.
 AC 042265;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE 20S PROTEASOME SUBUNIT C2.
 GN CC2.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STING I., WAGNER B.J.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF027978; G3136063; -.
 DR PFAM: PF00227; proteasome; 1.
 KW PROTEASOME.
 QY SEQUENCE 260 AA; 28925 MW; EF38499F CRC32;
 Query Match 69.9%; Score 51; DB 13; Length 260;
 Best Local Similarity 62.5%; Pred. No. 7.05e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 120 QRYGRPY 127
 QY 1 QKYNRPY 8
 RESULT 11
 ID 044677 PRELIMINARY; PRT; 521 AA.
 AC 044677;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE NEUTRAL PROTEASE.
 OS BACILLUS AMILOLOEFACIENS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SHIMADA H., HONJO M., MITA I., NAKAYAMA A., AKAKA A., MANABE K.,
 RA FURUTANI Y.,
 RL J. BIOTECHNOL. 2:75-85(1985).

DR EMBL: M36723; G143353; -.
 DR PFAM: PF00099; zn-protease; 1.
 KW PROTEASE.
 QY SEQUENCE 521 AA; 56725 MW; 64AFEE5F CRC32;
 Query Match 69.9%; Score 51; DB 2; Length 521;
 Best Local Similarity 75.0%; Pred. No. 7.05e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 308 QKYNRSY 315
 QY 1 QKYNRPY 8
 RESULT 12
 ID 058663 PRELIMINARY; PRT; 1009 AA.
 AC 058663;
 DT 01-JAN-1999 (TREMBLREL. 09, CREATED)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL PROTEIN MJ1468.
 GN MJ1468
 OS METHANOCOCCUS JANNASCHII.
 OC ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
 OC METHANOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DSM 2661.
 RX MEDLINE: 96337999.
 RA BOLT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
 RA KUTLON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
 RA KERULAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
 RA OVERBERGER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLADER A.,
 RA SCOTT J.L., GOGCHEN N.S.M., WEIDMAN J.F., FUHRMAN J.L., NGUYEN D.,
 RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
 RA COTTON M.D., ROBERTS K.M., HURST M.A., KATNE B.P., BORODOVSKI M.,
 RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
 RL SCIENCE 273:1058-1073(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 DR EMBL: U67588; G2826412; -.
 DR PFAM: PF00801; PHD; 3. TRANSMEMBRANE.
 KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
 FT TRANSMEM 6
 FT TRANSMEM 985 1005 POTENTIAL.
 FT DOMAIN 293 298 POLY-ASN.
 SQ SEQUENCE 1009 AA; 115119 MW; FAF4611 CRC32;
 Query Match 69.9%; Score 51; DB 1; Length 1009;
 Best Local Similarity 62.5%; Pred. No. 7.05e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 776 HXYRPGY 783
 QY 1 QKYNRPY 8
 RESULT 13
 ID 019008 PRELIMINARY; PRT; 192 AA.
 AC 019008;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE COSMID D2096.
 GN D2096.2
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVIELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SANDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SOLTSTON J.,
 RA THERIAULT-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLIDMAN P.,
 RA *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans*;
 RL MATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.

RA GEISEL C.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.

RA WATERSTON R.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U40800; G1065953; -
 SQ SEQUENCE 192 AA; 21669 MW; 93B8E6AC CRC32;

Query Match 68.5%; Score 50; DB 5; Length 192;
 Best Local Similarity 50.0%; Pred. No. 1.11e+01;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 30 DRYERPF 37
 :|||:
 QY 1 OKYNRPY 8

RESULT 14
 ID 074961 PRELIMINARY; PRT; 231 AA.
 AC 074961;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 25.6 KD PROTEIN (FRAGMENT).
 GN SPC736.16.

OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EURARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
 OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 OC SCHIZOSACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-972H-;
 RA WOOD V., RAJANDREAN M.A., BARRELL B.G., MURPHY L., HARRIS D.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AL023705; E1294543; -

RA HYPOTHETICAL PROTEIN.
 NON_TER 1
 SQ SEQUENCE 231 AA; 25584 MW; FB84EB08 CRC32;

Query Match 68.5%; Score 50; DB 3; Length 231;
 Best Local Similarity 62.5%; Pred. No. 1.11e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 120 DKYARSPY 127
 :|||:
 QY 1 OKYNRPY 8

RESULT 15
 ID 050244 PRELIMINARY; PRT; 307 AA.
 AC 050244;

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE TRANSPOSASE HOMOLOG.
 OS AGROBACTERIUM TUMEFACIENS.

OC PLASMID PTIC38.
 OC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
 OC RHIZOBIACEAE; AGROBACTERIUM.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C58;
 RA KALOGERAKI V.S., WINANS S.C.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF034769; G2655340; -
 SQ SEQUENCE 307 AA; 35022 MW; 3104224E CRC32;

Query Match 68.5%; Score 50; DB 2; Length 307;
 Best Local Similarity 71.4%; Pred. No. 1.11e+01;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 159 RYNRPY 165
 :|||:
 QY 2 KYNRPY 8

Search completed: Thu Sep 2 12:17:14 1999
 Job time : 23 secs.

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CC GENERAL INFORMATION:
CC APPLICANT: Conti-Fine, B. M.
CC TITLE OF INVENTION: DIPHTHERIA TOXIN EPITOPES
CC NUMBER OF SEQUENCES: 79
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
CC STREET: P.O. Box 2938
CC CITY: Minneapolis
CC STATE: MN
CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,972
CC FILING DATE: 30-NOV-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Woessner, Warren D
CC REGISTRATION NUMBER: 30,440
CC REFERENCE/DOCKET NUMBER: 600.344US1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 612-339-0331
CC TELEFAX: 612-339-3061
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 43:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: Internal
CC ORIGINAL SOURCE:
CC SEQUENCE 20 AA; 2314 MW; 2453 CN;
SQ

Query Match 67.1%; Score 49; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 6,486+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
5 YNRPAYS 11
|||||:
3 YNRPPT 9

RESULT 5
ID US-08-564-972-57 STANDARD; PRT; 180 AA.
XX xxxxxx
DE Sequence 57, Application US/08564972
XX Sequence 57, Application US/08564972
CC Patent No. 5843462
CC GENERAL INFORMATION:
CC APPLICANT: Conti-Fine, B. M.
CC TITLE OF INVENTION: DIPHTHERIA TOXIN EPITOPES
CC NUMBER OF SEQUENCES: 79
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
CC STREET: P.O. Box 2938
CC CITY: Minneapolis
CC STATE: MN

CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,972
CC FILING DATE: 30-NOV-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Woessner, Warren D
CC REGISTRATION NUMBER: 30,440
CC REFERENCE/DOCKET NUMBER: 600.344US1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 612-339-0331
CC TELEFAX: 612-339-3061
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 57:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 180 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: Internal
CC ORIGINAL SOURCE:
CC SEQUENCE 180 AA; 19086 MW; 175296 CN;
SQ

Query Match 67.1%; Score 49; DB 2; Length 180;
Best Local Similarity 71.4%; Pred. No. 6,486+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
105 YNRPAYS 111
|||||:
3 YNRPPT 9

RESULT 6
ID US-08-564-972-9 STANDARD; PRT; 331 AA.
XX xxxxxx
DE Sequence 9, Application US/08564972
XX Sequence 9, Application US/08564972
CC Patent No. 5843462
CC GENERAL INFORMATION:
CC APPLICANT: Conti-Fine, B. M.
CC TITLE OF INVENTION: DIPHTHERIA TOXIN EPITOPES
CC NUMBER OF SEQUENCES: 79
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
CC STREET: P.O. Box 2938
CC CITY: Minneapolis
CC STATE: MN
CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,972

CC FILING DATE: 30-NOV-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Woessner, Warren D
CC REGISTRATION NUMBER: 30,440
CC REFERENCE/DOCKET NUMBER: 600.344051
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 612-339-0331
CC TELEFAX: 612-339-3061
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 331 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: C-terminal
CC ORIGINAL SOURCE:
SQ SEQUENCE 331 AA: 36133 MW: 593181 CN;

Query Match 67.1%; Score 49; DB 2; Length 331;
Best Local Similarity 71.4%; Pred. No. 6.48e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 171 YNRPAYS 177
|||:|:
QY 3 YNRPYPT 9

RESULT 7
ID US-08-564-972-1 STANDARD; PRT; 535 AA.
AC xxxxxx
DT
DE Sequence 1, Application US/08564972
XX
CC Sequence 1, Application US/08564972
CC Patent No. 5843462
CC GENERAL INFORMATION:
CC APPLICANT: Conli-Fine, B. M.
CC TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
CC NUMBER OF SEQUENCES: 79
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.
CC STREET: P.O. Box 2938
CC CITY: Minneapolis
CC STATE: MN
CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,972
CC FILING DATE: 30-NOV-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Woessner, Warren D
CC REGISTRATION NUMBER: 30,440
CC REFERENCE/DOCKET NUMBER: 600.344051

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 612-339-0331
CC TELEFAX: 612-339-3061
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 535 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: Internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 335 AA: 38340 MW: 1522803 CN;

Query Match 67.1%; Score 49; DB 2; Length 535;
Best Local Similarity 71.4%; Pred. No. 6.48e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 375 YNRPAYS 381
|||:|:
QY 3 YNRPYPT 9

RESULT 8
ID US-08-484-993B-4 STANDARD; PRT; 536 AA.
AC xxxxxx
DT
DE Sequence 4, Application US/08484993B
XX
CC Sequence 4, Application US/08484993B
CC Patent No. 5837497
CC GENERAL INFORMATION:
CC APPLICANT: Harris Ph.D., Jeffrey D.
CC APPLICANT: Hsu, Kuang T.
CC APPLICANT: Podolski, Joseph S.
CC TITLE OF INVENTION: Materials and Methods for Immunoreception
CC NUMBER OF SEQUENCES: 59
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,993B
CC FILING DATE: 09-NOV-1993
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/012,990
CC FILING DATE: 29-JAN-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/973,341
CC FILING DATE: 09-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clough, David W.
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 31745
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6653
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856

CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 536 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 536 AA; 59333 MW; 1586589 CN;

Query Match 67.1%; Score 49; DB 2; Length 536;
Best Local Similarity 71.4%; Pred. No. 6.48e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 499 HKYRPP 505
QY 1 OKYRPP 7

RESULT 9
ID US-07-805-567-2 STANDARD; PRT; 316 AA.
XX xxxxxx

Sequence 2, Application US/07805567
CC Sequence 2, Application US/07805567
CC Patent No. 5378457
CC GENERAL INFORMATION:
CC APPLICANT: Paoletti, Enzo
CC APPLICANT: Tartaglia, James
CC TITLE OF INVENTION: INTERFERON SENSITIVE RECOMBINANT
CC TITLE OF INVENTION: POXYIRUS VACCINE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Curtis, Morris & Safford
CC ADDRESSEE: c/o William S. Frommer
CC STREET: 530 Fifth Avenue
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/805,567
CC FILING DATE: 19911216
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/638,080
CC FILING DATE: 07-JAN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Frommer, William S.
CC REGISTRATION NUMBER: 25,506
CC REFERENCE/DOCKET NUMBER: 454310-2281
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 840-3333
CC TELEFAX: (212) 840-0712
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 316 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 316 AA; 36218 MW; 474239 CN;

Query Match 65.8%; Score 48; DB 1; Length 316;
Best Local Similarity 62.5%; Pred. No. 8.22e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 141 DKYRPGY 148
QY 1 OKYRPPY 8

RESULT 10
ID US-08-564-972-42 STANDARD; PRT; 20 AA.
XX xxxxxx

Sequence 42, Application US/08564972
CC Sequence 42, Application US/08564972
CC Patent No. 5843462
CC GENERAL INFORMATION:
CC APPLICANT: Conti-Fine, B. M.
CC TITLE OF INVENTION: DIPHTHERIA TOXIN EPITOPES
CC NUMBER OF SEQUENCES: 79
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
CC STREET: P.O. Box 2938
CC CITY: Minneapolis
CC STATE: MN
CC COUNTRY: USA
CC ZIP: 55402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,972
CC FILING DATE: 30-NOV-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Woessner, Warren D
CC REGISTRATION NUMBER: 30,440
CC REFERENCE/DOCKET NUMBER: 600.344051
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 612-339-0331
CC TELEFAX: 612-339-3061
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 42:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 20 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: Internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 20 AA; 2364 MW; 2260 CN;

Query Match 64.4%; Score 47; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.04e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 15 YNRPAY 20
QY 3 YNRPY 8

RESULT 11
ID US-07-987-286-20 STANDARD; PRT; 25 AA.
XX xxxxxx

XX DE Sequence 20, Application 07/987286
XX CC Patent No. 5500366
XX CC Sequence 20, Application 07/987286
CC CC Patent No. 5500366
CC CC GENERAL INFORMATION:
CC CC APPLICANT: RUSSELL-JONES, GREGORY J
CC CC APPLICANT: GECY, ANDREW F
CC CC TITLE OF INVENTION: T-CELL EPITOPES
CC CC NUMBER OF SEQUENCES: 26
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: FOLEY & LARDNER
CC CC STREET: 3000 K STREET, N.W.
CC CC CITY: WASHINGTON, D.C.
CC CC COUNTRY: USA
CC CC ZIP: 20007-5109
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: 07/987,286
CC CC FILING DATE: 16-MAR-1993
CC CC CLASSIFICATION: 424
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: PCT/AU91/00429
CC CC FILING DATE: 17-SEP-1991
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: AU PK2361
CC CC FILING DATE: 18-SEP-1990
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: BENT, STEPHEN A.
CC CC REGISTRATION NUMBER: 29,768
CC CC REFERENCE/DOCKET NUMBER: 16786/175/CHAC
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: 202 672 5300
CC CC TELEFAX: 202 672 5399
CC CC TELEX: 904136
CC CC INFORMATION FOR SEQ ID NO: 20:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 25 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: peptide
CC CC FEATURE:
CC CC NAME/KEY: Modified-site
CC CC LOCATION: 1
CC CC OTHER INFORMATION: /note="RESIDUE 1 IS ACETYLALANINE"
CC CC FEATURE:
CC CC NAME/KEY: Modified-site
CC CC LOCATION: 25
CC CC OTHER INFORMATION: /note="RESIDUE 25 IS CYSTEINAMIDE"
CC CC SEQUENCE 25 AA: 2946 MW; 3853 CN;
Query Match 64.4%; Score 47; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.04e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 19 YNRPPY 24
OY 3 YNRPPY 8
RESULT 12
ID 5198342-2 STANDARD; PRT; 311 AA.
XX xxxxxx
AC
DT 01-JAN-1900
XX

DE Patent No. 5198342.
XX CC Patent No. 5198342
XX CC APPLICANT: MALISZEWSKI, CHARLES R.
CC CC TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
CC CC NUMBER OF SEQUENCES: 9
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/07/548,059
CC CC FILING DATE: 05-JUL-1990
CC CC SEQ ID NO: 2:
CC CC LENGTH: 287
CC CC SEQUENCE 311 AA; 34908 MW; 558002 CN;
Query Match 64.4%; Score 47; DB 4; Length 287;
Best Local Similarity 83.3%; Pred. No. 1.04e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSPY 202
OY 3 YNRPPY 8
RESULT 13
ID US-07-971-092-2 STANDARD; PRT; 287 AA.
XX xxxxxx
AC
DT
XX DE Sequence 2, Application US/07971092
XX CC Sequence 2, Application US/07971092
CC CC Patent No. 5328987
CC CC GENERAL INFORMATION:
CC CC APPLICANT: Maliszewski, Charles R.
CC CC TITLE OF INVENTION: Huiga Fc Receptor
CC CC NUMBER OF SEQUENCES: 2
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: Immunex
CC CC STREET: 51 University
CC CC CITY: Seattle
CC CC STATE: WA
CC CC COUNTRY: USA
CC CC ZIP: 98101
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/07/971,092
CC CC FILING DATE: 19921104
CC CC CLASSIFICATION: 435
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Perkins, Patricia A.
CC CC REGISTRATION NUMBER: 34693
CC CC REFERENCE/DOCKET NUMBER: 2603
CC CC INFORMATION FOR SEQ ID NO: 2:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 287 amino acids
CC CC TYPE: AMINO ACID
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC SEQUENCE 287 AA; 32265 MW; 435416 CN;
Query Match 64.4%; Score 47; DB 1; Length 287;
Best Local Similarity 83.3%; Pred. No. 1.04e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSPY 202
OY 3 YNRPPY 8

RESULT 14
ID US-08-469-537A-97 STANDARD: PRT: 1135 AA.
AC xxxxxx
XX
XX
XX
XX
DE Sequence 97, Application US/08469537A
XX
XX Sequence 97, Application US/08469537A
CC Patent No. 5843749
CC GENERAL INFORMATION:
CC APPLICANT: Maisonglerre, et al.
CC TITLE OF INVENTION: EHK AND ROR TYROSINE
CC NUMBER OF SEQUENCES: 107
CC CORRESPONDENCE ADDRESSES:
CC ADDRESS: Regeneron Pharmaceuticals, Inc.
CC STREET: 777 Old Saw Mill River Road
CC CITY: Tarrytown
CC STATE: NY
CC COUNTRY: U.S.A.
CC ZIP: 10591
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/469,537A
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: USSN 08/406,247
CC FILING DATE: 17-MAR-1995
CC APPLICATION NUMBER: USSN 08/144,992
CC FILING DATE: 28-OCT-1993
CC APPLICATION NUMBER: USSN 07/736,559
CC FILING DATE: 26-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kempster, Ph.D., Gall M
CC REGISTRATION NUMBER: 32,143
CC REFERENCE/DOCKET NUMBER: REG 070C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 914-345-7400
CC TELEFAX: 914-345-7721
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 97:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1135 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC SEQUENCE 1135 AA; 125367 MW; 6510763 CN;
SQ
Query Match 64.4%; Score 47; DB 2; Length 1135;
Best Local Similarity 57.1%; Pred. No. 1.04e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 1092 YERPPFA 1098
QY 3 YNRPPYT 9
RESULT 15
ID US-08-323-474-8 STANDARD: PRT: 1138 AA.
AC xxxxxx
XX
XX
XX
XX
XX

DE Sequence 8, Application US/08323474
XX
XX Sequence 8, Application US/08323474
CC Patent No. 5447860
CC GENERAL INFORMATION:
CC APPLICANT: Ziegler, Steven F.
CC TITLE OF INVENTION: NOVEL TYROSINE KINASE
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESSES:
CC ADDRESS: Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: US
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/323,474
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/905,600
CC FILING DATE: 26-JUN-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2609
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 587-0430
CC TELEFAX: (206) 233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1138 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1138 AA; 125055 MW; 6525428 CN;
SQ
Query Match 64.4%; Score 47; DB 1; Length 1138;
Best Local Similarity 57.1%; Pred. No. 1.04e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 1095 YERPPFA 1101
QY 3 YNRPPYT 9

Search completed: Thu Sep 2 12:17:39 1999
Job time : 8 secs.

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CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 100.0%; Score 73; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2,53e+01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 QKYNRPYT 9
 |||||
 QY 1 QKYNRPYT 9

RESULT 2
 W27575 standard; peptide: 9 AA.

AC W27575:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manfovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 90.4%; Score 66; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.64e+00;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 QKYNRPYT 9
 |||||
 QY 1 QKYNRPYT 9

RESULT 3
 W27571 standard; peptide: 9 AA.

ID W27571:
 AC W27571:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manfovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 86.3%; Score 63; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3.60e+00;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 QKYNRPYT 9
 |||||
 QY 1 QKYNRPYT 9

RESULT 4
 W27568 standard; protein: 107 AA.

ID W27568:
 AC W27568:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody;

light chain: variable region; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; pyrexia; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HIVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
 Mankovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 N-PSDB: T88403.
 High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 15; Page 75; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 Sequence 107 AA:

Query Match 86.3% Score 63; DB 27; Length 107;
 Best Local Similarity 77.8%; Pred. No. 3,60e+00;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 89 grynarypt 97
 1:111:111
 1 OKNRPPT 9

RESULT 5
 ID W2572 standard; peptide: 9 AA.
 AC W2572:
 DE 19-WAR-1998 (first entry)
 PI Anti-TNF-alpha antibody light chain CDR3.
 PI Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 PI light chain; complementarity determining region 3; inhibition;
 PI treatment; sepsis; disease; autoimmune disease; infectious disease;
 PI malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 PI cardiac disorder; inflammatory bone disorder; reperfusion injury;
 PI bone resorption disease; coagulation disturbance; burn; ELAM-1;
 PI keloid formation; scar tissue formation; pyrexia; HIVEC;
 PI periodontal disease; obesity; radiation toxicity;
 PI endothelial cell leukocyte adhesion molecule-1;
 PI human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.

25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
 Mankovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 68; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 Sequence 9 AA;

Query Match 83.6% Score 61; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 6,06e+00;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkynarypt 9
 1:111:111
 1 OKNRPPT 9

RESULT 6
 ID W2579 standard; peptide: 9 AA.
 AC W2579:
 DE 19-WAR-1998 (first entry)
 PI Anti-TNF-alpha antibody light chain CDR3.
 PI Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 PI light chain; complementarity determining region 3; inhibition;
 PI treatment; sepsis; disease; autoimmune disease; infectious disease;
 PI malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 PI cardiac disorder; inflammatory bone disorder; reperfusion injury;
 PI bone resorption disease; coagulation disturbance; burn; ELAM-1;
 PI keloid formation; scar tissue formation; pyrexia; HIVEC;
 PI periodontal disease; obesity; radiation toxicity;
 PI endothelial cell leukocyte adhesion molecule-1;
 PI human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
 Mankovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 70; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g., rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 83.6%; Score 61; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 6.06e+00;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpy 8
 |||||:
 QY 1 QKYNRPY 8

RESULT 7
 ID W27585 standard; peptide: 9 AA.
 AC W27585;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 72; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g., rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 82.2%; Score 60; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.84e+00;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpy 9
 |||||:
 QY 1 QKYNRPY 9

RESULT 8
 ID W27562 standard; peptide: 9 AA.
 AC W27562;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9; Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g., rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 79.5%; Score 58; DB 27; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.31e+01;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpy 9
 |||||:
 QY 1 QKYNRPY 9

RESULT 9
 ID W27562 standard; peptide: 9 AA.
 AC W27562;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9; Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g., rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Db 1 qkynaspy 8
1:111:11
QY 1 OKYNRPPT 8

RESULT 9
ID W27574 standard; peptide: 9 AA.
AC W27574;

DE 19-MAR-1998 (first entry)
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PW 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PW: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; page 67; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).

SO Sequence 9 AA;
Query Match 76.7%; Score 56; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 2.18e+01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynaspy 9
1111:111
QY 1 OKYNRPPT 9

RESULT 10
ID W27570 standard; peptide: 9 AA.
AC W27570;

DE 19-MAR-1998 (first entry)
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

OS Homo sapiens.
PW 097229131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PW 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PW: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; page 67; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).

SO Sequence 9 AA;
Query Match 72.6%; Score 53; DB 27; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.63e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynaspy 9
1111:111
QY 1 OKYNRPPT 9

RESULT 11
ID W27582 standard; peptide: 9 AA.
AC W27582;

DE 19-MAR-1998 (first entry)
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

OS Homo sapiens.
PW 097229131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PW 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 72.6%; Score 53; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 4.63e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 qkysdpyt 9
 ||| |||
 QY 1 QKRNRPYT 9

RESULT 12
 ID W27573 standard; peptide: 9 AA.
 AC W27573;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 71.2%; Score 52; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 5.94e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkysdpyt 9
 ||| |||
 QY 1 QKRNRPYT 9

RESULT 13
 ID W27576 standard; peptide: 9 AA.
 AC W27576; (first entry)
 DT 19-MAR-1998
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 69.98; Score 51; DB 27; Length 9;
 Best Local Similarity 75.08; Pred. No. 7.60e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 gkyasapy 8
 |||| :||
 OY 1 OKYNRPY 8

RESULT 14
 ID W27577 standard; peptide: 9 AA.
 AC W27577:

DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 69.98; Score 51; DB 27; Length 9;
 Best Local Similarity 75.08; Pred. No. 7.60e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 gkyasapy 8
 |||| :||
 OY 1 OKYNRPY 8

RESULT 15
 ID W27578 standard; peptide: 9 AA.
 AC W27578:

DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 69.98; Score 51; DB 27; Length 9;
 Best Local Similarity 66.78; Pred. No. 7.60e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 1 gkyasapy 9
 |||| :||
 OY 1 OKYNRPY 9

Search completed: Thu Sep 2 12:15:39 1999
 Job time : 19 secs.

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WORLDWIDE
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Msrch:pp protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 12:21:34 1999; MasPar time 1.35 Seconds
Abular output not generated. 67.724 Million cell updates/sec

Title: >US-08-599-226-26
Description: (1-9) from US08599226.pep
Perfect Score: 70
Sequence: 1 QRYNRAPYA 9

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A.COMB 2:5B.COMB 3:PC79.COMB 4:backfile1

Statistics: Mean 15.796; Variance 50.501; scale 0.313

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	55	78.6	269	1	US-08-202-2	Sequence 4, Applicatio
2	50	71.4	287	4	5198342-2	Patent No. 5198342.
3	50	71.4	287	1	US-07-971-	Sequence 2, Applicatio
4	46	65.7	150	2	US-08-592-	Sequence 14, Applicati
5	46	65.7	218	2	US-08-343-	Sequence 20, Applicati
6	46	65.7	246	2	US-08-604-	Sequence 3, Applicatio
7	46	65.7	255	2	US-08-592-	Sequence 4, Applicatio
8	46	65.7	255	2	US-08-576-	Sequence 2, Applicatio
9	46	65.7	255	2	US-08-592-	Sequence 10, Applicati
10	46	65.7	255	2	US-08-592-	Sequence 8, Applicatio
11	46	65.7	273	2	US-08-592-	Sequence 8, Applicatio
12	46	65.7	300	2	US-08-592-	Sequence 2, Applicatio
13	46	65.7	466	2	US-08-604-	Sequence 4, Applicatio
14	46	65.7	507	3	PCT-US95-0	Sequence 4, Applicatio
15	46	65.7	507	3	US-08-604-	Sequence 5, Applicatio
16	46	65.7	1376	3	PCT-US95-1	Sequence 3, Applicatio
17	46	65.7	1376	2	US-08-420-	Sequence 87, Applicati
18	45	64.3	107	1	US-08-276-	Sequence 87, Applicati
19	45	64.3	107	3	PCT-US95-0	Sequence 87, Applicati
20	45	64.3	107	2	US-08-899-	Sequence 87, Applicati
21	45	64.3	107	2	US-08-899-	Sequence 87, Applicati
22	45	64.3	400	1	US-07-989-	Sequence 2, Applicatio
23	44	62.9	33	2	US-08-724-	Sequence 12, Applicati

RESULT	1	STANDARD	PRT	269	AA.
ID	US-08-202-857-4				
XX	xxxxxx				
AC					
XX					
DT					
XX					
DE	Sequence 4, Application US/08202857				
XX					
CC	Sequence 4, Application US/08202857				
CC	Patent No. 5635345				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Scherrier, Klaus				
CC	APPLICANT: Bureau, Jean-Paul				
CC	APPLICANT: Bey, Fay al				
CC	TITLE OF INVENTION: Diagnostic Method				
CC	NUMBER OF SEQUENCES: 4				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: PRO-SOMA, SARL C/O AKZO PHARMA				
CC	STREET: 1330-A PICCARD DRIVE				
CC	CITY: ROCKVILLE				
CC	STATE: MARYLAND				
CC	COUNTRY: USA				
CC	ZIP: 20850-4377				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PS/2				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: Microsoft word				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/202,857				
CC	FILING DATE:				
CC	CLASSIFICATION: 435				
CC	PRIOR APPLICATION DATA:				
CC	APPLICATION NUMBER: US/07/860,492				
CC	FILING DATE: 11-JUNE-1992				
CC	APPLICATION NUMBER: PCT/EP91/01945				
CC	FILING DATE: 10-OCT-1991				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: BOBROWICZ, DONNA				
CC	REGISTRATION NUMBER: 32,196				
CC	TELEPHONE: 301-258-5200				
CC	TELEFAX: 301-977-1403				
CC	INFORMATION FOR SEO ID NO: 4:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 269 amino acids				

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: human
SQ SEQUENCE 269 AA; 30227 MW; 341084 CN;
Query Match 78.6%; Score 55; DB 1; Length 269;
Best Local Similarity 66.7%; Pred. No. 1.52e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 127 QXGRPPY 135
111111
QY 1 QXNRAPYA 9
RESULT 2
ID 5198342-2 STANDARD; PRT; 311 AA.
XX xxxxxx
DT 01-JAN-1900
XX Patent No. 5198342.
DE
XX
CC Patent No. 5198342
CC APPLICANT: MALISZEWSKI, CHARLES R.
CC TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/548,059
CC FILING DATE: 05-JUL-1990
CC SEQ ID NO: 2;
CC LENGTH: 287
CC SEQUENCE 311 AA; 34908 MW; 558002 CN;
SQ
Query Match 71.4%; Score 50; DB 4; Length 287;
Best Local Similarity 71.4%; Pred. No. 5.11e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 196 WYNRSY 202
:111111
QY 2 RYNRAPY 8
RESULT 3
ID US-07-971-092-2 STANDARD; PRT; 287 AA.
XX xxxxxx
DT
XX
DE
XX
CC Sequence 2, Application US/07971092
CC Patent No. 5328987
CC GENERAL INFORMATION:
CC APPLICANT: Maliszewski, Charles R.
CC TITLE OF INVENTION: Huiga Fc Receptor
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex
CC STREET: 51 University
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/971,092
CC FILING DATE: 19921104
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Perkins, Patricia A.
CC REGISTRATION NUMBER: 34693
CC REFERENCE/DOCKET NUMBER: 2603
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 287 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 287 AA; 32265 MW; 435416 CN;
Query Match 71.4%; Score 50; DB 1; Length 287;
Best Local Similarity 71.4%; Pred. No. 5.11e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 196 WYNRSY 202
:111111
QY 2 RYNRAPY 8
RESULT 4
ID US-08-592-214A-14 STANDARD; PRT; 150 AA.
XX xxxxxx
DT
XX
DE
XX
CC Sequence 14, Application US/08592214A
CC Patent No. 581536
CC GENERAL INFORMATION:
CC APPLICANT: Yanofsky, Martin F.
CC TITLE OF INVENTION: Cauliflower Floral Meristem Identify
CC NUMBER OF SEQUENCES: 33
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Campbell and Flores
CC STREET: 4370 La Jolla Village Drive, Suite 700
CC CITY: San Diego
CC STATE: California
CC COUNTRY: United States
CC ZIP: 92122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/592,214A
CC FILING DATE: 26-JAN-1996
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Campbell, Cathryn A.
CC REGISTRATION NUMBER: 31,815
CC REFERENCE/DOCKET NUMBER: P-UD 1927
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 535-9001
CC TELEFAX: (619) 535-8949
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 150 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 150 AA; 17841 MW; 110457 CN;
Query Match 65.7%; Score 46; DB 2; Length 150;
Best Local Similarity 55.6%; Pred. No. 1.32e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 68 EYERYSYA 76
:11:11
OY 1 OYNRAPYA 9

RESULT 5
ID US-08-343-101A-20 STANDARD: PRT; 218 AA.

AC xxxxxx

DE Sequence 20, Application US/08343101A

CC Sequence 20, Application US/08343101A

CC Patent No. 5830759

CC GENERAL INFORMATION:

CC APPLICANT: Chang, Yuan

CC APPLICANT: Moore, Patrick S.

CC TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma

CC NUMBER OF SEQUENCES: 22

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Cooper & Dunham

CC STREET: 1185 Avenue of the Americas

CC CITY: New York

CC STATE: New York

CC COUNTRY: U.S.A.

CC ZIP: 10036

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.24

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/343,101A

CC FILING DATE:

CC CLASSIFICATION: 514

CC ATTORNEY/AGENT INFORMATION:

CC NAME: White Esq., John P.

CC REGISTRATION NUMBER: 28,678

CC REFERENCE/DOCKET NUMBER: 45185-A

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 212-278-0400

CC TELEFAX: 212-391-0526

CC INFORMATION FOR SEQ ID NO: 20:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 218 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC HYPOTHETICAL: N

CC ANTI-SENSE: N

CC FEATURE:

CC NAME/KEY: Peptide

CC LOCATION: 1..218

CC OTHER INFORMATION:

CC SEQUENCE 218 AA; 24345 MW; 253377 CN;

CC Query Match

CC Best Local Similarity 65.7%; Score 46; DB 2; Length 218;

CC Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 119 RYNRGLYT 126

OY 2 RYNRAPYA 9

RESULT 6
ID US-08-604-989A-3 STANDARD: PRT; 246 AA.

XX xxxxxx

DE Sequence 3, Application US/08604989A

CC Sequence 3, Application US/08604989A

CC Patent No. 5834208

CC GENERAL INFORMATION:

CC APPLICANT: Sakano, S.

CC TITLE OF INVENTION: No. 5834208el Tyrosine Kinase

CC NUMBER OF SEQUENCES: 11

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Pennie & Edmonds LLP

CC STREET: 1155 Avenue of the Americas

CC CITY: New York

CC STATE: New York

CC COUNTRY: USA

CC ZIP: 10036-2711

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC OPERATING SYSTEM: DOS

CC SOFTWARE: FastSeq Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/604,989A

CC FILING DATE: February 23, 1996

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Charles E. Miller

CC REGISTRATION NUMBER: 24,576

CC REFERENCE/DOCKET NUMBER: 1920-026

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (212) 790-9090

CC TELEX: 66141 PENNIE

CC INFORMATION FOR SEQ ID NO: 3:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 246 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC ORIGINAL SOURCE:

CC ORGANISM: human

CC STRAIN: UT-7

CC SEQUENCE 246 AA; 27425 MW; 326654 CN;

Query Match 65.7%; Score 46; DB 2; Length 246;
Best Local Similarity 71.4%; Pred. No. 1.32e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 188 YGRAPYP 194

OY 3 YNRAPYA 9

RESULT 7
ID US-08-592-214A-4 STANDARD: PRT; 253 AA.

AC xxxxxx

DE Sequence 4, Application US/08592214A

CC Sequence 4, Application US/08592214A

CC Patent No. 5811536

CC GENERAL INFORMATION:

CC APPLICANT: Yanofsky, Martin F.

CC TITLE OF INVENTION: Cauliflower Floral Meristem Identify

CC NUMBER OF SEQUENCES: 33

CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Campbell and Flores
CC STREET: 4370 La Jolla Village Drive, Suite 700
CC CITY: San Diego
CC STATE: California
CC COUNTRY: United States
CC ZIP: 92122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentln Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/592,214A
CC FILING DATE: 26-JAN-1996
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Campbell, Cathryn A.
CC REGISTRATION NUMBER: 31,815
CC REFERENCE/DOCKET NUMBER: P-UD 1927
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 535-9001
CC TELEFAX: (619) 535-8949
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 253 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 253 AA; 29840 MW; 293953 CN;

Query Match 65.7%; Score 46; DB 2; Length 253;
Best Local Similarity 55.6%; Pred. No. 1.32e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 68 ERYERSYA 76
:|||:|
QY 1 QRYNRAPYA 9

RESULT 8
ID US-08-576-156-2 STANDARD; PRT: 255 AA.
XX xxxxxx
AC
XX
DT
XX
CC Sequence 2, Application US/08576156
CC Patent No. 5844119
CC GENERAL INFORMATION:
CC APPLICANT: Weigel, Detlef
CC TITLE OF INVENTION: Genetically Modified Plants Having Modulated
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: US
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: Windows95
CC SOFTWARE: FastSeq for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/576,156
CC FILING DATE: 12-21-95
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/360,336
CC FILING DATE: 12-21-94
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Haile, Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07251/013001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-678-5070
CC TELEFAX: 619-678-5099
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 255 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 255 AA; 30026 MW; 303372 CN;

Query Match 65.7%; Score 46; DB 2; Length 255;
Best Local Similarity 55.6%; Pred. No. 1.32e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 68 ERYERSYA 76
:|||:|
QY 1 QRYNRAPYA 9

RESULT 9
ID US-08-592-214A-10 STANDARD; PRT: 255 AA.
XX xxxxxx
AC
XX
DT
XX
CC Sequence 10, Application US/08592214A
CC Patent No. 5811536
CC GENERAL INFORMATION:
CC APPLICANT: Yanofsky, Martin F.
CC TITLE OF INVENTION: Cauliflower Floral Meristem Identify
CC NUMBER OF SEQUENCES: 33
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Campbell and Flores
CC STREET: 4370 La Jolla Village Drive, Suite 700
CC CITY: San Diego
CC STATE: California
CC COUNTRY: United States
CC ZIP: 92122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentln Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/592,214A
CC FILING DATE: 26-JAN-1996
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Campbell, Cathryn A.
CC REGISTRATION NUMBER: 31,815
CC REFERENCE/DOCKET NUMBER: P-UD 1927
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 535-9001
CC TELEFAX: (619) 535-8949
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 255 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 255 AA; 30087 MW; 310226 CN;

Query Match 65.7%; Score 46; DB 2; Length 255;
Best Local Similarity 55.6%; Pred. No. 1.32e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 68 ERYERSYA 76
:||:|:|
QY 1 QRYNRPAY 9

RESULT 10
ID US-08-592-214A-6 STANDARD; PRT: 255 AA.

AC xxxxxx

DE Sequence 6, Application US/08592214A

CC Sequence 6, Application US/08592214A
CC Patent No. 5811536

CC GENERAL INFORMATION:

CC APPLICANT: Yanofsky, Martin F.

CC TITLE OF INVENTION: Cauliflower Floral Meristem Identify

CC NUMBER OF SEQUENCES: 33

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Campbell and Flores

CC STREET: 4370 La Jolla Village Drive, Suite 700

CC CITY: San Diego

CC STATE: California

CC COUNTRY: United States

CC ZIP: 92122

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/592,214A

CC FILING DATE: 26-JAN-1996

CC CLASSIFICATION: 536

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Campbell, Cathryn A.

CC REGISTRATION NUMBER: 31,815

CC REFERENCE/DOCKET NUMBER: P-UD 1927

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 535-9001

CC TELEFAX: (619) 535-8949

CC INFORMATION FOR SEQ ID NO: 6:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 255 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: Protein

CC SEQUENCE 255 AA; 30205 MW; 297546 CN;

CC Query Match 65.7%; Score 46; DB 2; Length 255;

CC Best Local Similarity 55.6%; Pred. No. 1.32e+02;

CC Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CC Db 68 ERYERSYA 76

CC :||:|:|

CC QY 1 QRYNRPAY 9

RESULT 11
ID US-08-592-214A-8 STANDARD; PRT: 273 AA.

AC xxxxxx

DE Sequence 8, Application US/08592214A

XX Sequence 8, Application US/08592214A
CC Patent No. 5811536

CC GENERAL INFORMATION:

CC APPLICANT: Yanofsky, Martin F.

CC TITLE OF INVENTION: Cauliflower Floral Meristem Identify

CC NUMBER OF SEQUENCES: 33

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Campbell and Flores

CC STREET: 4370 La Jolla Village Drive, Suite 700

CC CITY: San Diego

CC STATE: California

CC COUNTRY: United States

CC ZIP: 92122

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/592,214A

CC FILING DATE: 26-JAN-1996

CC CLASSIFICATION: 536

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Campbell, Cathryn A.

CC REGISTRATION NUMBER: 31,815

CC REFERENCE/DOCKET NUMBER: P-UD 1927

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 535-9001

CC TELEFAX: (619) 535-8949

CC INFORMATION FOR SEQ ID NO: 8:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 273 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: Protein

CC SEQUENCE 273 AA; 31248 MW; 337267 CN;

CC Query Match 65.7%; Score 46; DB 2; Length 273;

CC Best Local Similarity 55.6%; Pred. No. 1.32e+02;

CC Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CC Db 68 ERYERSYA 76

CC :||:|:|

CC QY 1 QRYNRPAY 9

RESULT 12
ID US-08-592-214A-2 STANDARD; PRT: 300 AA.

AC xxxxxx

DE Sequence 2, Application US/08592214A

CC Sequence 2, Application US/08592214A
CC Patent No. 5811536

CC GENERAL INFORMATION:

CC APPLICANT: Yanofsky, Martin F.

CC TITLE OF INVENTION: Cauliflower Floral Meristem Identify

CC NUMBER OF SEQUENCES: 33

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Campbell and Flores

CC STREET: 4370 La Jolla Village Drive, Suite 700

CC CITY: San Diego

CC STATE: California

CC COUNTRY: United States

CC ZIP: 92122

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/592,214A
CC FILING DATE: 26-JAN-1996
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Campbell, Cathryn A.
CC REGISTRATION NUMBER: 31,815
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 535-9001
CC TELEFAX: (619) 535-8949
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 300 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 300 AA; 35369 MW; 456889 CN;

Query Match 65.7%; Score 46; DB 2; Length 300;
Best Local Similarity 55.6%; Pred. No. 1.32e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 68 ERYERSYA 76
:|:|:|:|
QY 1 QRYNRAPYA 9

RESULT 13
ID US-08-604-989A-4 STANDARD; PRT; 466 AA.
XX xxxxxx

Sequence 4, Application US/08604989A
Patent No. 5834208
GENERAL INFORMATION:
CC APPLICANT: Sakano, S.
CC TITLE OF INVENTION: No. 5834208e1 Tyrosine Kinase
CC NUMBER OF SEQUENCES: 11
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds LLP
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036-2711
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/604,989A
CC FILING DATE: February 23, 1996
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Charles E. Miller
CC REGISTRATION NUMBER: 24,576
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-8864/9741
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 466 amino acids

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: human
CC STRAIN: vt-7
CC SEQUENCE 466 AA; 51898 MW; 1114727 CN;

Query Match 65.7%; Score 46; DB 2; Length 466;
Best Local Similarity 71.4%; Pred. No. 1.32e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 379 YGRAPYP 385
1|1|1|:
QY 3 YNRAPYA 9

RESULT 14
ID PCT-US95-05008-2 STANDARD; PRT; 507 AA.
XX xxxxxx

Sequence 2, Application PC/TUS9505008
GENERAL INFORMATION:
CC APPLICANT: Sugen, Inc.
CC APPLICANT: 515 Galveston Drive
CC APPLICANT: Redwood City, California 94063-4720
CC APPLICANT: United States of America
CC APPLICANT: Wissenschaften E.V.
CC APPLICANT: Hofgarten Str. 2
CC APPLICANT: Munchen 80359
CC APPLICANT: Germany
CC TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
CC TITLE OF INVENTION: Kinases
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/05008
CC FILING DATE: 24-APR-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/232,545
CC FILING DATE: 22-APR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Coruzzi, Laura A.
CC REGISTRATION NUMBER: 30,742
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212)790-9090
CC TELEFAX: (212)869-9741
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 507 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown

CC MOLECULE TYPE: Protein
SQ SEQUENCE 507 AA; 56469 MW; 1316735 CN;

Query Match 65.7%; Score 46; DB 3; Length 507;
Best Local Similarity 71.4%; Pred. No. 1.32e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 420 YGRAPYP 426
| | | | |
QY 3 YNRAPYA 9

RESULT 15
ID US-08-604-989A-5 STANDARD; PRT; 507 AA.
XX
AC xxxxxx
XX
DT
XX

Sequence 5, Application US/08604989A

CC Sequence 5, Application US/08604989A
CC Patent No. 5834208

CC GENERAL INFORMATION:

CC APPLICANT: Sakano, S.

CC TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
CC NUMBER OF SEQUENCES: 11

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Pennile & Edmonds LLP

CC STREET: 1155 Avenue of the Americas

CC CITY: New York

CC STATE: New York

CC COUNTRY: USA

CC ZIP: 10036-2711

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC COMPUTER: IBM Compatible

CC OPERATING SYSTEM: DOS

CC SOFTWARE: FASTSEQ Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/604,989A

CC FILING DATE: February 23, 1996

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Charles E. Miller

CC REGISTRATION NUMBER: 24,576

CC REFERENCE/DOCKET NUMBER: 1920-026

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (212) 790-9090

CC TELEFAX: (212) 869-8864/9741

CC TELEX: 66141 PENNIE

CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 507 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC ORIGINAL SOURCE:

CC ORGANISM: human

CC STRAIN: UT-7

CC SEQUENCE 507 AA; 56491 MW; 1317560 CN;

Query Match 65.7%; Score 46; DB 2; Length 507;
Best Local Similarity 71.4%; Pred. No. 1.32e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 420 YGRAPYP 426
| | | | |
QY 3 YNRAPYA 9

Search completed: Thu Sep 2 12:21:41 1999
Job time : 7 secs.

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Best Local Similarity 75.0%; Pred. No. 3.72e-01;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 81 ORYXRAY 88
1:1:1111

OY 1 ORYNRAPYA 8

RESULT 2
ID 027562; PRELIMINARY; PRT: 248 AA.

AC 027562; 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DE 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

GN DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

OC EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.

RL [1] SHAVITSKY G., ESCALANTE R., LOOMIS W.F.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S23A; ALSO KNOWN AS THE
PROTEASOME A-TYPE FAMILY.

CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
NEUTRAL OR SLIGHTLY BASIC PH.

CC THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY.

CC THE COMPONENT C3 MAY HAVE A POTENTIAL REGULATORY EFFECT ON
ANOTHER COMPONENT(S) OF THE PROTEASOME COMPLEX THROUGH TYROSINE
PHOSPHORYLATION.

CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
PROTEOLYTIC PATHWAY.

CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.

CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
ALSO IN THE NUCLEUS.

DR EMBL: U60168; G1405364; -

DR PROSITE: P500388; PROTEASOME_A; 1.

DR PFAM: PF00227; proteasome; 1.

KM PROTEASOME; HYDROLASE; PROTEASE.

SQ SEQUENCE 248 AA; 27968 MW; BEE84ACC CRC32;

Query Match
Best Local Similarity 76.6%; Score 55; DB 5; Length 248;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

121 ORYXRAY 129
1:1:1111

OY 1 ORYNRAPYA 9

RESULT 3
ID 042265; PRELIMINARY; PRT: 260 AA.

AC 042265; 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JUN-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

GN 20S PROTEASOME SUBUNIT C2.

OC GALLUS GALLUS (CHICKEN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASINIDAE; PHASININAE; GALLUS.

RL [1] SEQUENCE FROM N.A.
SINGH I., WAGNER B.J.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF027978; G3136063; -
DR PFAM: PF00227; proteasome; 1.

KM PROTEASOME; 260 AA; 28925 MW; EF38499F CRC32;

Query Match
Best Local Similarity 78.6%; Score 55; DB 13; Length 260;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 120 ORYXRAY 128
1:1:1111

OY 1 ORYNRAPYA 9

RESULT 4
ID 002441; PRELIMINARY; PRT: 448 AA.

AC 002441; 01-JUL-1997 (TREMBLREL. 04, CREATED)

DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

GN GDP-DISSOCIATION INHIBITOR.

OC GEODIA CYDONIUM (SPONGE).

OC EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; TETRACINOMORPHA;

OC ASTROPHORIDA; GEODIIDAE; GEODIA.

RL [1] SEQUENCE FROM N.A.

RA KRASKO A., SCHEFFER U., KOZLOV C., PANCER Z., BATEL R., BADRIA F.A.,
MUELLER W.E.G.;
AQUATIC TOXICOL. 37:157-168(1997).

DR EMBL: X94983; E218570; -

DR PFAM: PF00996; GDI; 1.

SQ SEQUENCE 448 AA; 50215 MW; 848511EC CRC32;

Query Match
Best Local Similarity 77.1%; Score 54; DB 5; Length 448;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

217 ORYXRAY 224
1:1:1111

OY 1 ORYNRAPYA 8

RESULT 5
ID 021017; PRELIMINARY; PRT: 509 AA.

AC 021017; 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

GN F58H12.1

OC CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;

OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RL [1] SEQUENCE FROM N.A.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKS M.,
BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RITKEN L., ROOPRA A., SANDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THERRIER-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROUT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
NATURE 368:32-38(1994).

RL [2] SEQUENCE FROM N.A.

RA MILLER N.;

RL [3] SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

RP SEQUENCE FROM N.A.

RA WATERSTON R.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U40416; G1065490; -
SQ SEQUENCE 509 AA; 55953 MW; D0EC1387 CRC32;

Query Match 77.1%; Score 54; DB 5; Length 509;
Best Local Similarity 62.5%; Pred. No. 1.63e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 268 RYORPTPYT 275
| | | | |
OY 2 RYNRAPYA 9

RESULT 6
ID 017517 PRELIMINARY; PRT: 1277 AA.

AC 017517;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE ZC132.5 PROTEIN.

CAENORHABDITIS ELEGANS.

EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

[1]
SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
MEDLINE: 94150718.

RA WILSON R., AINSKCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONTFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).

[2]
SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA BRADSHAW H., DEVLIN K.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

[3]
SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;

SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF014939; G2275629; -

SQ SEQUENCE 1277 AA; 146496 MW; 8A6DB899 CRC32;

Query Match 77.1%; Score 54; DB 5; Length 1277;
Best Local Similarity 100.0%; Pred. No. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 877 OYNRAP 883
| | | | |
OY 1 OYNRAP 7

RESULT 7
ID 055956 PRELIMINARY; PRT: 790 AA.

AC 055956;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE ABC TRANSPORTER.

SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.

[1]
SEQUENCE FROM N.A.

RC STRAIN-PCC6803;
RX MEDLINE: 96127529.

RA KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
RA SUGIURA M., TABATA S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. sequence features in the 1Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA RES. 2:153-166(1995).

[2]
SEQUENCE FROM N.A.

RC STRAIN-PCC6803;
RX MEDLINE: 97061201.

RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAKOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUO A., MURAKI A., NAKAZAKI N., NARO K., OKUMURA S.,
RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. PCC6803. II. Sequence determination of the entire
RT genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-136(1996).

DR EMBL: D64005; D1011375; -
DR PFAM: PF00005; ABC_tran; 1.
DR PFAM: PF00498; FHA; 2.

SQ SEQUENCE 790 AA; 87656 MW; 436DBE61 CRC32;

Query Match 75.7%; Score 53; DB 2; Length 790;
Best Local Similarity 62.5%; Pred. No. 2.64e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 475 OYRSRSY 482
| | | | |
OY 1 OYNRAPY 8

RESULT 8
ID 062346 PRELIMINARY; PRT: 90 AA.

AC 062346;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE R11.2 PROTEIN.

GN R11.2.
OS CAENORHABDITIS ELEGANS.

EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

[1]
SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;
RA MCMURRAY A.;
RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

[2]
SEQUENCE FROM N.A.

RC MEDLINE: 94150718.
RA WILSON R., AINSKCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONTFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).

DR EMBL: Z81577; E1348694; -
SQ SEQUENCE 90 AA; 10937 MW; 80B83F8F CRC32;

Query Match 74.3%; Score 52; DB 5; Length 90;
Best Local Similarity 75.0%; Pred. No. 4.24e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 21 QRYRAIY 28
 |||:|:|
 QY 1 QRYNRAIY 8

RESULT 9
 ID P92024 PRELIMINARY; PRT; 494 AA.

AC P92024;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE MEX-1.
 GN MEX-1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-N2;
 MEDLINE; 97195715.

RT "The C. elegans MEX-1 protein is present in germline blastomeres and
 is a P granule component."
 RL DEVELOPMENT 124:731-739(1997).

DR EMBL; U81043; G1899062; -
 DR PFIAM; PF00642; zif-CCCH; 2.

SQ SEQUENCE 494 AA; 56608 MW; 716506D2 CRC32;

Query Match 74.3%; Score 52; DB 5; Length 494;
 Best Local Similarity 62.5%; Pred. No. 4.24e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 263 QRYRPE 270
 |||:|:|
 QY 1 QRYNRAIY 8

RESULT 10
 ID Q48279 PRELIMINARY; PRT; 170 AA.

AC Q48279;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE SIMILARITY WITH HEAD COMPLETION/STABILIZATION PROTEIN.
 OS HAEMOPHILUS SOMNUS.

OC BACTERIA; PROTOBACTERIA; GAMMA SUBDIVISION; PASTREURELLACEAE;
 OC HAEMOPHILUS.

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-HS25;
 PONTAROLO R.A.;

RL THESES (1995); V. I. D. O., UNIVERSITY OF SASKATCHEWAN.
 DR EMBL; U8154; G915368; -

SQ SEQUENCE 170 AA; 19923 MW; 91428D5E CRC32;

Query Match 72.9%; Score 51; DB 2; Length 170;
 Best Local Similarity 75.0%; Pred. No. 6.79e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 107 QRYKRAIY 114
 |||:|:|
 QY 1 QRYNRAIY 8

RESULT 11
 ID O50511 PRELIMINARY; PRT; 450 AA.

AC O50511;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE ZINC PROTEASE.
 GN SC9B10.04.

OS STREPTOMYCES COELICOLOR.

OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);
 OLIVER K., HARRIS D.;

RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);
 PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;

RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);
 MEDLINE; 97000351.

RT KEDENBACH M., KIESER H.M., DENAPPAITE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL MOL. MICROBIOL. 21:77-96(1996).

DR EMBL; AL009204; E1202335; -
 KW PROTEASE.

SQ SEQUENCE 450 AA; 49045 MW; 3E30B71A CRC32;

Query Match 72.9%; Score 51; DB 2; Length 450;
 Best Local Similarity 55.6%; Pred. No. 6.79e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 147 QRYDNVPG 155
 |||:|:|
 QY 1 QRYNRAIY 9

RESULT 12
 ID Q92592 PRELIMINARY; PRT; 178 AA.

AC Q92592;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)

DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)

DE CD89.L10.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.

RN [1]
 RP SEQUENCE FROM N.A.

RA TOYABE S., KIWANO Y., TAKEDA K., UCHIYAMA M., ABO T.;

RT "Alternatively spliced forms of monocyte IgA Fc receptors in patients
 with IgA nephropathy."
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; D87861; D1014171; -
 SQ SEQUENCE 178 AA; 19593 MW; EC5B1F1C CRC32;

Query Match 71.4%; Score 50; DB 4; Length 178;
 Best Local Similarity 71.4%; Pred. No. 1.08e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 87 WYNSPY 93
 :|||:|:|
 QY 2 RYNNRAIY 8

RESULT 13
 ID Q99935 PRELIMINARY; PRT; 201 AA.

AC Q99935;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)

DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE BASIC PROLINE-RICH PROTEIN.
 GN BLP.

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96309097.
 RA DICKINSON D.P., THIESSE M.;
 RT "cDNA cloning of an abundant human lacrimal gland mRNA encoding a
 RT novel tear protein."
 RL CURR. EYE RES. 15:377-386(1996).
 DR EMBL: S83198; G1836022; -.
 SQ SEQUENCE 201 AA; 22870 MW; 650A8F70 CRC32;

Query Match 71.4%; Score 50; DB 4; Length 201;
 Best Local Similarity 62.5%; Pred. No. 1.08e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 22 ORFSRPY 29
 ||:| |
 QY 1 ORYNRAPY 8

RESULT 14
 082438 PRELIMINARY; PRT; 332 AA.
 082438.
 DT 01-NOV-1998 (TREMREL. 08, CREATED)
 DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
 DE ANTIFREEZE PROTEIN.
 GN AFP.
 OS DAUCUS CAROTA (CARROT).
 CC EUCAROTIA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 CC ASTERIDAE; ARALIALES; APIACEAE; DAUCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, AUTUMN KING; TISSUE-TAP ROOT;
 RX MEDLINE: 98429644.
 RA MORRALL D., ELIAS L., ASHFORD D., SMALLWOOD M., SIDEBOTTOM C.,
 RA LILLFORD P., TELFORD J., HOLT C., BOWLES D.;
 RT "A carrot leucine-rich-repeat protein that inhibits ice
 RT recrystallization."
 RL SCIENCE 282:115-117(1998).
 DR EMBL: AF053480; G3702803; -.
 SQ SEQUENCE 332 AA; 36845 MW; 67194791 CRC32;

Query Match 71.4%; Score 50; DB 10; Length 332;
 Best Local Similarity 50.0%; Pred. No. 1.08e+01;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 311 ORFDRYAY 318
 ||:| | | |
 QY 1 ORYNRAPY 8

RESULT 15
 ID 044677 PRELIMINARY; PRT; 521 AA.
 AC 044677;
 DT 01-NOV-1996 (TREMREL. 01, CREATED)
 DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
 DE NEUTRAL PROTEASE.
 OS BACILLUS AMYLOLIQUEFACIENS.
 CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SHIMADA H., HONDO M., MITA I., NAKAYAMA A., AKAOKA A., MANABE K.,
 RA FURUTANI Y.;
 RL J. BIOTECHNOL. 2:75-85(1985).
 DR EMBL: M36723; G143353; -.
 DR PFAM: PF00099; zn-protease; 1.
 KW PROTEASE.
 SQ SEQUENCE 521 AA; 56725 MW; 64AF9E5F CRC32;

Query Match 71.4%; Score 50; DB 2; Length 521;

Best Local Similarity 62.5%; Pred. No. 1.08e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 308 ORYNRSY 315
 ||:| | | |
 QY 1 ORYNRAPY 8

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 Job time : 27 secs.

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DR EMBL: X15497; G8382; -.
DR EMBL: X62285; G8388; -.
DR PIR: S05507; SNF5K.
DR PIR: S23450; S23450.
DR FLYBASE: FBgn0003151; Pros35.
DR PROSITE: PS00388; PROTEASOME_A.1.
DR HSSP: P25156; 1PMA.
KW PROTEASOME; HYDROLASE; PROTEASE; PHOSPHORYLATION.
FT MOD.RES 103 103 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 279 AA; 31058 MW; AA18BBD F CRC32;

Query Match 82.9%; Score 58; DB 1; Length 279;
Best Local Similarity 66.7%; Pred. No. 7.94e-02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 121 QRYRRPYG 129
||| | | |
QY 1 QRYNRPYA 9

RESULT 2
ID PRG2_RAT STANDARD; PRT; 263 AA.
AC P18420.
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
DE (PROTEASOME NU CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2)
GN PSMAL.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=LIVER;
RX MEDLINE: 90057428.
RA FUJIMURA T., TANAKA K., KUMATORI A., SHIN S., YOSHIMURA T.,
RA ICHIHARA A., TOKUNAGA F., ARUGA R., IWANAGA S., KAKIZUKA A.,
RA NAKANISHI S.;
AB "Molecular cloning of cDNA for proteasomes (multicatalytic proteinase complexes) from rat liver: primary structure of the largest component (C2)."
RT BIOCHEMISTRY 28:7332-7340(1989).
RN [2]
RP SEQUENCE OF 1-30.
RC TISSUE=LIVER;
RX MEDLINE: 90243011.
RA TOKUNAGA F., ARUGA R., IWANAGA S., TANAKA K., ICHIHARA A., TAKAO T.,
RA SHIMONISHI Y.;
AB "The NH2-terminal residues of rat liver proteasome (multicatalytic proteinase complex) subunits, C2, C3 and C8, are N
RT alpha-acetylated."
RL FEBS LETT. 263:373-375(1990).
RN [3]
RP FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY.
CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL PROTEOLYTIC PATHWAY.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND ALSO IN THE NUCLEUS.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL RAT TISSUES.
CC -1- PTH: ITS C-TERMINAL EXTENSION IS PARTIALLY CLEAVED OFF BY LIMITED PROTEOLYSIS LEADING TO A CONVERSION OF THE PROTEASOME FROM ITS LATENT INTO ITS ACTIVE FORM.
CC -1- SIMILARITY: BELONGS TO PERTINASE FAMILY T1A; ALSO KNOWN AS THE PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.

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DR EMBL: M29859; G206382; -.
DR EMBL: D90265; G220877; -.
DR PIR: A32968; SNR32.
DR PROSITE: PS00388; PROTEASOME_A.1.
DR PFM: PF00227; Proteasome; 1.
DR HSSP: P25156; 1PMA.
KW PROTEASOME; HYDROLASE; PROTEASE; ACETYLATION.
FT MOD.RES 1 1 ACETYLATION.
SQ SEQUENCE 263 AA; 29517 MW; 01D55620 CRC32;

Query Match 78.6%; Score 55; DB 1; Length 263;
Best Local Similarity 66.7%; Pred. No. 3.77e-01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 121 QRYRRPYG 129
||| | | |
QY 1 QRYNRPYA 9

RESULT 3
ID PRG2_HUMAN STANDARD; PRT; 263 AA.
AC P25786.
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
DE (PROTEASOME NU CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2) (30 KD PROSOMAL PROTEIN) (PROS-30).
GN PSMAL OR PSC2 OR PROS30.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93013039.
RA SILVA-PEREIRA I., BEY F., COUX O., SCHERRER K.;
AB "Two mRNAs exist for the He PROS-30 gene encoding a component of human prosomes."
RT GENE 120:235-242(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91223105.
RA TAMURA T., LEE D.H., OSAKA F., FUJIMURA T., SHIN S., CHUNG C.H.,
RA TANAKA K., ICHIHARA A.;
AB "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multi-catalytic proteinase complexes)."
RT BIOCHIM. BIOPHYS. ACTA 1089:95-102(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91363412.
RA DEKARTINO G.N., ORTH K., MCCULLOUGH M.L., LEE L.W., MUNN T.Z.,
RA MOONAW C.R., DAWSON P.A., SLAUGHTER C.A.;
AB "The primary structures of four subunits of the human, high-molecular-weight proteinase, macropain (proteasome), are distinct but homologous."
RL BIOCHIM. BIOPHYS. ACTA 1079:29-38(1991).
RN [4]
RP FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX

WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY.

-1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL PROTEOLYTIC PATHWAY.

-1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.

-1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOSOL AND ALSO IN THE NUCLEUS.

-1- ALTERNATIVE PRODUCTS: TWO FORMS (SHORT AND LONG) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE FOR THIS PROTEIN.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.

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DR EMBL: M64992; G190447; ALT_SEQ.
 DR EMBL: D00759; G220022; -
 DR EMBL: X61969; G296738; -
 DR PIR: S15897; S15897.
 DR PIR: J01445; J01445.
 DR AARHUS/GENET-2DPAGE; 2223; IEF.
 DR MIM: 602854; -
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PFAM: PF00227; proteasome; 1.
 DR HSSP: P25156; 1PMA.
 DR PROTEASOME: HYDROLASE; PROTEASE; ACETYLATION; ALTERNATIVE SPLICING.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT VARSPIC 1 1 M->MOLSKYR (IN LONG FORM).
 SQ SEQUENCE 263 AA; 29555 MW; 6CD09A93 CRC32;

Query Match 78.6%; Score 55; DB 1; Length 263;
 Best Local Similarity 66.7%; Pred. No. 3,77e-01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 121 ORYGRPPY 129
 ||| | | | |
 QY 1 ORYNRAPYA 9

RESULT 4
 GNRP_MOUSE STANDARD; PRT: 1262 AA.
 P27671;

RT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).
 GN RASGRF1 OR CDC25MM OR GRF1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC RODENTIA: SCIROGNATHI: MURIDAE: MORINAE: MUS.
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE: 93010996.
 RA CEN H.; LOWY D.D.;
 RT "Isolation of multiple mouse cDNAs with coding homology to
 RT Saccharomyces cerevisiae CDC25: Identification of a region related to
 RT Bcr, Vav, Dbl and CDC24.";
 RL EMBL J. 11:4007-4015(1992).
 RN [2]
 RP SEQUENCE OF 791-1262 FROM N.A.
 RC STRAIN-SWISS; TISSUE-BRAIN;
 RX MEDLINE: 92289680.
 RA MARTEGANI E., VANONI M., ZIPPEL R., COCCETTI P., BRAMBILLA R.,
 RA FERRARI C., STURANI E.P., ALBERGHINA L.;

RT "Cloning by functional complementation of a mouse cDNA encoding a
 RT homologue of CDC25, a Saccharomyces cerevisiae Ras activator.";
 RL EMBL J. 11:2151-2157(1992).

RP SEQUENCE OF 1031-1226 FROM N.A.
 RX MEDLINE: 9235779.
 RA WEI W., MOSTELLER R.D., SANTAL P., GONZALES E., MCKINNEY D.,
 RA DASGUPTA C., LI P., LIU B.X., BROEK D.;
 RT "Identification of a mammalian gene structurally and functionally
 RT related to the CDC25 gene of Saccharomyces cerevisiae.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 89:7100-7104(1992).
 CC -1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: TO OTHER GUANINE-NUCLEOTIDE RELEASING FACTORS OF THE
 CC CDC25 FAMILY.

-1- SIMILARITY: CONTAINS 2 PH DOMAINS.

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DR EMBL: L20899; G388247; -
 DR EMBL: X59868; G50358; -
 DR PIR: S20730; S20730.
 DR PIR: S22693; S22693.
 DR MGD: MGI:99694; RASGRF1.
 DR PROSITE: PS00720; GDS.CDC25; 1.
 DR PROSITE: PS00741; GDS.CDC24; 1.
 DR PROSITE: PS50003; PH.DOMAIN; 2.
 DR PFAM: PF00169; PH; 2.
 DR PFAM: PF00612; IQ; 1.
 DR PFAM: PF00617; RASGEF; 1.
 DR PFAM: PF00618; RASGEF; 1.
 DR PFAM: PF00621; RHOGEP; 1.
 KW GUANINE-NUCLEOTIDE RELEASING FACTOR.
 FT DOMAIN 22 130 PH.
 FT DOMAIN 460 588 PH.
 FT CONFLICT 1033 1033 E->D (IN REF. 3).
 SQ SEQUENCE 1262 AA; 144101 MW; 021C787F CRC32;

Query Match 72.9%; Score 51; DB 1; Length 1262;
 Best Local Similarity 50.0%; Pred. No. 2,77e+00;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1060 EKERPPY 1067
 ::::|::|
 QY 1 ORYNRAPY 8

RESULT 5
 FCAR_HUMAN STANDARD; PRT: 287 AA.
 ID P24071; Q15728; Q15727; Q13603; Q13604;

DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR (IGA FC RECEPTOR) (CD89
 DE ANTIGEN).
 GN FCAR OR CD89.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
 OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91079769.
 RA MALISZEWSKI C.R., MARCH C.J., SCHOENBORN M.A., GIMPEL S., SHEN L.;
 RT "Expression cloning of a human fc receptor for Iga.";
 RL J. EXP. MED. 172:1665-1672(1990).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE-BONE MARROW;
 RX MEDLINE: 95363085.
 RA DE WIT T.P.M., MORTON H.C., CAPEL P.J.A., VAN DE WINKEL J.G.J.;
 RT "Structure of the gene for the human myeloid Iga Fc receptor (CD89).";
 RL J. IMMUNOL. 155:1203-1209(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (FORMS A.2 AND A.3).
 RC TISSUE-ALVEOLAR MACROPHAGE, AND MONOCYTES;
 RX MEDLINE: 96247667.
 RA PATRY C., SIBILLE Y., LEHUEU A., MONTEIRO R.C.;
 RT "Identification of Fc alpha receptor (CD89) isoforms generated by
 RT alternative splicing that are differentially expressed between blood
 RT monocytes and alveolar macrophages.";
 RL J. IMMUNOL. 156:4442-4448(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (FORMS B AND B-DELTA-S2).
 RA VAN DIJK T.B., MORTON H.C., CALDENHOVEN E., BRACKE M.,
 RA RAALMAERS J.A.M., LAMMERS J.W.J., KOENDEMAN L., GROOT R.P.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANS.
 RN [5]
 RP SEQUENCE FROM N.A. (FORM A.3/RLA2).
 RX MEDLINE: 96433090.
 RA PLESS R.J., ANDREWS P.D., KERR M.A., MOOF J.M.;
 RT "Alternative splicing of the human Iga Fc receptor CD89 in
 RT neutrophils and eosinophils.";
 RL BIOCHEM. J. 318:771-777(1996).
 RN [6]
 RP SUBUNITS.
 RX MEDLINE: 94375887.
 RA PEPPERKORN L.C., YEAMAN G.R.;
 RT "Association of Iga-Fc receptors (Fc alpha R) with Fc epsilon RI
 RT gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
 RT phosphorylation of gamma 2.";
 RL J. IMMUNOL. 153:3228-3236(1994).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN ALPHA.
 CC MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
 CC -1- SUBUNIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
 CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
 CC (FORM B).
 CC -1- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN BLOOD AND
 CC MUCOSAL MYELOID CELLS. MONOCYTES EXPRESS ISOPFORMS A.1, A.2 AND A.3
 CC WHILE ALVEOLAR MACROPHAGES EXPRESS A.1 AND A.2 TRANSCRIPTS;
 CC HOWEVER THEY EXPRESS ONLY ONE ISOPFORM AT THEIR SURFACES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FIVE FORMS; A.1 (SHOWN HERE), A.2,
 CC A.3, B AND B-DELTA-S2 ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD89 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd89.htm".
 CC -----
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 CC -----
 DR EMBL: X54150; G31330; -
 DR EMBL: X87767; G1054737; -
 DR EMBL: X87768; G1054737; JOINED.
 DR EMBL: X87769; G1054737; JOINED.
 DR EMBL: X87766; G1054737; JOINED.
 DR EMBL: X87765; G1054737; JOINED.
 DR EMBL: U43774; G1439556; -
 DR EMBL: U56236; G1326228; -
 DR EMBL: U56237; G1326231; -
 DR EMBL: S82919; E302400; -
 DR PIR: JH0332; JH0332.
 DR MIM: 147045; -
 KW RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; IGA-BINDING PROTEIN;

KW IMMUNOGLOBULIN FOLD; SIGNAL; ALTERNATIVE SPLICING.
 FT SIGNAL 1 21
 FT CHAIN 22 287
 FT DOMAIN 22 227
 FT TRANSMEM 228 246
 FT DOMAIN 247 287
 FT DOMAIN 42 107
 FT DOMAIN 139 200
 FT DISULFID 146 100
 FT DISULFID 149 193
 FT CARBOHYD 65 65
 FT CARBOHYD 79 79
 FT CARBOHYD 141 141
 FT CARBOHYD 177 177
 FT CARBOHYD 186 186
 FT CARBOHYD 198 198
 FT CARBOHYD 12 23
 FT VARSPLIC 121 216
 FT VARSPLIC 195 216
 FT VARSPLIC 217 287
 FT FT
 FT FT
 FT FT
 SQ SEQUENCE 287 AA: 32265 MW: 189010DB CRC32:
 B-DELTA-S2).
 Query Match 71.4%; Score 50; DB 1; Length 287;
 Best Local Similarity 71.4%; Pred. No. 4,49e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 DB 196 WYRSPY 202
 Qy 2 RYRABY 8
 RESULT 5
 ID DCAM_SOLITU STANDARD; PRT; 360 AA.
 AC 004694;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETOC)
 DE (SANDC) (INDUCED STOLEN TIP PROTEIN TUB13).
 GN SANDC OR TUB13.
 OS SOLANUM TUBEROSUM (POTATO).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 OC ASTERIDE; SOLANACEAE; SOLANACEAE; SOLANUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. RECORD; TISSUE-STOLON TIP;
 RX MEDLINE: 93081725.
 RA TAYLOR M.A., MAD ARIF S.A., KUMAR A., DAVIES H.V., SCOBBE L.A.,
 RA PEARCE S.R., FLAVELL A.J.;
 RT "Expression and sequence analysis of cDNAs induced during the early
 RT stages of tuberisation in different organs of the potato plant
 RT (Solanum tuberosum L.).";
 RL PLANT MOL. BIOL. 20:641-651(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. DESIRED;
 RX MEDLINE: 95036004.
 RA MAD ARIF S.A., TAYLOR M.A., GEORGE L.A., BUTLER A.R., BURCH L.R.,
 RA DAVIES H.V., STARK M.J., KUMAR A.;
 RT "Characterisation of the S-adenosylmethionine decarboxylase (SANDC)
 RT gene of potato.";
 RL PLANT MOL. BIOL. 26:327-338(1994).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE - (5'-DEOXY-5'-ADENOSYL)
 CC (3'-AMINOPROPYL)METHYLSTUFONIDUM SALT + CO(2).
 CC -1- COFACTOR: THIS ENZYME REQUIRES A PYRUVYL GROUP FOR ITS ACTIVITY.
 CC -1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
 CC AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMIN
 CC BIOSYNTHESIS FROM PUTRESCINE.
 CC -1- TISSUE SPECIFICITY: STOLON, ALSO EXPRESSED IN LEAVES, STEMS

CC AND ROOTS.
 CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING THE
 CC EARLY STAGES OF TUBERIZATION. MAXIMUM EXPRESSION WAS IN NON-
 CC SWELLING STOLON TIPS FROM STAGE B, AND LEVEL DECLINED AS THE
 CC TUBER INCREASED IN SIZE.
 CC -----
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 CC -----
 CC EMBL: Z11680; G21485; -
 CC DR EMBL: S74514; G807094; -
 CC DR PIR: S28047; S28047; -
 CC KW SPERMIDINE BIOSYNTHESIS; LYASE; DECARBOXYLASE; PYRUVATE; ZMOGEN.
 CC FT CHAIN 1 72 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
 CC CHAIN 73 360 CHAIN (BY SIMILARITY).
 CC SITE 72 73 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
 CC MOD_RES 73 73 CLEAVAGE (NONHYDROLYTICAL)
 CC ACT_SITE 13 13 CONVERTED TO A PYRUVYL GROUP
 CC ACT_SITE 16 16 IMPORTANT FOR CATALYTIC ACTIVITY (BY
 CC ACT_SITE 87 87 SIMILARITY).
 CC ACT_SITE 87 87 IMPORTANT FOR CATALYTIC ACTIVITY (BY
 CC CONFLICT 174 174 S -> P (IN REF. 2).
 CC CONFLICT 257 257 T -> S (IN REF. 2).
 CC CONFLICT 291 291 V -> I (IN REF. 2).
 CC CONFLICT 305 305 I -> T (IN REF. 2).
 CC SEQUENCE 360 AA; 39726 MW; 4F29EF84 CRC32;
 SQ

Query Match 70.0%; Score 49; DB 1; Length 360;
 Best Local Similarity 50.0%; Pred. No. 7.22e+00;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 332 QKTRTPY 339
 1:1:1:1
 1 QRYNRPY 8

RESULT 7
 RS2_ARATH STANDARD; PRT; 285 AA.
 P49688; Q22936;
 01-FEB-1996 (REL. 33, CREATED)
 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 40S RIBOSOMAL PROTEIN S2.
 RPS2 OR T11A07.6.
 GN ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 CC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC CAPRARIACE; BRASSICACEAE; ARABIDOPSIS.
 CC CAPRARIACE; BRASSICACEAE; ARABIDOPSIS.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-CV. COLUMBIA;
 CC ROUNDSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 CC SPRIGGS T.A., MASON T.M., KERLAVAGE A.R., ADAMS M.D., SOMERVILLE C.R.,
 CC VENTER J.C.;
 CC SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC [2]
 CC SEQUENCE OF 119-285 FROM N.A.
 CC STRAIN-CV. COLUMBIA;
 CC RAYNAL M., GREILET F., LAUDIE M., MEYER Y., COOKE R., DELSENY M.;
 CC SUBMITTED (OCT-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----

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 CC -----
 CC EMBL: AC002339; G2335095; -
 CC DR EMBL: Z17622; G16781; -
 CC DR PROSITE: PS00585; RIBOSOMAL_S5; 1.
 CC DR PIR: PF00333; S5; 1.
 CC DR HSSP: P02357; 1KP.
 CC KW RIBOSOMAL PROTEIN.
 CC FT CONFLICT 268 269 AS -> ST (IN REF. 2).
 CC FT CONFLICT 272 281 LISTKDPVV -> VSAKRYTTEG (IN REF. 2).
 CC SEQUENCE 285 AA; 30878 MW; 4684B4BF CRC32;
 SQ

Query Match 68.6%; Score 48; DB 1; Length 285;
 Best Local Similarity 57.1%; Pred. No. 1.15e+01;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 254 RFSRSPY 260
 1:1:1:1
 2 RYRNPY 8

RESULT 8
 HY14_PIG STANDARD; PRT; 14 AA.
 P01155;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE HYPOTHALMIC TETRADECAPEPTIDE.
 OS SUS SCROFA (PIG).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
 CC [1]
 CC SEQUENCE.
 CC SCHLESINGER D.H., NIAL H.D., LINTHICUM G.L., DUPONT A.,
 CC RA SCHALLI A.V.;
 CC SUBMITTED (NOV-1976) TO THE PIR DATA BANK.
 CC DR PIR: A01419; NYPG14.
 CC DR HSSP: P21856; 1GND.
 CC AMIDATION.
 CC KW MOD_RES 14 14 AMIDATION.
 CC SEQUENCE 14 AA; 1648 MW; 59F08C0B CRC32;
 SQ

Query Match 67.1%; Score 47; DB 1; Length 14;
 Best Local Similarity 57.1%; Pred. No. 1.83e+01;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2 RYKSPY 8
 1:1:1:1
 2 RYRNPY 8

RESULT 9
 KV11_HUMAN STANDARD; PRT; 108 AA.
 AC P01604;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (KUE).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 CC [1]
 CC SEQUENCE.
 CC MEDLINE: 79237924.
 CC RA EDLITZ M., KLEY H.-P., ZEITLER H.-J.;
 CC "The primary structure of the Bence-Jones protein Kue. The amino acid
 CC sequence of the variable part of a human L-chain of the kappa-type."
 CC -----

```

RL HOPE-SEYLER'S 2. PHYSIOL. CHEM. 360:725-734(1979).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01870; KIHUKU
DR PFAM: PF00047; 18; 1.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; AA01BE9 CRC32;

Query Match
Best Local Similarity 67.1%; Score 47; DB 1; Length 108;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 69 QOQSRPPY 97
OY 1 QRYNRPYA 9

RESULT 10
ID LASR_PSEAE STANDARD; PRT: 239 AA.
AC P25084; 051475; 051476;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE LASR REGULATORY PROTEIN.
GN LASR
OS PSEUDOMONAS AERUGINOSA.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
OC PSEUDOMONAS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PAOI:
RX MEDLINE: 91210193.
RA GAMBELLO M.J., IGLEWSKI B.H.;
RT "Cloning and characterization of the Pseudomonas aeruginosa lasR
RT gene, a transcriptional activator of elastase expression.";
RL J. BACTERIOL. 173:3000-3009(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PA103, AND IFO 3455;
RX MEDLINE: 95023115.
RA FUKUSHIMA J., ISHIMATA T., KURATA M., YUO Z., OKUDA K.;
RT "Intracellular receptor-type transcription factor, lasR, contains a
RT highly conserved amphipathic region which precedes the putative
RT helix-turn-helix DNA binding motif.";
RL NUCLEIC ACIDS RES. 22:3706-3707(1994).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF ELASTASE STRUCTURAL GENE
CC (LASB). BINDS TO THE PAI AUTOINDUCER.
CC -1- LASR IN STRAIN PA103 IS NOT ACTIVE, THIS IS PROBABLY DUE TO THE
CC CHANGE IN POSITION 180 OF THE SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE LUXR/CHPA FAMILY OF TRANSCRIPTIONAL
CC REGULATORS. AUTOINDUCER REGULATED SUBFAMILY.
CC -----
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CC -----
DR EMBL: M59425; G151326; -
DR EMBL: D30813; G541659; -
DR EMBL: D30812; G541657; -

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DR PIR: A43660; A43660.
DR PROSITE: PS00622; ETH_LUXR_FAMILY; 1.
DR PFAM: PF00196; GcrE; 1.
KW TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR;
KW AUTOINDUCER INDUCTION.
FT DNA_BIND 194 213 H-T-H MOTIF (BY SIMILARITY).
FT VARIANT 144 144 M -> I (IN STRAINS IFO 3455 AND PA103).
FT VARIANT 180 180 R -> W (IN STRAIN PA103).
SQ SEQUENCE 239 AA; 26618 MW; CC6B1BD CRC32;

Query Match
Best Local Similarity 67.1%; Score 47; DB 1; Length 239;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 62 EHYDRAGYA 70
OY 1 QRYNRPYA 9

RESULT 11
ID TRAE_MEIME STANDARD; PRT: 288 AA.
AC 000840;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1106 (ORF 1).
OS NEISSERIA MENINGITIDIS.
OC BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B15;
RX MEDLINE: 92326641.
RA KNIGHT A.I., NI H., CARTWRIGHT K.A.V., MCPADDEN J.;
RT "Identification and characterization of a novel insertion sequence,
RT IS1106, downstream of the pora gene in B15 Neisseria meningitidis.";
RL MOL. MICROBIOL. 6:1565-1573(1992).
CC -1- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
CC SEQUENCE.
CC -----
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CC -----
DR EMBL: Z11857; G45066; -
DR PIR: S22628; S22628.
KW TRANSPOSABLE ELEMENT; TRANSPOSITION; DNA-BINDING; DNA RECOMBINATION.
SQ SEQUENCE 288 AA; 32758 MW; 068FF8FA CRC32;

Query Match
Best Local Similarity 71.4%; Score 47; DB 1; Length 288;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 250 RYARAAY 256
OY 2 RYNRPYA 8

RESULT 12
ID GDIA_MOUSE STANDARD; PRT: 323 AA.
AC P50396;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALPHA) (GDI-1)
DE (FRAGMENT).
GN GDI OR RABGDI.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.

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RM [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C: TISSUE-SKELETAL MUSCLE;
 RX MEDLINE: 94217740.
 RA SHISHEVA A., SUDHOF T.C., CZECH M.P.;
 RT Cloning, characterization, and expression of a novel GDP
 RT dissociation inhibitor isoform from skeletal muscle.";
 RL MOL. CELL. BIOL. 14:3459-3468(1994).
 CC -1- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB
 CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
 CC SUBSEQUENT BINDING OF GTP TO THEM.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, LOWER IN OTHER
 CC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE TCD/MR6 FAMILY OF GDP DISSOCIATION
 CC INHIBITOR.
 CC -----
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 CC -----
 CC EMBL: U07950; G516537; .
 CC DR MGD: MGI:99846; GD11.
 CC DR PFAM: PF00996; GDI: 1.
 CC DR HSSP: P21856; 1GND.
 CC KW GTPASE ACTIVATION.
 CC FT NON_TER
 CC SQ SEQUENCE 323 AA; 36601 MW; EF8EC281 CRC32;

Query Match 67.1%; Score 47; DB 1; Length 323;
 Best Local Similarity 57.1%; Pred. No. 1.83e+01;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 94 RYKSPY 100
 11 :|||
 QY 2 RYRABPY 8

RESULT 13
 ID TRPE_SULSO STANDARD; PRT; 421 AA.
 AC 006128;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 CC ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
 CC TRPE.
 CC SULFOLOBUS SOLEFATRICUS.
 CC ARCHAEA; CRENARCHAEOTA; SULFOLOBALES; SULFOLOBUS.
 CC (1)
 CC SEQUENCE FROM N.A.
 CC STRAIN-ATCC 49255 / MT4;
 CC RX MEDLINE: 93106970.
 CC RA TUTTINO M.L., SCARANO G., MARINO G., SANNITA G., CUBELLIS M.V.;
 CC Triptophan biosynthesis genes trpEGC in the thermocacidophilic
 CC Archaeobacterium Sulfolobus solfataricus.";
 CC RT J. BACTERIOL. 175:299-302(1993).
 CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE - ANTHRANILATE +
 CC PYRUVATE + L-GLUTAMATE.
 CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
 CC -1- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
 CC SIMILARITY).
 CC -1- COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA
 CC RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE
 CC AMIDOTRANSFERASE ACTIVITY.
 CC -----
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 CC -----
 CC EMBL: M98048; G152937; .
 CC DR EMBL: Z50014; G1004323; .
 CC DR PIR: A40635; A40635.
 CC DR PFAM: PF00425; chorismate bind; 1.
 CC KW TRYPTOPHAN BIOSYNTHESIS; LYASE.
 CC SQ SEQUENCE 421 AA; 47736 MW; 658F857F CRC32;

Query Match 67.1%; Score 47; DB 1; Length 421;
 Best Local Similarity 71.4%; Pred. No. 1.83e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 352 YNRGPPA 358
 11 :|||

QY 3 YNRABPY 9

RESULT 14
 ID PRS7_CAEEL STANDARD; PRT; 435 AA.
 AC Q18787;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROBABLE 26S PROTEASE REGULATORY SUBUNIT 7.
 GN C52E4.4.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-BRISTOL N2;
 CC RA HOLT R.;
 CC RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDJ DATA BANKS.
 CC -1- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
 CC DEGRADATION OF UBICUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
 CC COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
 CC 26S COMPLEX (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
 CC -----
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DR EMBL: Z78012; E1344748; .
 DR WORMPEP: C52E4.4; CE08946.
 DR PROSITE: PS00674; AAA: 1.
 DR PFAM: PF00004; AAA: 1.
 CC KX HYPOTHETICAL PROTEIN; PROTEASOME; ATP-BINDING; NUCLEAR PROTEIN.
 CC FT NP_BIND 218 225 ATP (POTENTIAL).
 CC SQ SEQUENCE 435 AA; 48610 MW; D47E7317 CRC32;

Query Match 67.1%; Score 47; DB 1; Length 435;
 Best Local Similarity 62.5%; Pred. No. 1.83e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 37 RYGGPPA 44
 11 :|||

QY 2 RYRABPY 9

RESULT 15
 ID VIT2_DROME STANDARD; PRT; 442 AA.
 AC P02844;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

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DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE VITELLOGENIN II PRECURSOR (YOLK PROTEIN 2).
GN YP2.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83189120.
RA HUNG M.-C., WENSINK P.C.;
RT "Sequence and structure conservation in yolk proteins and their
   genes."
RL J. MOL. BIOL. 164:481-492(1983).
CC -1- FUNCTION: VITELLOGENIN IS THE MAJOR YOLK PROTEIN OF EGGS WHERE
CC IT IS USED AS A FOOD SOURCE DURING EMBRYOGENESIS.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE FAT BODY AND OVARIAN
CC FOLLICLE CELLS AND ACCUMULATE IN THE OOCYTE.
CC -1- INDUCTION: IN MALES BY BETA-ECDYSONE.
CC -1- SIMILARITY: PARTIAL, TO LIPASES. STRONG TO OTHER VITELLOGENINS.
CC -----
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CC -----
DR EMBL: J01157; -, NOT_ANNOTATED_CDS.
DR PIR: A03333; VJFF2.
DR FLYBASE: FBgn0005391; YP2.
DR PFAM: PF00151; Lipase; 1.
KW YOLK; SIGNAL.
FT SIGNAL. 1 20
FT CHAIN 21 442 VITELLOGENIN II.
SQ SEQUENCE 442 AA; 49678 MW; A433872E CRC32;

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Query Match 67.1%; Score 47; DB 1; Length 442;
Best local Similarity 75.0%; Pred. No. 1,83e+01;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 160 QRYNLOPY 167
   |||||
QY 1 QRYNRAPY 8

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Search completed: Thu Sep 2 12:20:32 1999
Job time : 8 secs.

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CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 100.0%; Score 70; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.25e-01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 grynrapy 9
 |||||||
 QY 1 QRYNRAPYA 9

RESULT 2
 ID W27568 standard; Protein; 107 AA.

AC W27568;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
 KW light chain; variable region; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Seifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 DR N-PSDB: T88403.
 DT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 S Claim 15; Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 107 AA:

Query Match 97.1%; Score 68; DB 27; Length 107;
 Best Local Similarity 88.9%; Pred. No. 1.06e+00;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 89 grynrapy 97
 |||||||
 QY 1 QRYNRAPYA 9

RESULT 3
 ID W27562 standard; peptide; 9 AA.

AC W27562;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Seifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 DT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 S Claim 9; Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Location/Qualifiers
 MISC-difference 9 /label= Thr, Ala

Query Match 94.3%; Score 66; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.79e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 grynrapy 8
 |||||||
 QY 1 QRYNRAPYA 8

RESULT 4
 ID W27571 standard; peptide; 9 AA.
 AC W27571;

DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B, Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SO

Query Match 92.9%; Score 65; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.33e+00;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpya 9
 |:|||||
 Oy 1 QRYNRPYA 9

RESULT 5
 ID W27575 standard; peptide; 9 AA.
 AC W27575;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.

PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B, Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SO

Query Match 90.0%; Score 63; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3.91e+00;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpyt 9
 |:|||||
 Oy 1 QRYNRPYA 9

RESULT 6
 ID W27579 standard; peptide; 9 AA.
 AC W27579;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B, Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70; 102pp; English.

The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).

Sequence 9 AA:

Query Match 87.1%; Score 61; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.54e+00;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 gkynrpy 8
1:|||||
QY 1 QRYNRPY 8

RESULT 7
ID W27584 standard; peptide; 9 AA.

AC W27584:
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
NM WO9729131-A1.
PI 14-AUG-1997.
PR 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 72; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).

Sequence 9 AA:

Query Match 85.7%; Score 60; DB 27; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.45e+00;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 gkynrpy 9
1:|||||
QY 1 QRYNRPY 9

RESULT 8
ID W27572 standard; peptide; 9 AA.

AC W27572:
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
NM WO9729131-A1.
PI 14-AUG-1997.
PR 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 68; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).

Sequence 9 AA:

Query Match 82.9%; Score 58; DB 27; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.41e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkyrpyt 9
1:11111:
QY 1 QRYNRAPYA 9

RESULT 9

ID W27570 standard; peptide: 9 AA.

W27570:

19-MAR-1998 (first entry)

Anti-TNF-alpha antibody light chain CDR3.

Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

light chain; complementarity determining region 3; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

malignancy; pulmonary disorder; intestinal disorder; hepatitis;

cardiac disorder; inflammatory bone disorder; reperfusion injury;

bone resorption disease; coagulation disturbance; burn; ELAM-1;

periodontal disease; scar tissue formation; pyrexia; HUVEC;

keloid formation; obesity; radiation toxicity;

endothelial cell leukocyte adhesion molecule-1;

human umbilical vein endothelial cell.

Homo sapiens.

WO9729131-A1.

14-AUG-1997.

10-FEB-1997: U02219.

25-NOV-1996: US-031476.

09-FEB-1996: US-599226.

(BADI) BASF AG.

Allen DJ, Hoogenboom HRJM, Kaymakcan Z, Labkovsky B,

Manfroid JA, McGuinness BT, Roberts AJ, Sakoraitas P,

Salfeld JC, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

WPI: 97-415302/38.

High affinity antibodies against human TNF alpha - useful to inhibit

TNF alpha activity, e.g. to treat autoimmune diseases and cancer

Claim 20: Page 67; 102pp; English.

The present sequence is a novel anti-human tumour necrosis

factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

determining region 3 (CDR3).

The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

less (both determined by surface plasmon resonance), and

neutralises human TNF-alpha cytotoxicity in a standard in vitro

assay with an IC50 of 1x10 power -7 M or less. The Ab, which

inhibits TNF-alpha activity, can be used to treat sepsis,

autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

syndrome, infectious diseases, malignancy, pulmonary, intestinal,

cardiac or inflammatory bone disorders, bone resorption disease,

alcoholic, viral or fulminant hepatitis, coagulation disturbances,

burns, reperfusion injury, keloid formation, scar tissue formation,

pyrexia, periodontal disease, obesity and radiation toxicity. The

Ab also inhibits TNF-alpha induced expression of endothelial cell

leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

endothelial cells (HUVEC).

Sequence 9 AA:

Query Match 78.6%; Score 55; DB 27; Length 9;

Best Local Similarity 77.8%; Pred. No. 2.99e+01;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkyrpyt 9
1:11111:
QY 1 QRYNRAPYA 9

RESULT 10

ID R22957 standard; Protein: 263 AA.

R22957:

15-OCT-1992 (first entry)

Human proteasome component HC2.

HC2; HC5; HC9; Alzheimer's disease; cancer.

Homo sapiens.

J04077498-A.

PD 11-MAR-1992. 193313.
PE 20-JUL-1990: JP-193313.
PR 20-JUL-1990: JP-193313.
PA (SARA) OTSUKA PHARM KK.
DR WPI: 92-135767/17.
DR N-NSDB: Q23894.

Human proteasome - has specified aminoacid sequence and gene base

sequence, used for e.g. investigation of Alzheimer's disease

Claim 1: Page 1; 24pp; Japanese.

Human proteasome HC2 and its gene can be used in the investigation,

diagnosis, and treatment of diseases associated with proteasome

abnormality such as cancers and Alzheimer's disease.

Human proteasome is purified from the soluble liver fractions of

human liver cell HepG2 cell. A probe was prepared, and a cDNA

library constructed using plasmid Bluescript KS-. A clone was

isolated and its DNA sequenced to give Q23894.

See also Q23894-7, R22957-60.

Sequence 263 AA:

Query Match 78.6%; Score 55; DB 4; Length 263;

Best Local Similarity 66.7%; Pred. No. 2.99e+01;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 121 qryrpyt 129
1:11111:
QY 1 QRYNRAPYA 9

RESULT 11

ID R22666 standard; Protein: 269 AA.

R22666:

06-NOV-1992 (first entry)

Protein used to raise anti-p33K antibodies.

HIV; human immunodeficiency virus; promosomal; cell surface; p27K.

OS Homo sapiens.

WO9207269-A.

30-APR-1992.

10-OCT-1990: E01945.

11-OCT-1990: EP-402838.

(PROS-) PRO-SOMA SARL.

Bey F, Bureau JP, Scherrer K;

WPI: 92-167288/20.

N-PSDB: Q24128.

Method for diagnosing HIV infection - comprises using

immunochromatological reagent contg. monoclonal antibodies against

proosomal cell surface proteins.

Claim 13: Fig 9; 34pp; English.

The 269 amino acid sequence is used to raise antibodies against the

proosomal surface protein p33K. The anti-p33K antibodies raised against

this protein can detect proosomal surface antigens. HIV infected cells

express these proteins on their surface, thus the antibodies may be used

to detect HIV infection and to determine whether T4 cells have been

infected even before they are killed by HIV.

See also R22665.

Sequence 269 AA:

Query Match 78.6%; Score 55; DB 1; Length 269;

Best Local Similarity 66.7%; Pred. No. 2.99e+01;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 127 qryrpyt 135
1:11111:
QY 1 QRYNRAPYA 9

RESULT 12

ID W27574 standard; peptide: 9 AA.

W27574:

19-MAR-1998 (first entry)

Anti-TNF-alpha antibody light chain CDR3.

Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

light chain; complementarity determining region 3; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 69; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 75.7%; Score 53; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 4.91e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapyt 9
 Oy 1 QRYNRAHYA 9

RESULT 13
 ID W27577 standard: peptide: 9 AA.
 AC W27577;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha: TNF-alpha: antibody: CDR3;
 KM light chain: complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 70; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 72.9%; Score 51; DB 27; Length 9;
 Best Local Similarity 75.0%; Pred. No. 8.02e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapyt 8
 Oy 1 QRYNRAHY 8

RESULT 14
 ID W27576 standard: peptide: 9 AA.
 AC W27576;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha: TNF-alpha: antibody: CDR3;
 KM light chain: complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 69; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 72.9% Score 51; DB 27; Length 9;
 Best Local Similarity 75.0% Pred. No. 8.02e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 qkynsapy 8
 ||:| |||
 QY 1 QRYNAPY 8

RESULT 15

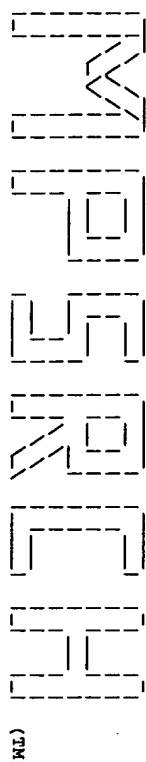
ID R42371 standard; Protein; 170 AA.
 AC R42371;
 DT 19-APR-1994 (first entry)
 DE Prod. of ORF5 of plasmid PRAP501.
 KW Haemophilus somnus; immunogenic; haemolysin; lppb; lppc;
 KW thromboembolic meningencephalitis; septicemia; arthritis;
 KW pneumonia; haemolysin-binding protein.
 OS Haemophilus somnus.
 PN WO9321323-A.
 PD 28-OCT-1993.
 PE 05-APR-1993; CA0135.
 PR 09-APR-1992; US-865050.
 PR 04-JUN-1992; US-893424.
 PR 04-JUN-1992; US-893426.
 PR 29-MAR-1993; US-038287.
 PR 29-MAR-1993; US-038288.
 PR 29-MAR-1993; US-038719.
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 PI WPI; 93-351733/44.
 N-PSDB; 051080.
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemolysin-binding protein, haemolysin, lppb and lppc,
 PT and corresp. DNA
 PS Disclosure: Fig 2; 119pp; English.
 CC A genomic cosmid library of Haemophilus somnus HS25 DNA was screened
 CC for clones capable of binding bovine haemolysin and having haemolytic
 CC activity. Positive clones were subcloned various times, resulting
 CC in plasmid PRAP501, which binds haemolysin but is not haemolytic. The
 CC clone was sequenced and was found to contain several open reading
 CC frames, potentially encoding 8 proteins. The haemolysin binding protein
 CC (encoded by the hmb gene) was encoded by ORF1. The protein can be
 CC used in vaccines for preventing or treating H. somnus infections,
 CC which cause thromboembolic meningo-encephalitis, septicemia,
 CC arthritis and pneumonia in vertebrates. The protein shown is
 CC potentially encoded by ORF5, and has an unknown function.
 CC See also R42370-86.
 SQ Sequence 170 AA:

Query Match 72.9% Score 51; DB 8; Length 170;
 Best Local Similarity 75.0% Pred. No. 8.02e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 107 qykxavy 114
 ||:| |||

QY 1 QRYNAPY 8

Search completed: Thu Sep 2 12:19:33 1999
 Job time : 19 secs.

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MUSCH_PP protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:19:51 1999; Maspar time 3.08 Seconds
 117.273 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-599-226-26
 Description: (1-9) from US06599226.ppe
 Perfect Score: 70
 Sequence: 1 QRYNAPYA 9

Scoring table:

GAP 150
 GAP 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

PLR60
 1:PLR1 2:PLR2 3:PLR3 4:PLR4

Statistics: Mean 23.338; Variance 31.114; scale 0.750

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	58	82.9	279	1	SNF5K	multicatalytic endope	3.16e+01
2	55	78.6	263	1	SNR2C	multicatalytic endope	1.29e+00
3	55	78.6	269	2	JC1445	multicatalytic endope	1.29e+00
4	53	75.7	790	2	S77032	ABC-type transport pr	3.20e+00
5	52	74.3	321	2	B71854	type II DNA modificat	5.09e+00
6	51	72.9	1260	2	S28407	guanine nucleotide-ex	7.79e+00
7	50	71.4	239	2	G02630	fealphanb - human	1.20e+01
8	50	71.4	287	2	JH0332	IGA (Fc) receptor, my	1.20e+01
9	50	71.4	521	2	I39956	neutral proteinase (E	1.20e+01
10	50	71.4	534	2	S71800	transcription factor	1.20e+01
11	49	70.0	342	2	H71258	protein Tpp3 precursor	1.85e+01
12	49	70.0	355	2	S76940	hypothetical protein	1.85e+01
13	49	70.0	360	2	S28047	TUBB3 protein - potat	1.85e+01
14	49	70.0	360	2	S52662	S-adenosylmethionine	1.85e+01
15	49	70.0	440	2	F70792	hypothetical protein	1.85e+01
16	48	68.6	367	2	S49009	fork head protein 2 -	2.83e+01
17	48	68.6	370	2	S49008	fork head protein - A	2.83e+01
18	48	68.6	419	3	JEO389	catalolite repressor	2.83e+01
19	48	68.6	1032	2	S74487	hypothetical protein	2.83e+01
20	47	67.1	64	2	G69747	hypothetical protein	4.30e+01
21	47	67.1	239	2	S53693	transcription factor	4.30e+01
22	47	67.1	239	2	S53692	transcription factor	4.30e+01
23	47	67.1	239	2	A43660	transcription activat	4.30e+01

24	47	67.1	288	2	S22628	hypothetical protein	4.30e+01
25	47	67.1	423	2	C56024	GDP dissociation inh1	4.30e+01
26	47	67.1	421	2	JC5323	anthranilate synthase	4.30e+01
27	47	67.1	442	1	VJF2	vitellogenin II precu	4.30e+01
28	47	67.1	445	2	B54091	rab GDP dissociation	4.30e+01
29	47	67.1	445	2	C56956	GDP dissociation inh1	4.30e+01
30	47	67.1	445	2	A56024	GDP dissociation inh1	4.30e+01
31	47	67.1	447	2	A54091	rab GDP dissociation	4.30e+01
32	47	67.1	447	2	I37082	GDP-dissociation inh1	4.30e+01
33	47	67.1	447	2	A35652	smg p23a regulatory p	4.30e+01
34	47	67.1	447	2	B56024	GDP dissociation inh1	4.30e+01
35	47	67.1	448	2	S36746	GDP dissociation inh1	4.30e+01
36	47	67.1	515	2	T03070	hypothetical protein	4.30e+01
37	47	67.1	520	2	B71143	hypothetical protein	4.30e+01
38	47	67.1	561	2	S01957	hypothetical protein	4.30e+01
39	47	67.1	689	2	S45901	probable membrane pro	4.30e+01
40	47	67.1	722	2	C71411	hypothetical protein	4.30e+01
41	47	67.1	956	2	G70327	isooleucyl-tRNA synthe	4.30e+01
42	47	67.1	1320	2	D64843	proline dehydrogenase	4.30e+01
43	47	67.1	1320	2	S66279	proline dehydrogenase	4.30e+01
44	47	67.1	2410	1	JQ1948	genome polypeptide 1	4.30e+01
45	47	67.1	2412	1	JQ1537	genome polypeptide 1	4.30e+01

ALIGNMENTS

RESULT ENTRY TITLE	1
SNF5K	#type complete
multicatalytic endopeptidase complex (EC 3.4.99.46) 35K chain	
- fruit fly (Drosophila melanogaster)	
19S cylinder particle 35K chain; multicatalytic proteinase	
35K chain; prosome 35K chain; proteasome 35K chain	
ORGANISM	#formal_name Drosophila melanogaster
DATE	30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Sep-1997
ACCESSIONS	S23450; S05507; A38761
REFERENCE	S23450
#authors	Frentzel, S.; Troxell, M.; Haass, C.; Resold-Hurt, B.; Glaetzer, K.H.; Kloetzel, P.M.
#journal	Eur. J. Biochem. (1992) 205:1043-1051
#title	Molecular characterization of the genomic regions of the Drosophila alpha-type subunit proteasome genes PROS-Dm28.1 and PROS-Dm35
#cross-references	EMBL:X62285; NID:g8387; PID:g8388
#accession	S23450
#molecule_type	DNA
#residues	1-279 ##label FREN
#cross-references	EMBL:X62285; NID:g8387; PID:g8388
#experimental_source	strain Canton S
REFERENCE	S05507
#authors	Haass, C.; Resold-Hurt, B.; Multhaup, G.; Beyreuther, K.; Kloetzel, P.M.
#journal	EMBO J. (1989) 8:2373-2379
#title	The PROS-35 gene encodes the 35 kd protein subunit of Drosophila melanogaster proteasome.
#cross-references	EMBL:X15497; NID:g8381; PID:g8382
#accession	A38761
#molecule_type	protein
#residues	4-18; 194-206 ##label HMA2
GENETICS	
#gene	PROS-35
#cross-references	FLYBase:FBgn0003151
#map_position	89F-90A
#introns	1/3; 211/3
CLASSIFICATION	#superfamily multicatalytic endopeptidase complex chain C9
KEYWORDS	hydrolase; phosphoprotein; proteinase
SUMMARY	#length 279 #molecular-weight 31058 #checksum 365
Query Match	82.9%; Score 58; DB 1; Length 279;

Best Local Similarity 66.7%; Pred. No. 3,16e-01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 121 QRYDRPXYG 129

QY 1 QRYNRPAY 9

RESULT 2
ENTRY SNRTC2 #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2

ALTERNATE_NAMES multicatalytic proteinase component C2; proteasome chain C2
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 17-Oct-1997

ACCESSIONS A32968; A38799; S09741

REFERENCE

#authors

#journal Fujiiwara, T.; Tanaka, K.; Kumatori, A.; Shin, S.; Yoshimura, T.; Ichihara, A.; Tokunaga, F.; Aruga, R.; Iwanaga, S.; Kakizuka, A.; Nakenishi, S.
#title Biochemistry (1989) 28:7332-7340
Molecular cloning of cDNA for proteasomes (multicatalytic proteinase complexes) from rat liver: primary structure of the largest component (C2).

#cross-references MVID:90057428

#accession A32968

#molecule_type mRNA

#residues 1-263 ##label FUJ1

#cross-references EMBL:M29859; NID:g206381; PID:g206382

#accession A38799

#molecule_type protein

#residues 2-25;42-58;63-74,'X',76-79,'X',81,116-135;190-203;
218-226,'XX',229,'X',231;244-246,'X',248-262 ##label FU2

REFERENCE

#authors

#journal Tokunaga, F.; Aruga, R.; Iwanaga, S.; Tanaka, K.; Ichihara, A.; Takao, T.; Shimonishi, Y.
#title FEBS Lett. (1990) 263:373-375
The NH2-terminal residues of rat liver proteasome (multicatalytic proteinase complex) subunits, C2, C3 and C8, are N-alpha-acetylated.

#cross-references MVID:90243011
#accession S09741
#molecule_type protein
#residues 1-30 ##label TOK
#classification #superfamily multicatalytic endopeptidase complex chain C9
#keywords acetylated amino end; hydrolase; proteinase

CLASSIFICATION #product multicatalytic endopeptidase complex chain C2
#status experimental #label MAT
#modified site acetylated amino end (Met) #status experimental
FEATURE 1-263

SUMMARY #length 263 #molecular-weight 29517 #checksum 9238

Query Match 78.6%; Score 55; DB 1; Length 263;
Best Local Similarity 66.7%; Pred. No. 1.29e+00;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 121 QRYGRPYG 129

QY 1 QRYNRPAY 9

RESULT 3

ENTRY

TITLE

ALTERNATE_NAMES JCI445 #type complete
multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2,
long splice form - human
macropain nu chain; multicatalytic endopeptidase complex HC2
chain; multicatalytic endopeptidase complex nu chain;
multicatalytic proteinase chain C2; prosome 30-33k chain;
proteasome alpha 1 subunit; proteasome chain C2; proteasome
nu chain

CONTAINS

multicatalytic endopeptidase complex chain C2, short splice form

ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997

ACCESSIONS JCI445; S15897; S17520; S25410; PC3321

REFERENCE

#authors

#journal

#title

Gene (1992) 120:235-242
Two mRNAs exist for the Hs PROS-30 gene encoding a component of human prosomes.

#accession JCI445

#molecule_type mRNA

#residues 1-269 ##label PER

#cross-references GB:M64992

REFERENCE

#authors

#journal

#title

Tamura, T.; Lee, D.H.; Osaka, F.; Fujiiwara, T.; Shin, S.; Chung, C.H.; Tanaka, K.; Ichihara, A.
Biochim. Biophys. Acta (1991) 1089:95-102
Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multi-catalytic proteinase complexes).

#cross-references MVID:91223105

#accession S15897

#molecule_type mRNA

#residues 'M',8-269 ##label TAM

#cross-references EMBL:D00759; NID:g220021; PID:d1001114; PID:g220022

REFERENCE

#authors

#journal

#title

Demartino, G.N.; Orth, K.; McCullough, M.L.; Lee, L.W.; Munn, T.Z.; Moosaw, C.R.; Dawson, P.A.; Slaughtter, C.A.
Biochim. Biophys. Acta (1991) 1079:29-38
The primary structures of four subunits of the human, high-molecular-weight proteinase, macropain (proteasome), are distinct but homologous.

#cross-references MVID:91363412

#accession S17520

#molecule_type mRNA

#residues not compared with conceptual translation

#cross-references GB:M61969; NID:g286737; PID:g286738

#accession S25410

#molecule_type protein

#residues 10-40;46-61;68-75;89-95;103-128;132-148;164-168;176-195;
203-223;225-267 ##label DE2

REFERENCE

#authors

#journal

#title

Kristensen, P.; Johnsen, A.H.; Derkx, W.; Tanaka, K.; Hendill, K.B.
Biochem. Biophys. Res. Commun. (1994) 205:1785-1789
Human proteasome subunits from 2-dimensional gels identified by partial sequencing.

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

#cross-references MVID:95110324

#accession PC3321

#molecule_type protein

#residues 69-88 ##label KRI

Query Match 78.6%; Score 55; DB 2; Length 269;

Best Local Similarity 66.7%; Pred. No. 1.29e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 127 ORGNRPPY 135
OY 1 ORYNRAPY 9

RESULT 4
ENTRY 577032 #type complete
TITLE ABC-type transport protein sl10778 - *Synechocystis* sp.
(strain PCC 6803)
ALTERNATE_NAMES protein sl10778
ORGANISM #formal name *Synechocystis* sp.
#variety PCC 6803
DATE 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998

ACCESSIONS 577032
REFERENCE 574322
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; Hirosewa, M.; Sugitara, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpō, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. (1996) 3:109-116

#journal #title Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MUID:97061201
#accession 577032
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-790 #label KAN
#cross-references EMBL:D64005; GB:AB001339; NID:g1001779; PID:d1011375; PID:g1006575

#note the nucleotide sequence was submitted to the EMBL Data Library, June 1996
CLASSIFICATION #superfamily ATP-binding cassette homology
KEYWORDS P-loop; transport protein
FEATURE 244-434 #domain ATP-binding cassette homology #label ABC\
261-268 #region nucleotide-binding motif A (P-loop)
SUMMARY #length 790 #molecular-weight 87656 #checksum 7314

Query Match 75.7%; Score 53; DB 2; Length 790;
Best Local Similarity 62.5%; Pred. No. 3.20e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 475 ORXRSST 482
OY 1 ORYNRAPY 8

RESULT 5
ENTRY B71854 #type complete
TITLE type II DNA modification enzyme (methyltransferase) - *Helicobacter pylori* (strain J99)
ORGANISM #formal name *Helicobacter pylori*
#variety strain J99
DATE 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 12-Feb-1999

ACCESSIONS B71854
REFERENCE A71800
#authors Alm, R.A.; Lind, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.R.; Noonan, B.; Guld, B.C.; deJonge, B.L.; Carmel, G.; Tsumino, P.J.; Caruso, A.; Urita-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Voyts, G.F.; Trust, T.J.
Nature (1999) 397:176-180

#journal #title Genomic sequence comparison of two unrelated isolates of the

human gastric pathogen *Helicobacter pylori*.
#cross-references MUID:99120557
#accession B71854
#status preliminary
#molecule_type DNA
#residues 1-321 #label ARN
#cross-references GB:AE001533; GB:AE001439; NID:g4155636; PID:g4155654
#experimental_source strain J99

GENETICS
#gene jhp1050
SUMMARY #length 321 #molecular-weight 36919 #checksum 5430

Query Match 74.3%; Score 52; DB 2; Length 321;
Best Local Similarity 75.0%; Pred. No. 5.00e+00;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 204 ORYNRPY 211
OY 1 ORYNRAPY 8

RESULT 6
ENTRY S28407 #type complete
TITLE guanine nucleotide-exchange activator CDC25 homology - mouse
ORGANISM #formal name *Mus musculus* #common name house mouse
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 10-Sep-1997

ACCESSIONS S28407; S22693; B46199; S20730
REFERENCE S28407
#authors Cen, H.; Papageorge, A.G.; Zippel, R.; Lowy, D.R.; Zhang, K.; EMBO J. (1992) 11:4007-4015
#journal #title Isolation of multiple mouse cDNAs with coding homology to Saccharomyces cerevisiae CDC25: identification of a region related to Bcr, Vav, Dbl and CDC24.
#cross-references MUID:93010996
#accession S28407
#status not compared with conceptual translation
#molecule_type mRNA
#residues 1-1260 #label CEN

REFERENCE S22693
#authors Martegani, E.; Vanoni, M.; Zippel, R.; Cocchetti, P.; Brambilla, R.; Ferrari, C.; Sturani, E.; Alberghina, L.; EMBO J. (1992) 11:2151-2157
#journal #title Cloning by functional complementation of a mouse cDNA encoding a homologue of CDC25, a Saccharomyces cerevisiae RAS activator.
#cross-references MUID:92289680
#accession S22693
#molecule_type mRNA
#residues 789-1260 #label MAR

REFERENCE A46199
#cross-references EMBL:X59688; NID:g50357; PID:g50358
#authors Wei, W.; Mosteller, R.D.; Sanyal, P.; Gonzales, E.; McKlincy, D.; Dasgupta, C.; Li, P.; Liu, B.X.; Broek, D.; Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104
#journal #title Identification of a mammalian gene structurally and functionally related to the CDC25 gene of *Saccharomyces cerevisiae*.
#cross-references MUID:92357779
#accession B46199
#status preliminary
#molecule_type nucleic acid
#residues 1029-1030, 'D', 1032-1224 #label WEI
#experimental_source fetus
#note sequence extracted from NCBI backbone (NCBIN:111101, NCBI:P111102)

CLASSIFICATION #superfamily CDC25-type guanine nucleotide exchange activator
homology: CDC24 homology; pleckstrin repeat homology
FEATURE 242-428 #domain CDC24 homology #label CD24\
1021-1257 #domain CDC25-type guanine nucleotide exchange activator homology #label SOS
SUMMARY #length 1260 #molecular-weight 143900 #checksum 9725

Query Match 72.9%; Score 51; DB 2; Length 1260;
Best Local Similarity 50.0%; Pred. No. 7.79e+00;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1058 EXERTPY 1065
:::1111
QY 1 QRYNRPY 8

SUMMARY

RESULT 7
ENTRY G02630 #type complete
TITLE FcalphaRb - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998

ACCESSIONS
REFERENCE G02630
#authors H01508
van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.; Raaijmakers, J.A.M.; Lammers, J.
#submission submitted to the EMBL Data Library, April 1996
#accession G02630
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-239 #label VAN
#cross-references EMBL:U56236; NID:g1326229
SUMMARY #length 239 #molecular_weight 2696 #checksum 5338

Query Match 71.4%; Score 50; DB 2; Length 239;
Best Local Similarity 71.4%; Pred. No. 1.20e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 196 WYNRSFY 202
:::1111
QY 2 RYNRPY 8

SUMMARY

RESULT 8
ENTRY JH0332 #type complete
TITLE IGA (Fc) receptor, myeloid cell (CD89) precursor - human
ALTERNATE_NAMES myeloid glycoprotein CD89
ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 10-Sep-1997
JH0332; I37224; S14405
ACCESSIONS JH0332
REFERENCE JH0332
#authors Meliszewski, C.R.; March, C.J.; Schoenborn, M.A.; Gimpel, S.; Shen, L.
#journal J. Exp. Med. (1990) 172:1665-1672
#title Expression cloning of a human Fc receptor for IGA.
#cross-references MIM:91079769
#accession JH0332
#molecule_type mRNA
#residues 1-287 #label MAL
#cross-references GB:X54150; NID:g31329; PID:g31330
REFERENCE 137224
#experimental_source myeloid cell liver V937
#authors de Wit, T.P.; Morton, H.C.; Capel, P.J.; van de Winkel, J.G.
#journal J. Immunol. (1995) 155:1203-1209
#title Structure of the gene for the human myeloid IGA Fc receptor (CD89).
#cross-references MIM:95363085
#accession I37224
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-287 #label RES
#cross-references EMBL:X87767; NID:g963041; PID:g1054737
GENETICS
#gene GDB:FCAR; CD89
#cross-references GDB:127543; OMIM:147045
#map_position 19q13.2-19q13.4
#introns 12/1; 24/1; 121/1; 217/1
KEYWORDS glycoprotein; immunoglobulin receptor; transmembrane protein

FEATURE
1-21 #domain signal sequence #status predicted #label SIG
22-287 #product IGA receptor Fc alpha #status predicted #label MFC
228-246 #domain transmembrane #status predicted #label TRA
65,79,141,177,186 #binding_site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 287 #molecular_weight 32265 #checksum 5963

Query Match 71.4%; Score 50; DB 2; Length 287;
Best Local Similarity 71.4%; Pred. No. 1.20e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 196 WYNRSFY 202
:::1111
QY 2 RYNRPY 8

SUMMARY

RESULT 9
ENTRY I39956 #type complete
TITLE neutral protease (EC 3.4.24.-) - Bacillus amyloliquefaciens
ORGANISM #formal_name Bacillus amyloliquefaciens
DATE 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 18-Mar-1997
ACCESSIONS I39956
REFERENCE I39956
#authors Shimada, H.; Honjo, M.; Mita, I.; Nakayama, A.; Akeoka, A.; Manabe, K.; Furutani, Y.
#journal J. Biochemol. (1985) 2:75-85
#title The nucleotide sequence and some properties of the neutral protease gene of Bacillus amyloliquefaciens.
#accession I39956
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-521 #label RES
#cross-references GB:M36723; NID:g143352; PID:g143353
GENETICS
#start_codon GTG
CLASSIFICATION #superfamily thermolysin
KEYWORDS hydrolase; metalloprotease
SUMMARY #length 521 #molecular_weight 56725 #checksum 6816

Query Match 71.4%; Score 50; DB 2; Length 521;
Best Local Similarity 62.5%; Pred. No. 1.20e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 308 QRYNRSY 315
1-1111
QY 1 QRYNRPY 8

SUMMARY

RESULT 10
ENTRY S71800 #type fragment
TITLE transcription factor FAS7-1 - African clawed frog (fragment)
ALTERNATE_NAMES forkhead activin signal transducer 1
ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 05-Dec-1997
ACCESSIONS S71800
REFERENCE S71800
#authors Chen, X.; Rubock, M.J.; Whitman, M.
#journal Nature (1996) 383:691-696
#title A transcriptional partner for MAD proteins in TGF-beta signalling.
#cross-references MIM:97032727
#accession S71800
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-534 #label CHP
#cross-references EMBL:U70980
CLASSIFICATION #superfamily unassigned fork head proteins; fork head
KEYWORDS DNA binding; transcription factor

FEATURE
117-209 #domain fork head DNA-binding domain homology #label FHD
SUMMARY
#length 534 #checksum 6119

Query Match 71.4%; Score 50; DB 2; Length 534;
Best Local Similarity 44.4%; Pred. No. 1.20e+01;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 113 HRYKPPYS 121
:11::11:
QY 1 QRYNRPYA 9

RESULT 11
ENTRY H71258 #type complete
TITLE protein Tps3 precursor - syphilis spirochete
ORGANISM #formal_name Treponema pallidum subsp. pallidum #common_name syphilis spirochete
DATE 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999
ACCESSIONS H71258; S19825; S18232
H71250
#authors Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin, M.; Hickey, E.K.; Clayton, R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Petersen, J.; Khaila, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald, L.; Artlich, P.; Bowman, C.; Cotton, M.D.; Fujii, C.; Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Watthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
#journal Science (1998) 281:375-388
#title Complete genome sequence of Treponema pallidum, the syphilis spirochete.
#cross-references MIMD:98332770
#accession H71258
#molecule_type DNA
#status nucleic acid sequence not shown; translation not shown
#residues 1-342 #label COL
#cross-references GB:AE001264; GB:AE00520; NID:93323278; PID:93323279
#experimental_source strain Nichols
REFERENCE S19825
#authors Bianco, D.
#submission submitted to the EMBL Data Library, August 1991
#accession S19825
#molecule_type DNA
#residues 1-9,'S',11-16,'A',18-28 #label BIA1
#cross-references EMBL:X61228; GB:S84879; NID:948228; PID:948229
REFERENCE S18230
#authors Bianco, D.R.; Giladi, M.; Champion, C.I.; Haake, D.A.; Chikani, G.K.; Miller, J.N.; Lovett, M.A.
#journal Mol. Microbiol. (1991) 5:2405-2415
#title Identification of Treponema pallidum subspecies pallidum genes encoding signal peptides and membrane-spanning sequences using a novel alkaline phosphatase expression vector.
#cross-references MIMD:92167806
#accession S18232
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-16,'A',18-28 #label BIA2
#cross-references EMBL:X61228; GB:S84879; NID:948228
GENETICS
#gene Tps3; TP0957
FEATURE
1-17 #domain signal sequence #status predicted #label SIG
SUMMARY
#length 342 #molecular-weight 38312 #checksum 7408

Query Match 70.0%; Score 49; DB 2; Length 342;
Best Local Similarity 85.7%; Pred. No. 1.85e+01;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 156 YTRAPYA 162
:1::1::1:
QY 1 QRYNRPYA 9

QY 3 YNRPYA 9

RESULT 12
ENTRY S76940 #type complete
TITLE hypothetical protein - Synechocystis sp. (strain PCC 6803)
ORGANISM #formal_name Synechocystis sp.
#variety PCC 6803
DATE 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 18-Sep-1998
ACCESSIONS S76940
S74322
#authors Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MIMD:97061201
#accession S76940
#status preliminary
#molecule_type DNA
#residues 1-355 #label KAN
#cross-references EMBL:D90917; GB:AB001339; NID:91653836; PID:d1019585; PID:91653942
#note The nucleotide sequence was submitted to the EMBL Data Library, June 1996

CLASSIFICATION
#superfamily Ribonucleoside diphosphate reductase beta chain
SUMMARY
#length 355 #molecular-weight 41603 #checksum 88

Query Match 70.0%; Score 49; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.85e+01;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 310 RYKSPYT 317
:1::1:
QY 2 RYNRPYA 9

RESULT 13
ENTRY S28047 #type complete
TITLE TUB13 protein - potato
ORGANISM #formal_name Solanum tuberosum #common_name potato
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
ACCESSIONS S28047
S28046
#authors Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flavell, A.J.
#journal Plant Mol. Biol. (1992) 20:641-651
#title Expression and sequence analysis of cDNAs induced during the early stages of tuberisation in different organs of the potato plant (Solanum tuberosum L.).
#accession S28047
#molecule_type mRNA
#residues 1-360 #label TAY
#cross-references EMBL:Z11680; NID:921484; PID:921485
GENETICS
#gene TUB13
SUMMARY
#length 360 #molecular-weight 39726 #checksum 7941

Query Match 70.0%; Score 49; DB 2; Length 360;
Best Local Similarity 50.0%; Pred. No. 1.85e+01;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 332 QRTTRPY 339
:1::1::1:
QY 1 QRYNRPYA 8

Search completed: Thu Sep 2 12:20:07 1999
Job time : 16 secs.

```

RESULT      14
ENTRY       S52662      #type complete
TITLE       S-adenosylmethionine decarboxylase (SAMDC) - potato
ORGANISM    #formal_name Solanum tuberosum #common_name potato
DATE        14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
          21-Jul-1995

ACCESSIONS  S52662
REFERENCE    S52662
#authors     Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.;
#journal     Burch, L.R.; Davies, H.V.; Stark, M.J.R.; Kumar, A.
#title       Plant Mol. Biol. (1994) 26:327-338
          Characterisation of the S-adenosylmethionine decarboxylase
          (SAMDC) gene of potato.

#accession   S52662
#status      Preliminary
#molecule_type DNA
#residues    1-360 #label ARI
MMARY        #length 360 #molecular-weight 39724 #checksum 8045

Query Match      70.0% Score 49; DB 2; Length 360;
Best Local Similarity 50.0% Pred. NO. 1.85e+01;
Matches          4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB      332 OKFRTPT 339
      1::1::1
QY      1 GRYNRAPY 8

RESULT      15
ENTRY       F70792      #type complete
TITLE       hypothetical protein RV3693 - Mycobacterium tuberculosis
          (strain H37RV)
ORGANISM    #formal_name Mycobacterium tuberculosis
DATE        17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
          17-Jul-1998

ACCESSIONS  F70792
REFERENCE    A70500
#authors     Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
          C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry
          III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
          Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
          Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
          Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
          Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
          Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
          Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.;
          Taylor, K.; Whitehead, S.; Barrall, B.G.
          Taylor, K.; Whitehead, S.; Barrall, B.G.
          Nature (1998) 393:537-544
          Deciphering the biology of Mycobacterium tuberculosis from
          the complete genome sequence.

#cross-references MIMD:98295987
#accession      F70792
#status          preliminary; nucleic acid sequence not shown;
          translation not shown
#molecule_type DNA
#residues        1-440 #label COL
#cross-references GB:AL023121; GB:AL123456; NID:g3261559; PID:el264553;
          PID:g2960117
#experimental_source strain H37RV

GENETICS
#gene           RV3693
SUMMARY         #length 440 #molecular-weight 47687 #checksum 5593

Query Match      70.0% Score 49; DB 2; Length 440;
Best Local Similarity 50.0% Pred. NO. 1.85e+01;
Matches          4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB      53 RFTSPYT 60
      1::1::1
QY      2 RYNRAPY 9

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 WIRENET (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Sep 2 12:24:39 1999; Maspar time 4.47 Seconds
 Modular output not generated. 146.469 Million cell updates/sec

Title: >US-08-599-226-27
 Description: (1-12) from US08599226.pep
 Perfect Score: 68
 Sequence: 1 ASYLSTSSSIDN 12

Scoring table:
 PAM 150
 Gap 15

Searched: 179066 seqs, 54579741 residues
 Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: sptrembl9
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mmc 8:sp_organelle
 9:sp_phage 10:sp_plant 11:sp_protent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 23.036; Variance 26.585; scale 0.867

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	53	77.9	127	14	011696	NUCLEOPROTEIN (FRAGMENT)	1.02e+00
2	52	76.5	377	2	084397	HYPOHETICAL 41.4 KD P	1.77e+00
3	51	75.0	471	10	023552	HYPOHETICAL 52.8 KD P	2.85e+00
4	50	73.5	293	2	051095	CONSERVED HYPOHETICAL	4.72e+00
5	49	72.1	384	2	011197	HYPOHETICAL 41.9 KD P	7.77e+00
6	49	72.1	650	2	050417	MULTI-FUNCTIONAL ENZYME	7.77e+00
7	48	70.6	149	11	061836	MYELIN BASIC PROTEIN (1.27e+01
8	48	70.6	195	11	001585	MYELIN BASIC PROTEIN (1.27e+01
9	48	70.6	197	4	015339	GOLGI-MBP	1.27e+01
10	48	70.6	250	11	003139	MYELIN BASIC PROTEIN (1.27e+01
11	48	70.6	304	4	015340	GOLGI-MBP	1.27e+01
12	48	70.6	649	3	060167	PROTEIN COMPLEX ASSEMB	1.27e+01
13	47	69.1	2150	5	023863	HISTIDINE KINASE A.	2.06e+01
14	46	67.6	188	10	081650	THYMIDYLATE KINASE (FR	3.31e+01
15	46	67.6	236	3	012282	CHROMOSOME XV READING	3.31e+01
16	46	67.6	327	5	062500	Y70CSC.4 PROTEIN.	3.31e+01
17	46	67.6	361	4	015595	ORF1A.	3.31e+01
18	46	67.6	416	4	015407	RTSBEA.	3.31e+01
19	46	67.6	428	5	P91535	COSMID ZC204.	3.31e+01
20	46	67.6	437	2	008305	INDLIN FRUCTOTRANSFERA	3.31e+01

Result ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
21	46	67.6	1022	6	028628	A-KINASE ANCHORING PRO	3.31e+01
22	46	67.6	1088	5	000905	HYPOHETICAL 129.9 KD	3.31e+01
23	46	67.6	2697	5	001438	SMIARITY TO THE P13/	5.28e+01
24	45	66.2	88	14	079008	ENVELOPE PROTEIN (FRAG	5.28e+01
25	45	66.2	94	14	079006	ENVELOPE PROTEIN (FRAG	5.28e+01
26	45	66.2	160	5	027302	GLOBIN.	5.28e+01
27	45	66.2	214	10	081901	HYPOHETICAL 24.3 KD P	5.28e+01
28	45	66.2	239	2	000510	SMKX PROTEIN.	5.28e+01
29	45	66.2	243	1	028075	HYDROXYMETHYLPRIMIDIN	5.28e+01
30	45	66.2	250	5	023509	COSMID ZK470.	5.28e+01
31	45	66.2	338	5	016949	APC/BP.	5.28e+01
32	45	66.2	484	5	023173	W05E10.1 PROTEIN.	5.28e+01
33	45	66.2	657	3	005931	SMIAR TO HEAT-SHOCK	5.28e+01
34	45	66.2	831	5	021574	M28.8 PROTEIN.	5.28e+01
35	45	66.2	832	4	092831	P/CAF.	5.28e+01
36	45	66.2	1001	2	025314	TYPE III RESTRICTION E	5.28e+01
37	45	66.2	3623	11	070244	INTRINSIC FACTOR-B12 R	5.28e+01
38	44	64.7	247	2	P70914	BRIT1, ATR, FBID & FBI	8.35e+01
39	44	64.7	460	3	002321	EXOCELLIOHOLINOLASE.	8.35e+01
40	44	64.7	471	4	000425	ROTATIVE RAS INHIBITOR	8.35e+01
41	44	64.7	583	5	018517	C39B10.1 PROTEIN.	8.35e+01
42	44	64.7	608	10	P92973	CCAI.	8.35e+01
43	44	64.7	696	5	023264	ZC373.1 PROTEIN (FRAG	8.35e+01
44	44	64.7	705	2	P94888	CADMIUM RESISTANCE PRO	8.35e+01
45	44	64.7	4836	11	088473	RJS.	8.35e+01

ALIGNMENTS

Result 1
 ID 011696: PRELIMINARY; PRT: 127 AA.
 AC 011696:
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-NOV-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DE NUCLEOPROTEIN (FRAGMENT).
 OS MEASLES VIRUS (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).
 OC VIRUSES, SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
 OC PARAMYXOVIRINAE; PARAMYXOVIRINAE; MORBILLIVIRUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-92-E;
 RX MEDLINE: 97278133.
 RA YAMAGUCHI S.;
 RT Identification of three lineages of wild measles virus by nucleotide
 RT sequence analysis of N, P, M, F, and L genes in Japan. "
 RL J. MED. VIROL. 52:113-120(1997).
 DR EMBL: D87487; D1020995; -
 KW NUCLEOPROTEIN.
 FT NON_TER
 SQ SEQUENCE 127 AA; 13950 MW; 42D75A2C CRC32;

Query Match 77.9%; Score 53; DB 14; Length 127;
 Best Local Similarity 63.6%; Pred. No. 1.02e+00;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 66 AAYLPTSTPLD 76
 QY 1 ASYLSTSSSID 11

Result 2
 ID 084397: PRELIMINARY; PRT: 377 AA.
 AC 084397:
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DE HYPOHETICAL 41.4 KD PROTEIN.
 OS CHLAMYDIA TRACHOMATIS.
 OC BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA.
 RN (1)
 RP SEQUENCE FROM N.A.

RC STRAIN-D/DW-3/CX;
 RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
 RA MITCHELL W.P., OLINGER L., TATISOV R.L., ZHAO Q., KOONIN E.V.,
 RA DAVIS R.W.;
 RT "Genome Sequence of an Obligate Intracellular Pathogen of Humans:
 RT Chlamydia trachomatis.";
 RL SCIENCE 0:0-0(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D/DW-3/CX;
 RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
 RA MITCHELL W.P., OLINGER L., TATISOV R.L., ZHAO Q., KOONIN E.V.,
 RA DAVIS R.W.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AE001312; G3328818; -
 KM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 377 AA; 41449 MW; 2879B006 CRC32;
 SO
 Query Match 76.5%; Score 52; DB 2; Length 377;
 Best Local Similarity 58.3%; Pred. No. 1.71e+00;
 Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Db 324 ASYLSSSPSYED 335
 QY 1 ASYLSTSSSLD 12

RESULT 3
 ID 023552 PRELIMINARY; PRT; 471 AA.
 AC 023552;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 52.8 KD PROTEIN.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRAALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BEVAN M., STRIEMA W., MURPHY G., WAMBUIT R., POHL T., TERRYN N.,
 RA KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R.,
 RA FUGIOMENECH P., HATZIOPOULOS P., OBERMAIER B., DUESTERHOFT A.,
 RA JONES J., PALME K., ANSORGE W., DEISEN M., BANCROFT I., MEMES H.W.,
 RA SCHUELLER C., CHALMATZIS N.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 ED ARABIDOPSIS SEQUENCING PROJECT, ESSA;
 DR SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 297342; E327038; -
 KM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 471 AA; 52785 MW; 4EBA8315 CRC32;
 SO
 Query Match 75.0%; Score 51; DB 10; Length 471;
 Best Local Similarity 63.6%; Pred. No. 2.85e+00;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 19 AGYTSSSD 29
 QY 1 ASYLSTSSSLD 11

RESULT 4
 ID 051095 PRELIMINARY; PRT; 293 AA.
 AC 051095;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN BB0068.
 OS BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).
 OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; BORRELIA.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35210 / B31;
 RX MEDLINE: 98065943
 RA FRASER C.M., CASSENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
 RA LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,
 RA DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
 RA PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
 RA VAN VUOT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
 RA UTERBACK T., MATHEY L., McDONALD L., ARTICH P., BOWMAN C.,
 RA GARLAND S., FULLI C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
 RA SMITH H.O., VENTER J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi.";
 RL NATURE 390:580-586(1997).
 DR EMBL: AE001120; G2687956; -
 DR TIGR: BB0068; -
 SQ SEQUENCE 293 AA; 33278 MW; 3FB9B9E2 CRC32;
 SO
 Query Match 73.5%; Score 50; DB 2; Length 293;
 Best Local Similarity 60.0%; Pred. No. 4.72e+00;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Db 198 AYLTSPNSLE 207
 QY 2 SYLTSSSLD 11

RESULT 5
 ID 011197 PRELIMINARY; PRT; 384 AA.
 AC 011197;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 41.9 KD PROTEIN IN CAN1 3 REGION (ORF2).
 OS MYCOBACTERIUM TUBERCULOSIS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; CORYNEBACTERINAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RA.
 RX MEDLINE: 95327699.
 RA YUAN Y., LEE R.E., BESRA G.S., BELISLE J.T., BARRY C.E. III;
 RT "Identification of a gene involved in the biosynthesis of
 RT cyclooperanated mycolic acids in Mycobacterium tuberculosis.";
 RL PROC. NTL. ACAD. SCI. U.S.A. 92:6630-6634(1995).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC FAMILY (SDR).
 DR EMBL: U27357; G886103; -
 DR PFAM: PF00106; adh_short; 1.
 KM HYPOTHETICAL PROTEIN; OXIDOREDUCTASE.
 SQ SEQUENCE 384 AA; 41995 MW; 9FB8465A CRC32;
 SO

Query Match 72.1%; Score 49; DB 2; Length 384;
 Best Local Similarity 54.5%; Pred. No. 7.77e+00;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 235 SYLTPTKAALD 245
 QY 1 ASYLSTSSSLD 11
 RESULT 6
 ID 050417 PRELIMINARY; PRT; 650 AA.
 AC 050417;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MULTI-FUNCTIONAL ENZYME.
 GN MY0004.49.
 OS MYCOBACTERIUM TUBERCULOSIS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; CORYNEBACTERINAE; MYCOBACTERIACEAE; MYCOBACTERIUM.

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-H37RV;
 RC OLIVER K., SKELTON J., BADCOCK K., CHURCHER C.M., HARRIS D.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-H37RV;
 RC PARKHILL J., BARRELL B.G., RAINDREAM M.A.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-H37RV;
 RC MEDLINE: 96181548;
 RX PHILLIP W.J., POULET S., EIGMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 RT leprae.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
 EMBL: AL009198; E1203309; -;
 SO SEQUENCE 650 AA; 70939 MW; 1E552EAS CRC32;

Query Match 72.1%; Score 49; DB 2; Length 650;
 Best Local Similarity 54.5%; Pred. No. 7.77e+00;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 501 SSYLPKALD 511
 :|||:|:|:
 QY 1 ASYLSTSSLDN 11

RESULT 7
 ID 061836 PRELIMINARY; PRT: 149 AA.
 AC 061836;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MYELIN BASIC PROTEIN (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-BRAIN;
 RX MEDLINE: 87118269;
 RA NEWMAN S., KITAMURA K., CAMPAGNONI A.T.;
 RT "Identification of a cDNA coding for a fifth form of myelin basic
 RT protein in mouse.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 84:886-890(1987).
 EMBL: M15062; G19051; -;
 DR PROSITE: PS00569; MYELIN_MBP; 1.
 KM ALTERNATIVE SPLICING; MYELIN.
 FT NON_TER 1
 SO SEQUENCE 149 AA; 16226 MW; A6DC1599 CRC32;

Query Match 70.6%; Score 48; DB 11; Length 149;
 Best Local Similarity 41.7%; Pred. No. 1.27e+01;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

DB 2 SKYLASTMDH 13
 :|||:|:|:
 QY 1 ASYLSTSSLDN 12

RESULT 8
 ID 001585 PRELIMINARY; PRT: 195 AA.
 AC 001585;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MYELIN BASIC PROTEIN (MBP).

GN MBP.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57 BL/6J; TISSUE-BONE MARROW;
 RX MEDLINE: 93057537;
 RA GRINA B., ZELENKA D., PESSAC B.;
 RT "A novel transcript overlapping the myelin basic protein gene.";
 RT J. NEUROCHEM. 59:2318-2323(1992).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-C57BL/6; TISSUE-BRAIN;
 RC MEDLINE: 93186801; PRIBYL T.M., CAMPAGNONI C.W., KAMPE K.,
 RA CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPE K.,
 RA AMOR-DUARTEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBAY B.,
 RA KITAMURA K.;
 RT "Structure and developmental regulation of Goli1-mbp, a 105-kilobase
 RT gene that encompasses the myelin basic protein gene and is expressed
 RT in cells in the oligodendrocyte lineage in the brain.";
 RT J. BIOL. CHEM. 268:4930-4938(1993).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 DR EMBL: X67319; G51333; -;
 DR EMBL: L07508; G193587; -;
 DR MGD: MGI:96925; MBP.
 KM MYELIN; STRUCTURAL PROTEIN; ACETYLATION; METHYLATION; PHOSPHORYLATION;
 KM AUTOIMMUNE ENCEPHALOMYELITIS; ALTERNATIVE SPLICING.
 SO SEQUENCE 195 AA; 21004 MW; 557D83EA CRC32;

Query Match 70.6%; Score 48; DB 11; Length 195;
 Best Local Similarity 41.7%; Pred. No. 1.27e+01;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

DB 144 SKYLASTMDH 155
 :|||:|:|:
 QY 1 ASYLSTSSLDN 12

RESULT 9
 ID 015339 PRELIMINARY; PRT: 197 AA.
 AC 015339;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GOLI1-MBP.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 94068468;
 RA PRIBYL T.M., CAMPAGNONI C.W., KAMPE K., KASHIMA T., HANDLEY V.W.,
 RA MCMAHON J., CAMPAGNONI A.T.;
 RT "The human myelin basic protein gene is included within a
 RT 179-kilobase transcription unit: expression in the immune and central
 RT nervous systems.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 90:10695-10699(1993).
 EMBL: L18865; G435060; -;
 DR EMBL: L18865; G435060; -;
 SO SEQUENCE 197 AA; 21522 MW; DBA8A5BF CRC32;

Query Match 70.6%; Score 48; DB 4; Length 197;
 Best Local Similarity 41.7%; Pred. No. 1.27e+01;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

DB 146 SKYLASTMDH 157
 :|||:|:|:
 QY 1 ASYLSTSSLDN 12

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RESULT 10
ID 003139 PRELIMINARY; PRT; 250 AA.
AC 003139;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE MYELIN BASIC PROTEIN (MBP).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE-BRAIN;
RA MEDLINE; 93186801.
RA CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPE K.,
RA AMUR-UMARJEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBAR B.,
RA KITAMURA K.;
RT "Structure and developmental regulation of Goll1-mbp, a 105-kilobase
gene that encompasses the myelin basic protein gene and is expressed
in cells in the oligodendrocyte lineage in the brain.";
DE J. BIOL. CHEM. 268:4930-4938(1993).
EMBL; L07507; G193585; -.
DR MYELIN: STRUCTURAL PROTEIN: ACETYLATION; METHYLATION; PHOSPHORYLATION;
KW AUTOLIMONE ENCEPHALOMYELITIS; ALTERNATIVE SPLICING.
SQ SEQUENCE 250 AA; 27167 MW; 3A08ADE7 CRC32;

Query Match 70.6%; Score 48; DB 11; Length 250;
Best Local Similarity 41.7%; Pred. No. 1.27e+01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 144 SKYLASTASTMDH 155
: |||: ||:
QY 1 ASYLSTSSSDN 12

RESULT 11
ID 015340 PRELIMINARY; PRT; 304 AA.
AC 015340;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE GOL1-MBP.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE; 94068468.
RA PRIBYL T.M., CAMPAGNONI C.W., KAMPE K., KASHIWA T., HANDLEY V.W.,
RA MCMAHON J., CAMPAGNONI A.T.;
RT "The human myelin basic protein gene is included within a
179-kilobase transcription unit: expression in the immune and central
nervous systems.";
DE PROC. NATL. ACAD. SCI. U.S.A. 90:10695-10699(1993).
EMBL; L18866; G435062; -.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 304 AA; 33117 MW; 4E98B0AE CRC32;

Query Match 70.6%; Score 48; DB 4; Length 304;
Best Local Similarity 41.7%; Pred. No. 1.27e+01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 146 SKYLASTASTMDH 157
: |||: ||:
QY 1 ASYLSTSSSDN 12

RESULT 12
ID 060167 PRELIMINARY; PRT; 649 AA.
AC 060167;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

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DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE PROTEIN COMPLEX ASSEMBLY PROTEIN.
GN SPBC19F8.03C.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIAESOMYCETES;
OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA BECK A., REINHARDT R., WOOD V., RAJANDREAM M.A., BARRELL B.G.;
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
EMBL; AL023594; E1293401; -.
DR SEQUENCE 649 AA; 72985 MW; 9C207DB2 CRC32;

Query Match 70.6%; Score 48; DB 3; Length 649;
Best Local Similarity 60.0%; Pred. No. 1.27e+01;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 234 NYLSTARSL 243
: |||: ||:
QY 2 SYLSTSSSDN 11

RESULT 13
ID 023863 PRELIMINARY; PRT; 2150 AA.
AC 023863;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE HISTIDINE KINASE A.
GN DHKA.
OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
OC EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA MEDLINE; 96324397.
RA WANG N., SHAULSKY G., ESCALANTE R., LOOMIS W.F.;
RT "A two-component histidine kinase gene that functions in
Dictyostelium development.";
DE EMBL J. 15:3890-3898(1996).
EMBL; U42597; G1136289; -.
DR PFWM; PF00072; response_reg; 1.
DR PFWM; PF00512; signal; 1.
SQ SEQUENCE 2150 AA; 239662 MW; 02F946CE CRC32;

Query Match 69.1%; Score 47; DB 5; Length 2150;
Best Local Similarity 63.6%; Pred. No. 2.06e+01;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 180 NYLNNSSSLN 190
: |||: |||:
QY 2 SYLSTSSSDN 12

RESULT 14
ID 081650 PRELIMINARY; PRT; 188 AA.
AC 081650;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE THYMIDYLATE KINASE (FRAGMENT).
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMEROPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPRALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RA ULLAH H., ROBERTSON N., FITES R.C.;
RT "Plant thymidylate kinase mRNA.";
EMBL; AF081570; G3493131; -.
DR

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FT	NON_TER	1	1
SQ	SEQUENCE	188 AA;	21248 MW; C306E7B8 CRC32;

Query Match	67.68;	Score 46;	DB 10;	Length 188;
Best Local Similarity	50.08;	Pred. No. 3.31e+01;		
Matches	6;	Conservative 3;	Mismatches 3;	Indels 0;
			Gaps	0;

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Db      43 SAYLSNKSQDD 54  
        ::||| | ||:  
QY      1 ASYLSTSSSLDN 12
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RESULT	15	
ID	Q12282	
AC	Q12282	
	PRELIMINARY;	PRT;
		236 AA

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE CHROMOSOME XV READING FRAME ORF YOR1214C
DE SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST)
EURKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMETES; SACCCHAROMYCETALES
SACCCHAROMYCETAEAL; SACCCHAROMYCES.

RN
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BOYER J., FAIRHEAD C., GAILLON L., GALISSON F., MICHAUX G.,
 RA THIERRY A., DUJON B.,
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MIRS.
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FY1679;
 RA GALLISON F., DOJON B.;
 RL SUBMITTED (CCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS
 DR EMBL: Z75122; ECT52081; -
 RN EMBL: X92441; GI1050786; -
 QD SEQUENCE 236 AA; 26156 MW; 97599C243 CRC32;

Query Match	67.68;	Score 46;	DB 3;	Length 236;
Best Local Similarity	66.78;	Pred. No. 3.31e+01;		
Matches	6;	Conservative	3;	Mismatches 0;
			Indels	0;
			Gaps	0;

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Db      176 SYLSSTTSL 184
      ||||::||
QY      2 SYLSTSSSL 10

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Search completed: Thu Sep 2 12:25:03 1999
Job time : 24 secs.

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 WISE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:24:11 1999; Maspar time 2.20 Seconds
 154.213 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-599-226-27
 Description: (1-12) from US08599226.pep
 Perfect Score: 68
 Sequence: 1 ASYLSTSSSLDN 12

Scoring table: PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: SWISS-Prot37
 1:swissprot

Statistics: Mean 23.947; Variance 24.229; scale 0.968

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	51	75.0	352	1	YDH3_SCHPO	7.63e+01
2	48	70.6	127	1	MBP_RAT	3.92e+00
3	48	70.6	167	1	MBP_CAVPO	3.92e+00
4	48	70.6	171	1	MBP_PANTR	3.92e+00
5	48	70.6	196	1	MBP_MOUSE	3.92e+00
6	48	70.6	194	1	MBP_HUMAN	3.92e+00
7	48	70.6	577	1	PYRH_YEAST	3.92e+00
8	47	69.1	132	1	YMH7_MYCTU	6.65e+00
9	47	69.1	543	1	YJF8_YEAST	6.65e+00
10	47	69.1	684	1	YV18_MYCTU	6.65e+00
11	47	69.1	687	1	VIDA_VIBCH	6.65e+00
12	47	69.1	800	1	PT11_YEAST	6.65e+00
13	46	67.6	301	1	P34_RICRI	1.12e+01
14	46	67.6	345	1	VCAN_BPT7	1.12e+01
15	46	67.6	398	1	VCAB_BPT7	1.12e+01
16	46	67.6	471	1	UF01_MAIZE	1.12e+01
17	46	67.6	471	1	UF03_MAIZE	1.12e+01
18	46	67.6	471	1	UF03_MAIZE	1.12e+01
19	45	66.2	169	1	MBP_BOVIN	1.86e+01
20	45	66.2	209	1	SOMA_ESOLD	1.86e+01
21	45	66.2	210	1	YGBL_HAEIN	1.86e+01
22	45	66.2	396	1	L1DD_ECOLI	1.86e+01
23	45	66.2	416	1	YEL1_ECOLI	1.86e+01

24	45	66.2	485	1	G6PD_ZYMO	1.86e+01
25	45	66.2	547	1	MERA_STAUV	1.86e+01
26	45	66.2	552	1	DHAK_CITFR	1.86e+01
27	45	66.2	633	1	Y102_YEAST	1.86e+01
28	45	66.2	750	1	YJN2_YEAST	1.86e+01
29	45	66.2	753	1	YBNJ_ECOLI	1.86e+01
30	44	64.7	141	1	Y221_MYCGE	3.07e+01
31	44	64.7	238	1	VGLG_HSV1	3.07e+01
32	44	64.7	371	1	CYSK_EMENT	3.07e+01
33	44	64.7	468	1	YPS7_CABEL	3.07e+01
34	44	64.7	483	1	KICL_MOUSE	3.07e+01
35	44	64.7	498	1	RPB2_METJA	3.07e+01
36	44	64.7	817	1	Y249_YEAST	3.07e+01
37	43	63.2	231	1	Y249_MYCTU	5.00e+01
38	43	63.2	238	1	ARD1_YEAST	5.00e+01
39	43	63.2	357	1	PHEE_PROMI	5.00e+01
40	43	63.2	505	1	RADA_SYN3	5.00e+01
41	43	63.2	545	1	4CL1_SOLTU	5.00e+01
42	43	63.2	678	1	PTN3_YEAST	5.00e+01
43	43	63.2	926	1	PTN4_HUMAN	5.00e+01
44	43	63.2	1255	1	ERR2_HUMAN	5.00e+01
45	43	63.2	3924	1	ANKR_HUMAN	5.00e+01

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	352 AA.
AC	092348:			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	HYPOTHETICAL 39.7 KD PROTEIN C669.03C IN CHROMOSOME I.			
GN	SPAC669.03C.			
OS	SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).			
OC	EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASTOMYCETES;			
CC	SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;			
CC	SCHIZOSACCHAROMYCES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-972;			
RA	MURPHY L., HARRIS D., BARRELL B.G., RAUANDREAM M.A., CONNOR R.E.;			
RL	SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC	-1- SIMILARITY: SOME TO YEAST YML206C.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; 281317; E276610; -			
KW	HYPOTHETICAL PROTEIN.			
SD	SEQUENCE 352 AA; 39679 MW; D92A9357 CRC32;			
DB	303 SYLNASSLEN 313			
OY	2 SYLSTSSSLDN 12			
Query Match	75.0%;	Score 51:	DB 1:	Length 352;
Best Local Similarity	63.6%;	Pred. No. 7.63e+01;		
Matches	7;	Conservative	3;	Mismatches 1;
			Indels	0;
			Gaps	0;
RESULT	2	STANDARD:	PRT:	127 AA.
AC	P02688:			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	MYELIN BASIC PROTEIN S (MBP S).			

GN MBP.
 OS EUTARIUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87026249.
 RA SCHACH M., BUDZINSKI R.M., STOFFEL W.;
 RT "Cloned proteolipid protein and myelin basic protein cDNA.
 RT Transcription of the two genes during myelination.";
 RL BIOL. CHEM. HOPE-SEYLER 367:825-834(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84026484.
 RA ROACH A., BOYLAN K., HORVATH S., PRUSINER S.B., HOOD L.E.;
 RT "Characterization of cloned cDNA representing rat myelin basic
 RT protein: absence of expression in brain of shiverer mutant mice.";
 RL CELL 34:799-806(1983).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE: 75127359.
 RA DUNKLEY P.R., CARREGIE P.R.;
 RT "Amino acid sequence of the smaller basic protein from rat brain
 RT myelin.";
 RL BIOCHEM. J. 141:243-255(1974).
 RN [4]
 RP SEQUENCE OF 45-85.
 RX MEDLINE: 73180720.
 RA MCFARLIN D.E., BLANK S.E., KIBLER R.F., MCKENALLY S., SHAPIRA R.;
 RT "Experimental allergic encephalomyelitis in the rat: response to
 RT SCIENCE 179:478-480(1973).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- ALTERNATIVE PRODUCTS: RATS HAVE TWO MYELIN BASIC PROTEINS. THE
 CC SMALLER ONE, SHOWN HERE, IS MISSING 40 RESIDUES (FOLLOWING RESIDUE
 CC 113 OR 114) WITH RESPECT TO THE LARGER ONE FROM OTHER SPECIES.
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 CC -----
 DR EMBL: M25889; G205322; -
 DR EMBL: K00512; -; NOT_ANNOTATED_CDS.
 DR PIR: A03142; MBRTS.
 DR PIR: B24351; B24351.
 DR PIR: A21062; A21062.
 DR PROSITE: PS00569; MYELIN_MBP; 1.
 KW MYELIN: STRUCTURAL PROTEIN; ACETYLTATION; METHYLATION; PHOSPHORYLTATION;
 KW AUTOIMMUNE ENCEPHALOMYEELITIS; ALTERNATIVE SPLICING.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLTATION.
 FT MOD_RES 104 104 METHYLATION (MONO-44% OR DI-11%).
 FT CONFLICT 46 47 SG -> GS (IN REF. 2).
 FT CONFLICT 124 124 M -> I (IN REF. 2).
 SQ SEQUENCE 127 AA; 14080 MW; 834EBB5 CRC32;
 Query Match 70.6%; Score 48; DB 1; Length 127;
 Best Local Similarity 41.7%; Pred. No. 3.92e+00;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 DB 12 SKYLATASTMDH 23
 QY 1 ASYLSTSSSLDN 12
 RESULT 3
 ID MBP_CAVPO STANDARD; PRT; 167 AA.

AC P25188;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE MYELIN BASIC PROTEIN (MBP).
 OS CAVIA PORCELLUS (GUINEA PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 84215086.
 RA DEIBLER G.E., MARTENSON R.E., KRUTZSCH H.C., KIES M.W.;
 RT "Sequence of guinea pig myelin basic protein.";
 RL J. NEUROCHEM. 43:100-105(1984).
 RN [2]
 RP SEQUENCE OF 45-87.
 RA SHAPIRA R., MCKENALLY S.S., CHOU F., KIBLER R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. BIOL. CHEM. 246:4630-4640(1971).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC PIR: A37246; A37246.
 DR PIR: C92087; C92087.
 DR PROSITE: PS00569; MYELIN_MBP; 1.
 KW MYELIN: STRUCTURAL PROTEIN; ACETYLTATION; METHYLATION; PHOSPHORYLTATION;
 KW AUTOIMMUNE ENCEPHALOMYEELITIS.
 FT MOD_RES 1 1 ACETYLTATION.
 FT MOD_RES 106 106 METHYLATION (MONO- OR DI-) (BY
 FT DOMAIN 114 122 SIMILARITY).
 FT INDICES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYEELITIS.
 SQ SEQUENCE 167 AA; 18213 MW; B31793AB CRC32;
 Query Match 70.6%; Score 48; DB 1; Length 167;
 Best Local Similarity 41.7%; Pred. No. 3.92e+00;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 DB 12 SKYLATASTMDH 23
 QY 1 ASYLSTSSSLDN 12
 RESULT 4
 ID MBP_PANTR STANDARD; PRT; 171 AA.

RA MEDLINE: 87311781.
 RA ROTH H.J., KRONQUIST K.E., DE ROSBO N., CRANDALL B.F.,
 RA CAMPAGNONI A.T.;
 RT "Evidence for the expression of four myelin basic protein variants in
 RT the developing human spinal cord through cDNA cloning.";
 RL J. NEUROSCI. RES. 17:321-328(1987).
 RN [3]
 RP SEQUENCE OF 1-58; 85-131 AND 143-196 FROM N.A.
 RA MEDLINE: 86308101.
 RA ROTH H.J., KRONQUIST K., PRETORIUS P.J., CRANDALL B.F.,
 RA CAMPAGNONI A.T.;
 RT "Isolation and characterization of a cDNA coding for a novel human
 RT 17.3k myelin basic protein (MBP) variant.";
 RL J. NEUROSCI. RES. 16:227-238(1986).
 RN [4]
 RP SEQUENCE OF 1-58 AND 85-196 FROM N.A.
 RA MEDLINE: 86259714.
 RA KAMHOLZ J., DE FERRA F., PUCKETT C., LAZZARINI R.A.;
 RT "Identification of three forms of human myelin basic protein by cDNA
 RT cloning.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 83:4962-4966(1986).
 RN [5]
 RP SEQUENCE OF 1-58 AND 85-196.
 RA MEDLINE: 72066400.
 RA KARNIGIE P.R.;
 RT "Amino acid sequence of the encephalitogenic basic protein from human
 RT myelin.";
 RL BIOCHEM. J. 123:57-67(1971).
 RN [6]
 RP SEQUENCE OF 45-58 AND 85-114, REVISIONS.
 RA SHAPIRA R., MCKENNA S.S., CHOU F., KIBLER R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. BIOL. CHEM. 246:4630-4640(1971).
 RN [7]
 RP SEQUENCE OF 1-58 FROM N.A.
 RA MEDLINE: 90152679.
 RA BOYLAN K.B., AVRES T.M., POPKO B., TAKAHASHI N., HOOD L.E.,
 RA PRUSINER S.B.;
 RT "Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a
 RT new form of oligonucleotide repetitive sequence showing length
 RT polymorphism.";
 RL GENOMICS 6:16-22(1990).
 RN [8]
 RP METHYLATION.
 RA MEDLINE: 72066401.
 RA BALDWIN G.S., CARNIGIE P.R.;
 RT "Isolation and partial characterization of methylated arginines from
 RT the encephalitogenic basic protein of myelin.";
 RL BIOCHEM. J. 123:69-74(1971).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- ALTERNATIVE PRODUCTS: HUMANS HAVE THREE FORMS OF MBP, 21.5K, 18.5K
 CC (THE MOST ABUNDANT), AND 17.2K. THE THREE FORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -----
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 CC -----
 DR EMBL: M13577; G307160; -
 DR EMBL: M30516; G307161; -
 DR EMBL: M30515; G307162; -
 DR EMBL: M30047; G307159; -
 DR EMBL: X17286; E221974; -
 DR EMBL: X17287; E221974; JOINED.
 DR EMBL: X17290; E221974; JOINED.
 DR EMBL: X17288; E221974; JOINED.

DR EMBL: X17369; E221974; JOINED.
 DR EMBL: X17289; E221974; JOINED.
 DR EMBL: M63589; G187403; -
 DR PIR: A24153; MBHRB.
 DR PIR: S10482; S10482.
 DR MIM: 159430; -
 DR PROSITE: PS00569; MYELIN_MBP; 1.
 DR MYELIN: STRUCTURAL PROTEIN; ACETYLATION; METHYLATION; PHOSPHORYLATION;
 DR AUTOIMMUNE ENCEPHALOMYELITIS; ALTERNATIVE SPLICING.
 FT INIT MET 0
 FT MOD_RES 1 1
 FT MOD_RES 133 133
 FT MOD_RES 45 114
 FT DOMAIN
 FT DOMAIN 138 148
 FT VARSPPLIC 59 84
 FT VARSPPLIC 132 142
 FT VARSPPLIC 196 AA; 21362 MM; 0A8864EE CRC32;
 SQ SEQUENCE 196 AA; 21362 MM; 0A8864EE CRC32;
 Db 12 SKYATFASTMDH 23
 Qy 1 ASYLISTSSLDN 12
 Query Match 70.6%; Score 48; DB 1; Length 196;
 Best Local Similarity 41.7%; Pred. No. 3.92e+00;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 RESULT 7
 ID PYRH YEAST STANDARD; PRT; 577 AA.
 AC P38627;
 DT 01-OCT-1994 (REL. 30. CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CTP SYNTHASE 2 (EC 6.3.4.2) (UTP--AMMONIA LIGASE 2) (CTP SYNTHETASE
 DE 2).
 GN URAB OR YUR103M OR J1962.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCCHAROMYCETALES;
 OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 28383 / FL100;
 RA MEDLINE: 94166752.
 RA OZIER-KALOGEROPOULOS O., ADELIN M.T., YANG W.L., CARMAN G.M.,
 RA LACHOUVE F.;
 RT "Use of synthetic lethal mutants to clone and characterize a novel
 RT CTP synthetase gene in Saccharomyces cerevisiae.";
 RL MOL. GEN. GENET. 242:431-439(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA RAMEZANI RAD M., KIRCHGATH L., HOLLENBERG C.P.;
 RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDJ DATA BANKS.
 CC -1- CATALYTIC ACTIVITY: ATP + UTP + GLUTAMINE -> ADP + ORTHOPHOSPHATE +
 CC CTP (AMMONIA CAN REPLACE GLUTAMINE).
 CC -1- PATHWAY: LAST STEP IN PYRIMIDINE BIOSYNTHESIS.
 CC -1- SIMILARITY: TO OTHER SPECIES CTP SYNTHASE.
 CC -1- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE
 CC AMIDOTRANSFERASES.
 CC -----
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 CC -----
 DR EMBL: X68196; G440163; -
 DR EMBL: Z49603; G1015810; -.

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DR PIR: S40000; S40000.
DR PIR: S42580; S42580.
DR SGD: L0002437; URA8.
DR PROSITE: PS00442; GATASE_TYPE_1; 1.
RM PYRIMIDINE BIOSYNTHESIS; LIGASE; GLUTAMINE AMIDOTRANSFERASE;
KM MULTIGENE FAMILY.
FT ACT_SITE 404 404 GATASE (BY SIMILARITY).
FT ACT_SITE 537 537 GATASE (BY SIMILARITY).
FT ACT_SITE 539 539 GATASE (BY SIMILARITY).
FT CONFLICT 96 97 OL -> HY (IN REF. 2).
FT CONFLICT 204 204 L -> S (IN REF. 2).
FT CONFLICT 440 446 PSSHHA -> QVVIYMP (IN REF. 2).
FT CONFLICT 557 577 QLRTCEVYIKDINLSEGENE -> AAPAHLYK (IN
REF. 2).
SQ SEQUENCE 577 AA; 64621 MW; ADAF6873 CRC32;

Query Match 70.6%; Score 48; DB 1; Length 577;
Best Local Similarity 54.5%; Pred. No. 3.92e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

318 SYLSTSSLDN 328
|||||:||||:
OY 2 SYLSTSSLDN 12

RESULT 8
ID YW07.MYCTU STANDARD; PRT: 132 AA.
AC Q10847;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 14.7 KD PROTEIN CY39.07C.
GN MTCY39.07C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORYNEBACTERIINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
[1]
RC SEQUENCE FROM N.A.
RP STRAIN-H37RV;
RA OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1 SIMILARITY: TO M.TUBERCULOSIS MTCY48.04C.
CC -----
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CC -----
DR EMBL; Z74025; E248788; -.
RM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 132 AA; 14731 MW; 3D577F11 CRC32;

Query Match 69.1%; Score 47; DB 1; Length 132;
Best Local Similarity 63.6%; Pred. No. 6.65e+00;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 10 AYLTSTSSLDN 20
:|||||:|
OY 2 SYLSTSSLDN 12

RESULT 9
ID YJF8.YEAST STANDARD; PRT: 543 AA.
AC P47041;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 60.8 KD PROTEIN IN BTN1-PEP8 INTERGENIC REGION.
GN YJ1058C OR J1141.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).

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OC EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCCHAROMYCETALES;
OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
[1]
RP SEQUENCE FROM N.A.
RA POHL T.M., ALJINOVIC G.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1 SIMILARITY: STRONG, TO YEAST YBR270C.
CC -----
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CC -----
DR EMBL; Z49333; G108201; -.
RM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 543 AA; 60840 MW; 8233FB93 CRC32;

Query Match 69.1%; Score 47; DB 1; Length 543;
Best Local Similarity 58.3%; Pred. No. 6.65e+00;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 182 ASFLDSSTLN 193
|||||:|:|:|
OY 1 ASYLTSSSLN 12

RESULT 10
ID YV18.MYCTU STANDARD; PRT: 684 AA.
AC Q11157;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 57.3 KD PROTEIN GMC-TYPE OXIDOREDUCTASE CY20G9.18C.
GN MTCY20G9.18C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORYNEBACTERIINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
[1]
RC SEQUENCE FROM N.A.
RP STRAIN-H37RV;
RA MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1 COFACTOR: FAD FLAVOPROTEIN (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
CC -----
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CC -----
DR EMBL; Z77162; E255032; -.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
RM HYPOTHETICAL PROTEIN; OXIDOREDUCTASE; FLAVOPROTEIN; FAD.
SQ SEQUENCE 684 AA; 72253 MW; F4A66D1F CRC32;

Query Match 69.1%; Score 47; DB 1; Length 684;
Best Local Similarity 70.0%; Pred. No. 6.65e+00;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 117 ASYLTGRSL 126
|||||:|:|
OY 1 ASYLTSSSL 10

RESULT 11
ID VJVA_VIBCH STANDARD; PRT: 687 AA.

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AC Q00964;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE VIBRIOACTIN RECEPTOR PRECURSOR.
GN VIDA.
OS VIBRIO CHOLERAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OGAWA 395;
RA MEDLINE: 92276356.
RT BUTTERTON J.R., STOEHRER J.A., PAYNE S.M., CALDERWOOD S.B.;
RT "Cloning, sequencing, and transcriptional regulation of *vib*, the
RT gene encoding the ferric vibriobactin receptor of *Vibrio cholerae*,"
RL J. BACTERIOL. 174:3729-3738(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OGAWA 395;
RA LIAO W.J., CHOI M.H., BUTTERTON J.R.;
RT SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR FERRIC VIBRIOACTIN.
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
CC -----
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CC -----
DR EMBL: AF030977; G2641147; -
DR PIR: A41905; A41905.
DR PFAM: PF00593; TonB_boxC: 1.
KM SIGNAL; RECEPTOR; OUTER MEMBRANE; IRON TRANSPORT.
FT SIGNAL 1 37
FT CHAIN 38 687
SQ SEQUENCE 687 AA; 76413 MW; 525D3D49 CRC32;
DB VIBRIOACTIN RECEPTOR.
QY 69.1%; Score 47; DB 1; Length 687;
Query Match
Best Local Similarity 66.7%; Pred. No. 6.65e+00;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 662 YLSTNTLD 670
QY 3 YLSTSSLD 11
RESULT 12
ID PT11 YEAST STANDARD; PRT; 800 AA.
AC P08468;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PET11 PROTEIN PRECURSOR.
GN PET11 OR YMR257C OR YMR920.11C.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCCHAROMYCETALES;
CC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 88038811.
RA STRICK C.A., FOX T.D.;
RT "Saccharomyces cerevisiae positive regulatory gene *PET11* encodes a
RT mitochondrial protein that is translated from an mRNA with a long 5'
RT leader,"
RL MOL. CELL. BIOL. 7:2728-2734(1987).
RN [2]
RP REVISIONS.
RA STRICK C.A., FOX T.D.;
RL SUBMITTED (XX-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA HUNT S., BOWMAN S., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RT SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: REQUIRED FOR TRANSLATION OF THE MITOCHONDRIAL GENE FOR
CC CYTOCHROME C OXIDASE SUBUNIT II (COX2).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -1- SIMILARITY: SOME, TO YEAST YH160C.
CC -----
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CC -----
DR EMBL: M17143; G387896; -
DR EMBL: 248639; G732935; -
DR PIR: A26915; A26915.
DR SGD: L0001393; PET11.
KM TRANSLATION REGULATION: ACTIVATOR; TRANSIT PEPTIDE; MITOCHONDRION.
FT TRANSIT 1 7
FT CHAIN 800
FT SIMILAR 637 685
FT CONFLICT 278 278
FT CONFLICT 709 709
SQ SEQUENCE 800 AA; 94522 MW; 14907869 CRC32;
DB 726 PAYSTASION 737
QY 69.1%; Score 47; DB 1; Length 800;
Query Match
Best Local Similarity 50.0%; Pred. No. 6.65e+00;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
DB 1 ASYLSTSSLDN 12
RESULT 13
ID P34.RICRI STANDARD; PRT; 301 AA.
AC P21559;
DT 01-MAY-1991 (REL. 18, CREATED)
DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROTEIN P34.
GN P34.
OS RICKETTSIA RICKETTSII.
OC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RICKETTSIALES;
CC RICKETTSIACEAE; RICKETTSIENAE; RICKETTSIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHETLA SMTH;
RA MEDLINE: 91088329.
RA ANDERSON B.E., BAUMSTARK B.R., BELLINI W.J.;
RT "Nucleotide sequence of the *p34* gene from *Rickettsia rickettsii*,"
RL NUCLEIC ACIDS RES. 18:7168-7168(1990).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE UPF0018 FAMILY.
CC -----
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CC -----
DR EMBL: X56068; G46397; -
DR PIR: S13095; S13095.
KM TRANSMEMBRANE.
FT TRANSMEM 15 35
FT TRANSMEM 40 60
FT TRANSMEM 83 103
FT TRANSMEM POTENTIAL.
FT TRANSMEM POTENTIAL.

FT TRANSMEM 120 140 POTENTIAL.
FT TRANSMEM 171 191 POTENTIAL.
SQ SEQUENCE 301 AA; 34686 MW; 28899720 CRC32;
Query Match 67.6%; Score 46; DB 1; Length 301;
Best Local Similarity 60.0%; Pred. No. 1.12e+01;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DB 13 ASYLSTSSSLD 22
OY 1 ASYLSTSSSL 10

RESULT 14
ID VCAABPT7 STANDARD; PRT: 345 AA.
AC P19726; P03717;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
MAJOR CAPSID PROTEIN 10A.
10 BACTERIOPHAGE T7,
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; PODOVIRIDAE.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 83241725.
RA DUNN J.J., STUDIER F.W.;
RT Complete nucleotide sequence of bacteriophage T7 DNA and the
RT locations of T7 genetic elements.*;
RL J. MOL. BIOL. 166:477-535(1983).
CC -1- SIMILARITY: TO THE T3 MAJOR CAPSID PROTEIN 10A.
CC -----
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CC -----
CC EMBL: V01146; G15604; -
DR PIR: A04344; VABPA7.
DR PIR: S42325; S42325.
KW COAT PROTEIN.
SQ SEQUENCE 345 AA; 36545 MW; D12C1BAE CRC32;
Query Match 67.6%; Score 46; DB 1; Length 345;
Best Local Similarity 41.7%; Pred. No. 1.12e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
DB 71 AAYLAGENLDD 82
OY 1 ASYLSTSSSLD 12

RESULT 15
ID VCAABPT7 STANDARD; PRT: 398 AA.
AC P19727; P03717;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE MINOR CAPSID PROTEIN 10B.
GN 10
OS BACTERIOPHAGE T7.
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; PODOVIRIDAE.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 83241725.
RA DUNN J.J., THOMPSON K.;
RT Complete nucleotide sequence of bacteriophage T7 DNA and the
RT locations of T7 genetic elements.*;
RL J. MOL. BIOL. 166:477-535(1983).
CC -1- THE MINOR CAPSID PROTEIN 10B IS DUE TO A TRANSLATIONAL SHIFT TO

CC THE -1 FRAME.
CC -1- SIMILARITY: TO THE T3 MINOR CAPSID PROTEIN 10B, EXCEPT IN THE
CC C-TERMINAL EXTENSIONS.
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CC -----
CC EMBL: V01146; G431193; -
DR PIR: B04344; VABPA7.
DR PIR: S42326; S42326.
KW COAT PROTEIN.
SQ SEQUENCE 398 AA; 41830 MW; 88D410FF CRC32;
Query Match 67.6%; Score 46; DB 1; Length 398;
Best Local Similarity 41.7%; Pred. No. 1.12e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
DB 71 AAYLAGENLDD 82
OY 1 ASYLSTSSSLD 12

Search completed: Thu Sep 2 12:24:21 1999
Job time : 10 secs.

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 (TM)

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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:23:34 1999; MasPar time 3.12 Seconds
 Tabular output not generated. 154.250 Million cell updates/sec

Title: >US-08-599-226-27
 Description: (1-12) from US08599226.pep
 Perfect Score: 68
 Sequence: 1 ASYLSTSSSLDN 12

Scoring table:
 PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: PIR60
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 23.467; Variance 26.716; scale 0.878

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	52	76.5	377	2	F71520	1.43e+00
2	51	73.0	471	2	C71439	2.39e+00
3	50	73.5	293	2	D70108	3.95e+00
4	49	72.1	650	2	F70974	6.50e+00
5	48	70.6	128	1	MBR85	1.06e+01
6	48	70.6	167	2	A37246	1.06e+01
7	48	70.6	171	1	MECZB	1.06e+01
8	48	70.6	197	1	MBHOB	1.06e+01
9	48	70.6	328	1	MBMSB	1.06e+01
10	48	70.6	564	2	S57124	1.06e+01
11	47	69.1	132	2	H70759	1.72e+01
12	47	69.1	543	2	S56830	1.72e+01
13	47	69.1	684	2	G70744	1.72e+01
14	47	69.1	687	2	A41905	1.72e+01
15	47	69.1	800	2	S53079	1.72e+01
16	47	69.1	2150	2	S71629	1.72e+01
17	46	67.6	236	2	S60941	2.76e+01
18	46	67.6	301	2	S13095	2.76e+01
19	46	67.6	345	1	VABPA7	2.76e+01
20	46	67.6	398	1	VBBPA7	2.76e+01
21	46	67.6	437	1	UC5459	2.76e+01
22	46	67.6	471	2	S01052	2.76e+01
23	46	67.6	471	2	S01037	2.76e+01

24	46	67.6	471	2	S08325	flavonol 3-O-glucosyl	2.76e+01
25	45	66.2	169	1	MBBOB	myelin basic protein	4.39e+01
26	45	66.2	171	1	MBGB	myelin basic protein	4.39e+01
27	45	66.2	210	2	B64108	L-fucose-phosphate	4.39e+01
28	45	66.2	239	2	S25204	srnx protein - Strept	4.39e+01
29	45	66.2	243	2	H69525	hydroxymethylpyrimidi	4.39e+01
30	45	66.2	338	2	A53066	CCAAT enhancer-binding	4.39e+01
31	45	66.2	381	2	G71906	probable transcription	4.39e+01
32	45	66.2	396	2	C49904	L-lactate dehydrogena	4.39e+01
33	45	66.2	416	2	H64984	hypothetical 43.4 kD	4.39e+01
34	45	66.2	485	2	B37855	glucose-6-phosphate 1	4.39e+01
35	45	66.2	547	2	E29504	mercury(II) reductase	4.39e+01
36	45	66.2	633	2	S49788	probable membrane pro	4.39e+01
37	45	66.2	657	2	S51387	dnAa-type molecular c	4.39e+01
38	45	66.2	662	2	H71676	DNA gyrase chain B (g	4.39e+01
39	45	66.2	730	2	S55180	phospholipase D homol	4.39e+01
40	45	66.2	761	2	C64813	ybnJ protein - Escher	4.39e+01
41	45	66.2	832	2	S71788	P/GAF protein - human	4.39e+01
42	45	66.2	1001	2	H64593	type III restriction	4.39e+01
43	44	64.7	370	2	S70157	CPSE protein, 40.6k -	6.93e+01
44	44	64.7	471	2	B38637	Ras inhibitor (clone	6.93e+01
45	44	64.7	619	2	A56519	CDC16 protein - human	6.93e+01

ALIGNMENTS

RESULT 1
 ENTRY F71520 #type complete
 TITLE hypothetical protein yprs - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 ORGANISM #formal_name Chlamydia trachomatis
 DATE 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 21-Nov-1998

ACCESSIONS F71520
 REFERENCE A71570
 #authors Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W.

#journal Science (1998) 282:754-759
 #title Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.

#cross-references MUID:9900809

#accession F71520

#status preliminary

#molecule_type DNA

#residues 1-377 #label ARN

#cross-references GB:AE001312; GB:AE001273; NID:g3328812; PID:g3328818

#experimental_source serotype D, strain UW-3/Cx

GENETICS

#gene

SUMMARY

Query Match 76.5%; Score 52; DB 2; Length 377;
 Best Local Similarity 58.3%; Pred. No. 1.43e+00;
 Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 324 ASYLSSPSVED 335

QY 1 ASYLSTSSSLDN 12

RESULT 2

ENTRY C71439 #type complete

TITLE hypothetical protein - Arabidopsis thaliana

ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear cress

DATE 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

ACCESSIONS C71439

REFERENCE A71400

#authors Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirke, W.; Van Staveren, M.;

Stiekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel, K.; Murphy, G.; Piffenelli, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzneger, T.; Pohl, T.M.; Terry, N.; Giesen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.; Lecharny, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.; Kavanagh, T.; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puldomenech, P.; Douka, A.; Vouklatou, E.; Milton, D.; Hatzopoulos, P.; Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhof, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansoorge, W.; Cooke, R.; Berger, C.; Delenay, M.; Voet, M.; Voickaert, G.; Mewes, H.W.; Klosterman, S.; Schueller, C.; Chaiwatzis, N.

Nature (1998) 391:485-488

Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana.

#journal #title Nature (1998) 391:485-488

#cross-references GB:297342; NID:g2245031; PID:g2245065

#accession C71439

#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-471 #label BEV

GENETICS

#cross-references GB:297342; NID:g2245031; PID:g2245065

SUMMARY

#map_position 4COP9-4G3845

#length 471 #molecular-weight 52785 #checksum 7455

Query Match 75.0%; Score 51; DB 2; Length 471; Best Local Similarity 63.6%; Pred. No. 2.39e+00; Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 19 AGYLTSSSD 29 1:||||| 11 1 ASYLTSSSD 11

QY 1 ASYLTSSSD 11

RESULT 3

ENTRY D70108 #type complete

TITLE conserved hypothetical protein BB0068 - Lyme disease

ORGANISM #formal_name Borrelia burgdorferi #common_name Lyme disease

DATE 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Jun-1998

ACCESSIONS D70108

REFERENCE A70100

#authors Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodeon, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weiman, J.; Uitterlbeck, T.; McInerney, L.; McDonald, L.; Artach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.

#journal #title Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

#cross-references NID:98065943

#accession D70108

#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-293 #label KLE

GENETICS

#cross-references GB:AE001120; GB:AE000783; NID:g2687951; PID:g2687956; TIGR:BB0068

SUMMARY

#experimental_source strain B31

#length 293 #molecular-weight 33278 #checksum 5223

Query Match 73.5%; Score 50; DB 2; Length 293; Best Local Similarity 60.0%; Pred. No. 3.95e+00; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 198 AYLTSPNSLE 207 :|||||:

QY 2 SYLTSSSD 11

RESULT 4

ENTRY F70974 #type complete

TITLE probable acral protein - Mycobacterium tuberculosis (strain H37RV)

ORGANISM #formal_name Mycobacterium tuberculosis

DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

ACCESSIONS F70974

REFERENCE A70500

#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.

Nature (1998) 393:537-544

Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.

#journal #title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.

#cross-references NID:98295987

#accession F70974

#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-650 #label COL

GENETICS

#cross-references GB:AL009198; GB:AL123456; NID:g3242262; PID:el202309; PID:g261670

SUMMARY

#experimental_source strain H37RV

#length 650 #molecular-weight 70939 #checksum 8551

Query Match 72.1%; Score 49; DB 2; Length 650; Best Local Similarity 54.5%; Pred. No. 6.50e+00; Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 501 SYLTPTKALD 511 :|||||:

QY 1 ASYLTSSSD 11

RESULT 5

ENTRY MBRTS #type complete

TITLE myelin basic protein S - rat

ALTERNATE_NAMES small myelin basic protein

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 24-Apr-1984 #sequence_revision 08-Feb-1996 #text_change 05-Sep-1997

ACCESSIONS B24351

REFERENCE A24351

#authors Schach, M.; Budzinski, R.M.; Stoffel, W.

#journal #title Biol. Chem. Hoppe-Seyler (1986) 367:825-834

#title Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the two genes during myelination.

#cross-references NID:87026249

#accession B24351

#molecule_type mRNA

#residues 1-128 #label SCH

REFERENCE A90275

#authors Dunkley, P.R.; Carnegle, P.R.

#journal #title Biochem. J. (1974) 141:243-255

#title Amino acid sequence of the smaller basic protein from rat brain myelin.

#cross-references MUID:75127359
#accession A90275
##molecule-type protein
##residues 2-128 #label DUN
#note at position 105, arginine, monomethylarginine, and dimethylarginine occur in the ratio 4:4:1
#note rats have two myelin basic proteins; the smaller one, shown above, is missing 40 residues (following residue 114 or 115) with respect to the larger ones from other species

REFERENCE
#authors A94243
McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKneally, S.; Shapiro, R.
#journal Science (1973) 179:478-480
#title Experimental allergic encephalomyelitis in the rat: response to encephalitogenic proteins and peptides.
#cross-references MUID:73180720
#accession A94243
##molecule-type protein
##residues 46-86 #label MCF
#note the sequence reported for this encephalitogenic peptide differs from that shown by a transposition of residues 47 and 48; two other differences are printing errors

REFERENCE
#authors A21062
Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.E.
#journal Cell (1983) 34:799-806
#title Characterization of cloned cDNA representing rat myelin basic protein: absence of expression in brain of shiverer mutant mice.
#cross-references MUID:84026484
#accession A21062
##molecule-type mRNA
##residues 1-124, 'I', 126-128 #label ROA
#note Experimental source strain Sprague-Dawley
#classification superfamily myelin basic protein
#keywords alternative splicing; blocked amino end; experimental autoimmune encephalomyelitis; methylated amino acid; myelin

FEATURE
2-128 #product myelin basic protein S #status experimental
2 #label MATV
#modified.site blocked amino end (Ala) (in mature form)
105 #modified.site omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (NR9) (partial) #status experimental

SUMMARY
#length 128 #molecular-weight 14211 #checksum 2812

Query Match
Best Local Similarity 41.7%; Pred. No. 1.06e+01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 13 SKYLASTMDH 24
: ||:|:|:|:
QY 1 ASYLSTSSSLDN 12

RESULT 6
ENTRY A37246 #type complete
TITLE myelin basic protein - guinea pig
ALTERNATE_NAMES myelin A1 protein
ORGANISM #formal_name Cavia porcellus #common_name guinea pig
DATE 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 07-Oct-1994
ACCESSIONS A37246; C92087; A03140
REFERENCE A37246
#authors Delbier, G.E.; Martenson, R.E.; Krutzsch, H.C.; Klee, M.W.
#journal J. Neurochem. (1984) 43:100-105
#title Sequence of guinea pig myelin basic protein.
#cross-references MUID:84215086
#accession A37246
#status Preliminary
#molecule-type protein

#residues 1-167 #label DEI
REFERENCE A92087
#authors Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
#journal J. Biol. Chem. (1971) 246:4630-4640
#title Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.

#accession C92087
##molecule-type protein
##residues 45-87 #label SHN
#classification superfamily myelin basic protein
#keywords myelin
SUMMARY #length 167 #molecular-weight 18213 #checksum 1628

Query Match
Best Local Similarity 41.7%; Pred. No. 1.06e+01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 12 SKYLASTMDH 23
: ||:|:|:|:
QY 1 ASYLSTSSSLDN 12

RESULT 7
ENTRY M8CZB #type complete
TITLE myelin basic protein - chimpanzee (tentative sequence)
ALTERNATE_NAMES MBP
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 06-Sep-1996
ACCESSIONS A03139
REFERENCE A03139
#authors Westall, F.C.; Thompson, M.; Kalter, S.S.
#journal Life Sci. (1975) 17:219-223
#title The proposed sequence of the encephalitogenic protein from chimpanzee brain.
#cross-references MUID:76009821
#accession A03139
##molecule-type protein
##residues 1-171 #label WBS
#note This protein may function in maintaining the proper structure of myelin.

CLASSIFICATION #superfamily myelin basic protein
KEYWORDS blocked amino end; methylated amino acid; myelin; structural protein

FEATURE
1 #modified.site blocked amino end (Ala) (probably acetylated) #status experimental
107 #modified.site omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (NR9) #status experimental

SUMMARY
#length 171 #molecular-weight 18560 #checksum 7537

Query Match
Best Local Similarity 41.7%; Pred. No. 1.06e+01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 12 SKYLASTMDH 23
: ||:|:|:|:
QY 1 ASYLSTSSSLDN 12

RESULT 8
ENTRY MBHDB #type complete
TITLE myelin basic protein - human
CONTAINS myelin basic protein precursor, 17-2K splice form; myelin basic protein precursor, 18.5K splice form; myelin basic protein precursor, 20.2K splice form; myelin basic protein precursor, 21.5K splice form
ORGANISM #formal_name Homo sapiens #common_name man
DATE 18-Dec-1981 #sequence_revision 25-Aug-1995 #text_change 20-Mar-1998
ACCESSIONS S10482; A94106; B94106; JH0802; A60862; A61420; A33273; I54219; I56567; I73634; I56565; S66383; A03139;

```

REFERENCE      A24153
#authors       S10482
#journal       Streicher, R.; Stoffel, W.
#title         Biol. Chem. Hoppe-Seyler (1969) 370:503-510
               The organization of the human myelin basic protein gene.
               Comparison with the mouse gene.
#cross-references MUID:89302693
#accession     S10482
               translation not shown
               ##status
               ##molecule_type DNA
               ##residues      1-197 ##label STR
REFERENCE      #cross-references EMBL:X17286; NID:g34490; PID:e221974; PID:g1184244
#authors       A94106
#journal       Kamholz, J.; De Ferra, F.; Puckett, C.; Lazzarini, R.
#title         Proc. Natl. Acad. Sci. U.S.A. (1986) 83:4962-4966
               Identification of three forms of human myelin basic protein
               by cDNA cloning.
#cross-references MUID:86259714
#accession     A94106
               ##molecule_type mRNA
               ##residues      1-59,86-197 ##label KAM
               ##cross-references GB:M1357; NID:g187408; PID:g307160
               ##note          18..5K splice form
REFERENCE      #accession     B94106
               ##molecule_type mRNA
               ##residues      1-197 ##label KA2
               ##note          antibody to the exon 2 encoded sequence detected a 21.5K
               splice form
               ##note          a 17.2K splice form is also described
               ##note          antibody to the exon 2 encoded sequence detected a 21.5K
               splice form; a 17.2K splice form is also described
REFERENCE      A90256
#authors       Carnegele, P.R.
#journal       Biochem. J. (1971) 123:57-67
#title         Amino acid sequence of the encephalitogenic basic protein
               from human myelin.
#cross-references MUID:72066400
#accession     A90256
               ##molecule_type protein
               ##residues      2-59,86-197 ##label CAR
REFERENCE      JH0802
#authors       Proost, P.; Van Damme, J.; Opdenkker, G.
#journal       Blochem. Biophys. Res. Commun. (1993) 192:1175-1181
#title         Leukocyte gelatinase B cleavage releases encephalitogens from
               human myelin basic protein.
#cross-references MUID:93282820
#accession     JH0802
               ##molecule_type protein
               ##residues      2-59,86-197 ##label PRO
               ##experimental_source brain
REFERENCE      AG0862
#authors       Scoble, H.A.; Whitaker, J.N.; Blemann, K.
#journal       J. Neurochem. (1986) 47:614-616
#title         Analysis of the primary sequence of human myelin basic
               protein peptides 1-44 and 90-170 by fast atom bombardment
               mass spectrometry.
#accession     AG0862
               ##molecule_type protein
               ##residues      2-45,117-197 ##label SCO
               ##note          evidence for acetylated amino end
REFERENCE      A61420
#authors       Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Blemann, K.
#journal       J. Biol. Chem. (1984) 259:5028-5031
#title         Amino acid sequence of human myelin basic protein peptide
               45-89 as determined by mass spectrometry.
#accession     A61420
               ##molecule_type protein
               ##residues      46-59,86-116 ##label GIB
REFERENCE      A33273
#authors       Wood, D.D.; Moscarello, M.A.
#journal       J. Biol. Chem. (1989) 264:5121-5127
#title         The isolation, characterization, and lipid-aggregating
               properties of a citrullin containing myelin basic protein.

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```

#cross-references MUID:89174797
#accession A33273
#molecule_type protein
#residues 15-25,'X',27-31,'X',33-59,86-148,'X',150-156,'X',
158-185,'X',187-196,'X' ##label WOO
form C-8: residues designated 'X' were determined as
citruiline

REFERENCE
#authors A90257
#journal Balclwin, G.S.; Carnegie, P.R.
#journal Blochem. J. (1971) 123:69-74
#title Isolation and partial characterization of methylated
arginines from the encephalitogenic basic protein of
myelin.

#cross-references MUID:72066401
#contents annotation; methylarginine
#note Arg-134 may be unmodified, monomethylarginine, or
dimethylarginine in the approximate ratio of 1:6:10
A92806

REFERENCE
#authors Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.
#journal J. Immunol. (1971) 105:1223-1230
#cross-references MUID:71088405
#contents annotation
#note a region including residues 139-149 induces experimental
autoimmune encephalomyelitis
154219

REFERENCE
#authors Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood,
L.E.; Prusiner, S.B.
#journal Genomics (1990) 6:16-22
#title Repetitive DNA (TGGA)n 5' to the human myelin basic protein
gene: a new form of oligonucleotide repetitive sequence
showing length polymorphism.
#cross-references MUID:90152679
#accession 154219
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type DNA
#residues 1-59 ##label RES
#cross-references GB:M63599; NID:9187402; PID:9187403
156567

REFERENCE
#authors Roth, H.J.; Kronquist, K.E.; Kerlero de Rosbo, N.; Crandall,
B.F.; Campanoni, A.T.
#journal J. Neurosci. Res. (1987) 17:321-328
#title Evidence for the expression of four myelin basic protein
variants in the developing human spinal cord through cDNA
cloning.
#cross-references MUID:87311781
#accession 156567
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-132,144-197 ##label RE2
#cross-references GB:M30516; NID:9187410; PID:9307161
173634

#accession
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-197 ##label RE3
#cross-references GB:M30515; NID:9187412; PID:9307162
156565

REFERENCE
#authors Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.;
Campanoni, A.T.
#journal J. Neurosci. Res. (1986) 16:227-238
#title Isolation and characterization of a cDNA coding for a novel
human 17.3k myelin basic protein (MBP) variant.
#cross-references MUID:86308101
#accession 156565
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-59,86-133,145-197 ##label RE4
#cross-references GB:M30047; NID:9187400; PID:9307159
566383

REFERENCE
#authors Boullas, C.; Pang, H.; Mastromarini, F.; Moscarello, M.A.
#journal Arch. Biochem. Biophys. (1995) 322:174-182
#title The isolation and characterization of four myelin basic
proteins from the unbound fraction during CMS2
chromatography.

```

#cross-references MUID:96004793
 #accession S66383
 #molecule_type protein
 #residues 23-25,'X',27-39 #label BOU
 COMMENT Four alternatively spliced forms of myelin basic protein have been observed, 21.5K, 20.2K, the most abundant 18.5K, and 17.2K.

GENETICS
 #gene GDB:MBP
 #cross-references GDB:119379; OMIM:159430
 #map-position 18q22-18qter
 #introns 59/3; 85/3; 120/3; 132/3; 143/3; 183/3

FUNCTION
 #description probably helps maintain myelin structure
 #superfamily myelin basic protein
 #acetylated amino end; alternative splicing; citrulline; experimental autoimmune encephalomyelitis; methylated amino acid; myelin; structural protein

KEYWORDS

FEATURE
 2-197
 2-132,144-197
 2-59,86-197
 2-59,86-132,144-197
 26,32,149,157,186,197
 134

SUMMARY
 #length 197 #molecular-weight 21493 #checksum 4642

Query Match 70.6%; Score 48; DB 1; Length 197;
 Best Local Similarity 41.7%; Pred. No. 1.06e+01;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 13 SKYLA7ASTMDH 24
 : |||:|:|:
 0Y 1 ASYLSTSSSLDN 12

RESULT 9
 ENTRY MBMSB #type complete
 TITLE golli-myelin basic protein precursor - mouse
 ALTERNATE_NAMES golli-emb protein; MBP
 CONTAINS myelin basic protein
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 17-Mar-1987 #sequence_revision 07-Oct-1994 #text_change 20-Feb-1998
 A45421; A545421; A90875; A90867; A26591; B26591; A60920; A46407; I58996; I54033; I53256; A03141; A24772; S5122 A45421
 Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry, C.F.; Handley, V.W.; Newman, S.L.; Garbay, B.; Kitamura, K.
 J. Biol. Chem. (1993) 268:4930-4938
 Structure and developmental regulation of Golli-emb, a 105-kilobase gene that encompasses the myelin basic protein gene and is expressed in cells in the oligodendrocyte lineage in the brain.

#cross-references MUID:93186801
 #accession A45421
 #molecule_type mRNA
 #residues 1-190;217-276;316-328 #label CAM1
 #cross-references GB:U07507; NID:g193584
 #experimental_source clone J37
 #note sequence extracted from NCBI backbone (NCBIN:126696) and modified

#accession B45421
 #status Preliminary
 #molecule_type mRNA
 #residues 1-191,'SSEP' #label CAM2
 #cross-references GB:U07508; NID:g193586; PID:g193587
 #experimental_source clone BG21
 #note sequence extracted from NCBI backbone (NCBIN:126700, NCBI:P:126715)

REFERENCE
 #authors A90875
 de Ferreira, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molinaux, S.; Lazzarini, R.A.
 Cell (1985) 43:721-727
 #journal Cell (1985) 43:721-727
 #title Alternative splicing accounts for the four forms of myelin basic protein.
 #cross-references MUID:86079555
 #accession A90875
 #molecule_type mRNA
 #residues 134-328 #label DEF
 #cross-references GB:U0404; GB:M1669; NID:g199060; PID:g387419
 #experimental_source 21.5K

REFERENCE
 #authors A90867
 Takahashi, N.; Roach, A.; Teplow, D.B.; Prusiner, S.B.; Hood, L.
 Cell (1985) 42:139-148
 #journal Cell (1985) 42:139-148
 #title Cloning and characterization of the myelin basic protein gene from mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate use of exons.
 #cross-references MUID:85254913
 #accession A90867
 #molecule_type DNA
 #residues 134-190;217-328 #label TAK
 #cross-references GB:M1533; NID:g199044; PID:g387414
 #experimental_source 18.5K

REFERENCE
 #authors A94188
 Newman, S.; Kitamura, K.; Campagnoni, A.T.
 Proc. Natl. Acad. Sci. U.S.A. (1987) 84:886-890
 #journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:886-890
 #title Identification of a cDNA coding for a fifth form of myelin basic protein in mouse.
 #cross-references MUID:87118269
 #accession A26591
 #molecule_type mRNA
 #residues 134-274;316-328 #label NEW1
 #cross-references GB:M15062; NID:g199049
 #experimental_source clone M722; splice form 17.2K

#accession B26591
 #molecule_type mRNA
 #residues 134-190;217-263;275-328 #label NEW2
 #cross-references GB:M15062; NID:g199050
 #experimental_source clone M78; splice form 17.24K

REFERENCE
 #authors A60920
 Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdil, J.M.; Mohandas, T.; Handley, V.W.; Campagnoni, A.T.
 J. Neurochem. (1990) 54:2032-2041
 #journal J. Neurochem. (1990) 54:2032-2041
 #title Expression of a novel transcript of the myelin basic protein gene.
 #accession A60920
 #status translation not shown
 #molecule_type mRNA
 #residues 134-190;217-274;316-328 #label KIT
 #experimental_source M41; splice form 14K

REFERENCE
 #authors I48407
 Grima, B.; Zelenika, D.; Pessac, B.
 J. Neurochem. (1992) 59:2318-2333
 #journal J. Neurochem. (1992) 59:2318-2333
 #title A novel transcript overlapping the myelin basic protein gene.
 #cross-references MUID:93057537
 #accession I48407
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-191,'SSEP' #label GRI
 #cross-references EMBL:X67319; NID:g51332; PID:g51333
 #note submitted to the EMBL Data Library, July 1992

REFERENCE
 #authors I58996
 Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.;

#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:18-22
 #title Characterization of mouse myelin basic protein messenger RNAs with a myelin basic protein cDNA clone.
 #cross-references M3119431
 #accession 158996
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule-type mRNA
 #residues 219-248 #label ZEL
 #cross-references GB:K00989; NID:g199037; PID:g554195
 #accession 154033
 #authors Mura, M.; Tamura, T.
 #journal Gene (1989) 75:31-38
 #title The promoter elements of the mouse myelin basic protein gene function efficiently in NG108-15 neuronal/glia cells.
 #cross-references M3119431
 #accession 154033
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule-type DNA
 #residues 134-157 #label MTU
 #cross-references GB:M24410; NID:g199052; PID:g554196
 #accession 153256
 #authors Okano, H.; Tamura, T.; Mura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.
 #journal EMBO J. (1988) 7:77-83
 #title Gene organization and transcription of duplicated MBP genes of myelin deficient (sh1-mld) mutant mouse.
 #cross-references M3119431
 #accession 153256
 #status translation not shown; translated from GB/EMBL/DBJ
 #molecule-type DNA
 #residues 217-229, 'HN', 232-250 #label OKA
 #cross-references GB:M36275; NID:g199069; PID:g293725
 #note hypothetical translation of the reversed and complementary sequence to that shown in Figure 7
 #comment Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and 14K.
 #GENETICS
 #gene Goll1-mbp; sh1-mld
 #introns 190/3; 250/3; 262/3; 273/3; 314/3
 #FUNCTION
 #description probably helps maintain myelin structure
 #CLASSIFICATION
 #superfamily myelin basic protein
 #KEYWORDS
 #FEATURE
 1-190, 217-276,
 316-328
 #product Goll1-mbp protein (clone J37) #status predicted
 134-328
 #product myelin basic protein, splice form 21.5K #status predicted
 134-274, 316-328
 #product myelin basic protein, splice form 17K-a #status predicted
 134-190, 217-328
 #product myelin basic protein, splice form 18.5K #status predicted
 134-190, 217-263,
 275-328
 #product myelin basic protein, splice form 17K-b #status predicted
 134-190, 217-274,
 316-328
 #product myelin basic protein, splice form 14K #status predicted
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 Best Local Similarity 41.7%; Pred. No. 1.06e+01;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 Db 144 SKYLASTASMDH 155
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 QY 1 ASYSTSSSDN 12
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 ENTRY S57124 #type complete

#TITLE Crp synthase (EC 6.3.4.2) URA8 - yeast (Saccharomyces cerevisiae)
 #ALTERNATE_NAMES protein J1962; protein YJR103w
 #ORGANISM #formal_name Saccharomyces cerevisiae
 #DATE 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 06-Feb-1998
 #ACCESSIONS S57124; S42580; S40000
 #REFERENCE S57111
 #authors Ramirez, R., M.; Kirchner, L.; Hollenberg, C.P.
 #submission submitted to the Protein Sequence Database, September 1995
 #accession S57124
 #molecule-type DNA
 #residues 1-564 #label RAM
 #cross-references EMBL:249603; NID:g1015809; PID:g1015810; MIPS:YJR103w
 #accession S42580
 #authors Orler, K.; Katsouras, O.; Adeline, M.T.; Yang, W.L.; Carman, G.M.; Lacroute, F.
 #journal Mol. Gen. Genet. (1994) 242:431-439
 #title Use of synthetic lethal mutants to clone and characterize a novel Crp synthase gene in Saccharomyces cerevisiae.
 #cross-references M3119431
 #accession S42580
 #molecule-type DNA
 #residues 1-95, 'QL', 98-203, 'L', 205-439, 'PSSHIA', 447-556, 'QLRHCET', 564, 'DINSEGENE', #label OZI
 #cross-references EMBL:X68196; NID:g440162; PID:g440163
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 #gene SGD:URA8
 #cross-references SGD:S0003864; MIPS:YJR103w
 #map_position 10R
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 #superfamily Crp synthase
 #KEYWORDS
 #length 564 #molecular-weight 63056 #checksum 5924
 #SUMMARY
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 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Db 318 SYLSTVRSSEH 328
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 QY 2 SYLSTSSSDN 12
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 ENTRY H70759 #type complete
 #TITLE hypothetical protein Rv2010 - Mycobacterium tuberculosis (strain H37RV)
 #ORGANISM #formal_name Mycobacterium tuberculosis
 #DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
 #ACCESSIONS H70759
 #REFERENCE A70500
 #authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garler, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, S.; Squares, S.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
 #journal Nature (1998) 393:537-544
 #title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
 #cross-references M3119431
 #accession H70759
 #status preliminary; nucleic acid sequence not shown; translation not shown
 #molecule-type DNA
 #residues 1-132 #label COL
 #cross-references GB:274025; GB:AL123456; NID:g3261586; PID:e248788; PID:g1403443

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##residues 1-277,'G',279-498,'R',500-568,'P',570-708,'QVALDKS',716,
'AL',#label STR
##cross-references EMBL:M17143
##note the authors translated the codon AGA for residue 297 as
Gly

GENETICS
#gene SGD:PET111
##cross-references SGD:S0004870; MIPS:YMR257C
#map_position 13R
KEYWORDS mitochondrion; transmembrane protein
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127-143 #domain transmembrane #status predicted #label TM1\
547-563 #domain transmembrane #status predicted #label TM2
SUMMARY #length 800 #molecular-weight 94522 #checksum 1456

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Best Local Similarity 50.08; Pred. No. 1.72e+01;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

726 PAYSTRASIDN 737
:::|::|::|
QY 1 ASYLSRSSIDN 12

Search completed: Thu Sep 2 12:23:55 1999
Job time : 21 secs.

WATERMAN

(TM)

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 12:25:22 1999; Maspar time 1.39 Seconds
87.949 Million cell updates/sec
Abular output not generated.

Title: >US-08-599-226-27
Description: (1-12) from US08599226.pep
Perfect Score: 68
Sequence: 1 ASYLSTSSSLDN 12

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCRT9_COMB 4:backfiles1

Statistics: Mean 15.565; Variance 46.626; Scale 0.334

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	50	73.5	426	3	PCR-US95-1	Sequence 2, Applicatio
2	50	72.5	426	1	US-08-336-	Sequence 2, Applicatio
3	49	72.1	384	1	US-08-457-	Sequence 5, Applicatio
4	48	70.6	20	2	US-08-468-	Sequence 2, Applicatio
5	48	70.6	21	2	US-08-787-	Sequence 33, Applicati
6	48	70.6	170	2	US-08-327-	Sequence 1, Applicatio
7	47	69.1	168	4	5194425-4	Patent No. 5194425.
8	46	67.6	314	4	US-08-040-	Sequence 2, Applicatio
9	45	66.2	170	4	5194425-3	Patent No. 5194425.
10	45	66.2	170	2	US-08-227-	Sequence 1, Applicatio
11	44	64.7	209	2	US-08-771-	Sequence 2, Applicatio
12	44	64.7	464	1	PCR-US91-0	Sequence 16, Applicati
13	44	64.7	464	1	US-07-688-	Sequence 16, Applicati
14	43	63.2	213	2	US-08-761-	Sequence 5, Applicatio
15	43	63.2	213	2	US-08-761-	Sequence 5, Applicatio
16	43	63.2	213	1	US-08-459-	Sequence 3, Applicatio
17	43	63.2	213	1	US-08-460-	Sequence 2, Applicatio
18	43	63.2	213	1	US-08-287-	Sequence 2, Applicatio
19	43	63.2	213	2	US-08-761-	Sequence 10, Applicati
20	43	63.2	213	1	US-08-459-	Sequence 2, Applicatio
21	43	63.2	213	3	PCR-US93-0	Sequence 2, Applicatio
22	43	63.2	238	1	US-08-928-	Sequence 5, Applicatio
23	43	63.2	240	1	US-08-261-	Sequence 80, Applicati

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25	43	63.2	345	2	US-08-446-	Sequence 40, Applicati	1.85e+02
26	43	63.2	1255	1	US-08-467-	Sequence 68, Applicati	1.85e+02
27	43	63.2	1255	2	US-08-466-	Sequence 68, Applicati	1.85e+02
28	43	63.2	1255	2	US-08-625-	Sequence 8, Applicatio	1.85e+02
29	43	63.2	1255	2	US-08-484-	Sequence 2, Applicatio	1.85e+02
30	43	63.2	1255	2	US-08-414-	Sequence 68, Applicati	1.85e+02
31	43	63.2	1255	2	US-08-486-	Sequence 68, Applicati	1.85e+02
32	43	63.2	1255	2	US-08-356-	Sequence 2, Applicatio	1.85e+02
33	42	61.8	158	2	US-08-828-	Sequence 3, Applicatio	2.36e+02
34	42	61.8	159	2	US-08-828-	Sequence 1, Applicatio	2.36e+02
35	42	61.8	170	4	5468481-3	Patent No. 5468481.	2.36e+02
36	42	61.8	238	1	US-08-588-	Sequence 2, Applicatio	2.36e+02
37	42	61.8	238	1	US-08-452-	Sequence 1, Applicatio	2.36e+02
38	42	61.8	238	3	PCR-US95-1	Sequence 2, Applicatio	2.36e+02
39	42	61.8	238	2	US-08-753-	Sequence 2, Applicatio	2.36e+02
40	42	61.8	238	1	US-08-337-	Sequence 2, Applicatio	2.36e+02
41	42	61.8	312	1	US-08-414-	Sequence 2, Applicatio	2.36e+02
42	42	61.8	326	4	5395759-2	Patent No. 5395759.	2.36e+02
43	42	61.8	822	2	US-08-222-	Sequence 7, Applicatio	2.36e+02
44	42	61.8	3666	2	US-08-222-	Sequence 12, Applicati	2.36e+02
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ALIGNMENTS

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XX				
DT				
XX				
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CC	Sequence 2, Application PC/TUS9513795			
CC	GENERAL INFORMATION:			
CC	APPLICANT: HOLLIS, GREGORY F.			
CC	TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS			
CC	NUMBER OF SEQUENCES: 4			
CC	CORRESPONDENCE ADDRESSES:			
CC	ADDRESS: CHRISTINE E. CARTY			
CC	STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000			
CC	CITY: RAHWAY			
CC	STATE: NEW JERSEY			
CC	COUNTRY: USA			
CC	ZIP: 07065-0907			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Patentin Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: PCT/US95/13795			
CC	FILING DATE:			
CC	CLASSIFICATION:			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: CARTY, CHRISTINE E.			
CC	REGISTRATION NUMBER: 36,099			
CC	REFERENCE/DOCKET NUMBER: 19211Y			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (908) 594-6734			
CC	TELEFAX: (908) 594-4720			
CC	INFORMATION FOR SEQ ID NO: 2:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 426 amino acids			
CC	TYPE: amino acid			
CC	STRANDEDNESS: single			
CC	TOPOLOGY: linear			
CC	MOLECULE TYPE: protein			
CC	SEQUENCE 426 AA; 47234 MW; 1032622 CN;			

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DB 214 TSYLSPSPSLD 224
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QY 1 ASYLSTSSSLD 11

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DE
Sequence 2, Application US/08336583
Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLDIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 426 AA: 4/234 MW: 1032622 CN;

Query Match 73.5%; Score 50; DB 1; Length 426;
Best Local Similarity 63.6%; Pred. No. 3.21e+01;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 214 TSYLSPSPSLD 224
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QY 1 ASYLSTSSSLD 11

RESULT 3
ID US-08-457-245-5 STANDARD; PRT: 384 AA.
AC xxxxxx
DT
DE

DE Sequence 5, Application US/08457245
XX Sequence 5, Application US/08457245
CC Patent No. 5573915
CC GENERAL INFORMATION:
CC APPLICANT: BARRY III, Clifton E.
CC APPLICANT: YUAN, Ying
CC TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA INVOLVED
CC TITLE OF INVENTION: IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOLIC ACIDS IN
CC TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: Stewart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/457,245
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Chambers, Guy W.
CC REGISTRATION NUMBER: 30,617
CC REFERENCE/DOCKET NUMBER: 15280-216000
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 384 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: ORF2 protein
CC SEQUENCE 384 AA: 41963 MW: 701271 CN;

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Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 235 SSYLPTRALD 245
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QY 1 ASYLSTSSSLD 11

RESULT 4
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AC xxxxxx
DT
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Sequence 2, Application US/08468540B
Sequence 2, Application US/08468540B
Patent No. 5858980
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Hailer, David
APPLICANT: Miller, Ariel
APPLICANT: Al-Sabbagh, Ahmad
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue

CC	CITY:	New York
CC	STATE:	NY
CC	COUNTRY:	USA
CC	ZIP:	10022
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Diskette
CC	OPERATING SYSTEM:	DOS
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	
CC	FILING DATE:	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Jacobs, Seth H
CC	REGISTRATION NUMBER:	32,140
CC	REFERENCE/DOCKET NUMBER:	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	212-527-7700
CC	TELEFAX:	
CC	TELEX:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	20 amino acids
CC	TYPE:	amino acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
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CC	Best Local Similarity	41.7%; Pred. NO. 5,34e+01;
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AC		
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XX		
Sequence 33, Application US/08787547		
Sequence No. 5783567		
Patent No. 5783567		
GENERAL INFORMATION:		
APPLICANT: Hedley, Mary Lynne		
APPLICANT: Curley, Joanne M.		
APPLICANT: Langer, Robert S.		
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY		
TITLE OF INVENTION: OF NUCLEIC ACID		
NUMBER OF SEQUENCES: 107		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: Fish & Richardson, P.C.		
STREET: 225 Franklin Street		
CITY: Boston		
STATE: MA		
COUNTRY: US		
ZIP: 02110-2804		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Diskette		
COMPUTER: IBM Compatible		
OPERATING SYSTEM: Windows95		
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CURRENT APPLICATION DATA:		

CC APPLICATION NUMBER: US/08/787,547
CC FILING DATE: 22-JAN-1997
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fraser, Janis K.
CC REGISTRATION NUMBER: 34,819
CC REFERENCE/DOCKET NUMBER: 08191/003001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617-542-5070
CC TELEFAX: 617-542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 33:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 21 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 21 AA; 2312 MW; 2012 CN;

Query Match 70.6%; Score 48; DB 2; Length 21;
Best Local Similarity 41.7%; Pred. No. 5,34e+01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 6 SKYLATASTMDH 17
 : ||::||::|
Qy 1 ASYLISTSSLDN 12

RESULT 6
ID US-08-327-357A-1 STANDARD; PRT; 170 AA.
AC xxxxxx
XX
DT
XX
DE Sequence 1, Application US/08327357A
XX
CC Sequence 1, Application US/08327357A
CC Patent No. 5817629
CC GENERAL INFORMATION:
CC APPLICANT: WARREN, Kenneth G.
CC APPLICANT: CATZ, Ingrid
CC TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
CC TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN IN
CC TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
CC NUMBER OF SEQUENCES: 1
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti
CC STREET: 1201 New York Avenue, N.W., Suite 1000
CC City: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/327,357A
CC FILING DATE: 21-OCT-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/798,099
CC FILING DATE: 27-NOV-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: CA 2,053,799-0
CC FILING DATE: 22-OCT-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.

CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 27052-115469
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 170 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC IMMEDIATE SOURCE:
CC CLONE: human myelin basic protein
SQ SEQUENCE 170 AA; 18459 MW; 143982 CN;

Query Match 70.6%; Score 48; DB 2; Length 170;
Best Local Similarity 41.7%; Pred. No. 5.34e+01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
DB 12 SKYLASTMDH 23
QY 1 ASYLSTSSLDN 12

RESULT 7
ID 5194425-4 STANDARD; PRT; 182 AA.
AC xxxxxx
DT 01-JAN-1900
DE Patent No. 5194425.
XX
XX
CC Patent No. 5194425
CC APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
CC BRIAN R.
CC TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
CC AMELIORATING AUTOIMMUNITY
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/367,751
CC FILING DATE: 21-JUN-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 210,594
CC FILING DATE: 23-JUN-1988
CC SEQ ID NO:4:
SQ SEQUENCE 168
LENGTH: 168
19707 MW; 182144 CN;

Query Match 69.1%; Score 47; DB 4; Length 168;
Best Local Similarity 50.0%; Pred. No. 6.87e+01;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
DB 12 YLASTMDH 21
QY 3 YLSTSSLDN 12

RESULT 8
ID US-08-040-753-2 STANDARD; PRT; 314 AA.
AC xxxxxx
DT
XX
XX
DE Sequence 2, Application US/08040753
XX
XX
CC Sequence 2, Application US/08040753
CC Patent No. 5464745
CC GENERAL INFORMATION:

CC APPLICANT: Merendorf, Robert
CC APPLICANT: Garber, Richard
CC APPLICANT: No. 5464745, Robert
CC APPLICANT: Hammer, Beth
CC TITLE OF INVENTION: Protein Ligand Binding
CC TITLE OF INVENTION: Region Mapping System
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Quarles and Brady
CC STREET: 1 South Plinckney St., Box 2113
CC CITY: Madison
CC STATE: WI
CC COUNTRY: USA
CC ZIP: 53701-2113
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PC-DOS/MS-DOS
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/040,753
CC FILING DATE: 19930331
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seay, Nicholas J
CC REGISTRATION NUMBER: 27386
CC REFERENCE/DOCKET NUMBER: 70-399-9001-1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 608-251-5000
CC TELEFAX: 608-251-9166
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 314 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 314 AA; 33533 MW; 495848 CN;

Query Match 67.6%; Score 46; DB 1; Length 314;
Best Local Similarity 41.7%; Pred. No. 8.82e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
DB 71 AYLAAGENDLD 82
QY 1 ASYLSTSSLDN 12

RESULT 9
ID 5194425-3 STANDARD; PRT; 184 AA.
AC xxxxxx
DT 01-JAN-1900
DE Patent No. 5194425.
XX
XX
CC Patent No. 5194425
CC APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
CC BRIAN R.
CC TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
CC AMELIORATING AUTOIMMUNITY
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/367,751
CC FILING DATE: 21-JUN-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 210,594
CC FILING DATE: 23-JUN-1988
CC SEQ ID NO:3:
SQ SEQUENCE 184 AA; 19952 MW; 183015 CN;

RESULT 11

CC GENERAL INFORMATION:
CC
CC APPLICANT: Wiggler, Michael H.
CC

CC APPLICATION NUMBER: US/08/761,258
CC FILING DATE:
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meigs, J. Timothy
CC REGISTRATION NUMBER: 38,241
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (919) 541-8587
CC TELEFAX: (919) 541-8689
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 213 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 213 AA; 23364 MW; 236956 CN;

Query Match 63.2%; Score 43; DB 2; Length 213;
Best Local Similarity 33.3%; Pred. No. 1.85e+02;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

DB 99 AGYLFRGAGLNE 110
|||:||||:
QY 1 ASYLTSSSLDN 12

RESULT 15
ID US-08-761-258-3 STANDARD; PRT: 213 AA.
XX xxxxxx
XX
XX
XX
XX
DE Sequence 3, Application US/08761258
CC Sequence 3, Application US/08761258
CC Patent No. 5756087
CC GENERAL INFORMATION:
CC APPLICANT: Ligon, James M.
CC APPLICANT: Hill, Dwight S.
CC APPLICANT: Lam, Stephen T.
CC APPLICANT: Gaffney, Thomas D.
CC APPLICANT: Torkewitz, Nancy
CC TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
CC TITLE OF INVENTION: with Enhanced Biocontrol Activity
CC NUMBER OF SEQUENCES: 11
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ciba-Geigy Corporation
CC STREET: 520 White Plains Road, P.O. Box 2005
CC CITY: Tarrytown
CC STATE: NY
CC COUNTRY: USA
CC ZIP: 10591
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/761,258
CC FILING DATE:
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meigs, J. Timothy
CC REGISTRATION NUMBER: 38,241
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (919) 541-8587
CC TELEFAX: (919) 541-8689
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 213 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear

CC MOLECULE TYPE: protein
SQ SEQUENCE 213 AA; 23364 MW; 236956 CN;

Query Match 63.2%; Score 43; DB 2; Length 213;
Best Local Similarity 33.3%; Pred. No. 1.85e+02;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

DB 99 AGYLFRGAGLNE 110
|||:||||:
QY 1 ASYLTSSSLDN 12

Search completed: Thu Sep 2 12:25:29 1999
Job time : 7 secs.

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CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 100.0%; Score 68; DB 27; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.53e-01;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 asylistsaldk 12
 |||
 QY 1 ASYLSTSSLDN 12

RESULT 2
 ID W27589 standard; peptide: 12 AA.
 AC W27589:

DE 19-MAR-1998 (first entry)
 KW Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JC, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 73; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 97.1%; Score 66; DB 27; Length 12;
 Best Local Similarity 91.7%; Pred. No. 1.45e+00;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 asylistsaldk 12
 |||
 QY 1 ASYLSTSSLDN 12

RESULT 3
 ID W27587 standard; peptide: 12 AA.
 AC W27587:

DE 19-MAR-1998 (first entry)
 KW Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JC, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 73; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 94.1%; Score 64; DB 27; Length 12;
 Best Local Similarity 91.7%; Pred. No. 2.47e+00;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 asylistsaldk 12
 |||
 QY 1 ASYLSTSSLDN 12

RESULT 4
 ID W27588 standard; peptide: 12 AA.
 AC W27588:

DE 19-MAR-1998 (first entry)
 KW Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW heavy chain: complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PS 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BR, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 73; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 12 AA:
 Query Match 92.6%; Score 63; DB 27; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3; 22e+00;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 asylstssld 11
 1 ASYLSSTSSLD 11
 RESULT 5
 ID W27594 standard: peptide; 12 AA.
 AC W27594; 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PS 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BR, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Disclosure; Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 12 AA:
 Query Match 91.2%; Score 62; DB 27; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4; 18e+00;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 2 SYLSSTSSLDN 12
 2 SYLSSTSSLDN 12

PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BR, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Disclosure; Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 12 AA:
 Query Match 91.2%; Score 62; DB 27; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4; 18e+00;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 2 SYLSSTSSLDN 12
 2 SYLSSTSSLDN 12
 RESULT 6
 ID W27593 standard: peptide; 12 AA.
 AC W27593;
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PS 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BR, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 12 AA:
 Query Match 91.2%; Score 62; DB 27; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4; 18e+00;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 2 SYLSSTSSLDN 12
 2 SYLSSTSSLDN 12

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, infectious diseases, autoimmune diabetes or nephrotic
 CC syndrome, inflammatory bone disorders, bone resorption disease,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 12 AA:

Query Match 88.2%; Score 60; DB 27; Length 12;
 Best Local Similarity 81.8%; Pred. No. 7.05e+00;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 asyistassle 11
 1111111111
 QY 1 ASYSTSSSLD 11

RESULT 7
 ID W27563 standard; peptide: 12 AA.
 AC W27563;
 DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 FT Key Location/Qualifiers
 FT Misc_difference 12 /label- Tyr. Asn
 FT W09729131-A1.
 DT 14-AUG-1997.
 PR 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakoraitas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9; Page 65; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 12 AA:

Query Match 83.8%; Score 57; DB 27; Length 12;
 Best Local Similarity 90.0%; Pred. No. 1.53e+01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 2 sylstassle 11
 1111111111
 QY 2 SYLSTSSSLD 11

RESULT 8
 ID W27592 standard; peptide: 12 AA.
 AC W27592;
 DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 FT Key Location/Qualifiers
 FT Misc_difference 12 /label- Tyr. Asn
 FT W09729131-A1.
 DT 14-AUG-1997.
 PR 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakoraitas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 74; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 12 AA:

Query Match 83.8%; Score 57; DB 27; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.53e+01;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 asylstsssl 11
 ||:|||||
 QY 1 ASYLSTSSSLD 11

RESULT 9
 ID W27591 standard; peptide; 12 AA.
 AC W27591:

DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody heavy chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM heavy chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 KM Homo sapiens.
 KW WO9729131-A1.

PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 PI Saifeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; page 76; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 12 AA;

Query Match 83.8%; Score 57; DB 27; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.53e+01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 asylstsssl 10
 |||||||
 QY 1 ASYLSTSSSL 10

RESULT 10
 ID W27569 standard; Protein; 121 AA.
 AC W27569:

DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody heavy chain variable region.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
 KM heavy chain; variable region; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;

KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 KM Homo sapiens.
 KW WO9729131-A1.

PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 PI Saifeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 16; page 76; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 121 AA;

Query Match 83.8%; Score 57; DB 27; Length 121;
 Best Local Similarity 90.0%; Pred. No. 1.53e+01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 100 sylstsssl 109
 |||||||
 QY 2 SYLSTSSSLD 11

RESULT 11
 ID W27590 standard; peptide; 12 AA.
 AC W27590:

DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody heavy chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM heavy chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 KM Homo sapiens.
 KW WO9729131-A1.

PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Manovic J, McGinness BT, Roberts AJ, Sakorafas P,
 PI Saleh JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 74: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 12 AA;

Query Match 80.9%; Score 55; DB 27; Length 12;
 Best Local Similarity 90.9%; Pred. No. 2.55e+01;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 asylstsfeld 11
 :|||||:111
 QY 1 ASYLSTSSLD 11

RESULT 12
 ID W23067 standard; Protein: 417 AA.
 AC W23067;
 DT 19-FEB-1998 (first entry)
 DE Canine IGE heavy chain constant region (exon 1-4 product).
 KW IGE: immunoglobulin; antibody; heavy chain constant region;
 KW allergy; hypersensitivity; therapy; dog; antisense;
 KW immunomodulation.
 CC Immunoglobulin.
 CC Canis familiaris.
 CC Key Location/Qualifiers
 FT MISC_difference 55 /note= "encoded by ACC"
 FT MISC_difference 56 /note= "encoded by TAC"
 FT MISC_difference 67 /note= "encoded by GCC"
 FT MISC_difference 83 /note= "encoded by GGC"
 FT MISC_difference 174 /note= "encoded by NNT"
 FT MISC_difference 175 /note= "encoded by GGN"
 FT MISC_difference 176 /note= "encoded by NNC"
 FT MISC_difference 176 /note= "encoded by TGN"
 FT MISC_difference 203 /note= "encoded by TCC"
 FT MISC_difference 204 /note= "encoded by GAC"
 FT WO9730156-A2.
 PN 21-AUG-1997.
 PD 14-FEB-1997: 002322.
 PR 14-FEB-1996: US-601197.
 PA (IDEX-) IDEX LAB INC.
 PI Harris RA, Mermer B, Steifring AE;

DR WPI: 97-425031/39.
 DR N-PSDB: T79278.
 PT Isolated canine IGE heavy chain constant region DNA - useful to
 PT develop products for treatment of canine allergies and for
 PT immunomodulation in dogs
 PS Disclosure: Page 35-39; 59pp: English.
 CC This polypeptide is encoded by exons 1-4 (see T79278) of canine
 CC IGE heavy chain constant region (epsilon) genomic DNA. Another
 CC polypeptide, comprising the exon 5 and 6 product, is given in
 CC W23068. Recombinant peptides encoded by exons 1-6 can be
 CC produced in eukaryotic or prokaryotic cells. Such peptides,
 CC and antibodies raised against them, are used in methods to treat
 CC the manifestation of allergy in dogs, e.g. to treatment Type I
 CC immediate hypersensitivity, and for immunomodulation.
 CC Sequence 417 AA;

Query Match 73.5%; Score 50; DB 26; Length 417;
 Best Local Similarity 63.6%; Pred. No. 8.92e+01;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 209 asylpspsld 219
 :||||:1111
 QY 1 ASYLSTSSLD 11

RESULT 13
 ID W06968 standard; Protein: 384 AA.
 AC W06968;
 DT 12-MAR-1997 (first entry)
 DE M. tuberculosis ORF 2 product.
 KW MACE: mycolic acid cyclopropanating enzyme; cyclopropanation; cma;
 KW pathogenic form; mycobacterium; non-pathogenic; screen; inhibitor;
 KW cyclopropane mycolic acid synthase; beta-ketoacyl reductase;
 KW Streptomyces cinamomensis; homology.
 OS Mycobacterium tuberculosis.
 PN US5573915-A.
 PD 12-NOV-1996.
 PE 01-JUN-1995: 457245.
 PR 01-JUN-1995: US-457245.
 PA (USGO) US GOVERNMENT.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Clifton B, Yuan Y;
 DR N-PSDB: T46163.
 DR WPI: 96-517880/51.
 PT Screening assay for anti-mycobacterial agents - based on inhibition
 PT of mycolic acid cyclopropanating enzyme
 PS Disclosure: Column 35-36; 35pp: English.
 CC This sequence is encoded by ORF 2 of Mycobacterium tuberculosis (see
 CC T46163). Three ORFs have been found all within a 7.2 kb BamHI fragment
 CC isolated from M. tuberculosis, and are believed to be related to the
 CC biosynthesis of mycolic acids. The ORF 2 gene product has homology to
 CC known enzymes involved in the oxidative/reductive interconversions of
 CC a ketone and an alcohol. It is most homologous (30 percent identity
 CC over 188 amino acids) to actiII, beta-ketoacyl reductase from
 CC Streptomyces cinamomensis which is involved in chain elongation in
 CC polyketide biosynthesis. Cyclopropanation of mycolic acids distinguishes
 CC pathogenic forms of mycobacterium from non-pathogenic forms. A method to
 CC determine the ability of a cpd. to inhibit cyclopropanation of mycolic
 CC acids in pathogenic mycobacterium is claimed.
 CC Sequence 384 AA;

Query Match 72.1%; Score 49; DB 20; Length 384;
 Best Local Similarity 54.5%; Pred. No. 1.14e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 235 asylptkaald 245
 :|||:1::|1
 QY 1 ASYLSTSSLD 11

RESULT 14
 ID R95335 standard; peptide: 19 AA.
 AC R95335;

DT 16-DEC-1996 (first entry)
 DE MBP-1.1 (11-29).
 KM Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KM CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KM CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KM relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KM diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 KM psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KM myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 OS Synthetic.
 PN W09612737-A2.
 PD 02-MAY-1996.
 PF 25-OCT-1995; U13682.
 PR 25-OCT-1994; US-328224.
 PR 15-MAR-1995; US-404228.
 PR 25-OCT-1995; ZA-009033.
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 PI Devaux B, Franzen H, Geller M, Hsu D, Pallard X;
 PI Rothenard J, Samson M, Shi J, Smilek D;
 PI WPI; 96-230552/23.
 MS Myelin basic derived peptide(s) and analogs - used in the treatment
 of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 CS Claim 1; Fig 2; 91pp; English.
 CC R53334-R53374 represent peptides derived from myelin basic protein (MBP).
 CC Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for treating
 CC MS in a mammal. The composition acts to down regulate the autoimmune
 CC response, and may be administered in an amount sufficient to prevent the
 CC onset of symptoms of MS. The compositions may also be used to treat
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive
 CC MS or benign MS. These peptides may also be used in the treatment of
 CC other diseases involving myelin autoantigens, including diabetes, Graves
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,
 CC thyroiditis, and rheumatoid arthritis. Peptides derived from other
 CC myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 SQ Sequence 19 AA;

Query Match 70.6%; Score 48; DB 19; Length 19;
 Best Local Similarity 41.7%; Pred. No. 1.46e+02;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

2 skylataastmdh 13
 : ||:|:|:|:
 1 ASYLSTSSSLDN 12

RESULT 15
 ID W37551 standard; peptide; 19 AA.
 AC W37551;
 DT 22-APR-1998 (first entry)
 DE Human myelin basic protein peptide MBP-1.1 (11-29).
 KM Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KM autoimmune response; MBP; myelin basic protein; demyelinating.
 OS Homo sapiens.
 PN W09735879-A1.
 PD 02-OCT-1997.
 PF 01-MAY-1996; U06072.
 PR 28-MAR-1996; US-623406.
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 PI Devaux B, Garman RD, Rothenard J, Smilek D, Wallner B;
 PI WPI; 97-489564/45.
 PT Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 PS Claim 101; page 35; 108pp; English.
 CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a

CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 SQ Sequence 19 AA;

Query Match 70.6%; Score 48; DB 27; Length 19;
 Best Local Similarity 41.7%; Pred. No. 1.46e+02;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

DB 2 skylataastmdh 13
 : ||:|:|:|:
 QY 1 ASYLSTSSSLDN 12

Search completed: Thu Sep 2 12:23:16 1999
 Job time : 20 secs.

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WIRE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Sep 2 12:29:09 1999: Maspar time 1.39 Seconds
Abular output not generated. 87.629 Million cell updates/sec

Title: >US-08-599-226-28
Description: (1-12) from US08599226.pep
Perfect Score: 70
Sequence: 1 ASYLSTSSSLDK 12

Scoring table:
PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfile1

Statistics: Mean 15.890; Variance 46.087; scale 0.345

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	50	71.4	426	3	PCT-US95-1	Sequence 2, Applicatio
2	50	71.4	426	1	US-08-336-	Sequence 2, Applicatio
3	49	70.0	384	1	US-08-457-	Sequence 5, Applicatio
4	48	68.6	238	3	PCT-US95-1	Sequence 2, Applicatio
5	48	68.6	238	1	US-08-588-	Sequence 2, Applicatio
6	48	68.6	238	1	US-08-337-	Sequence 2, Applicatio
7	48	68.6	238	1	US-08-452-	Sequence 1, Applicatio
8	48	68.6	238	2	US-08-753-	Sequence 2, Applicatio
9	48	68.6	312	1	US-08-414-	Sequence 2, Applicatio
10	47	67.1	540	1	US-08-367-	Sequence 2, Applicatio
11	46	65.7	20	2	US-08-468-	Sequence 2, Applicatio
12	46	65.7	21	2	US-08-787-	Sequence 3, Applicatio
13	46	65.7	170	2	US-08-327-	Sequence 1, Applicatio
14	45	64.3	168	4	5194425-4	Patent No. 5194425.
15	45	64.3	520	1	US-08-706-	Sequence 2, Applicatio
16	45	64.3	555	1	US-08-440-	Sequence 6, Applicatio
17	45	64.3	555	2	US-08-687-	Sequence 6, Applicatio
18	44	62.9	209	2	US-08-771-	Sequence 2, Applicatio
19	44	62.9	464	3	PCT-US91-0	Sequence 16, Applicati
20	44	62.9	464	1	US-07-688-	Sequence 16, Applicati
21	44	62.9	485	1	US-07-991-	Sequence 12, Applicati
22	44	62.9	501	1	US-08-434-	Sequence 2, Applicatio
23	44	62.9	501	1	US-07-687-	Sequence 2, Applicatio

24	44	62.9	501	4	5168064-4	Patent No. 5168064.
25	44	62.9	501	1	US-08-271-	Sequence 2, Applicatio
26	43	61.4	170	4	5194425-3	Patent No. 5194425.
27	43	61.4	170	2	US-08-227-	Sequence 1, Applicatio
28	43	61.4	238	2	US-08-928-	Sequence 5, Applicatio
29	43	61.4	240	3	PCT-US95-0	Sequence 80, Applicati
30	43	61.4	240	1	US-08-261-	Sequence 8, Applicatio
31	43	61.4	314	1	US-08-040-	Sequence 2, Applicatio
32	43	61.4	345	2	US-08-446-	Sequence 40, Applicati
33	43	61.4	980	1	US-08-413-	Sequence 5, Applicatio
34	43	61.4	980	1	US-08-220-	Sequence 5, Applicatio
35	43	61.4	1255	2	US-08-356-	Sequence 2, Applicatio
36	43	61.4	1255	2	US-08-484-	Sequence 8, Applicatio
37	43	61.4	1255	1	US-08-467-	Sequence 68, Applicati
38	43	61.4	1255	2	US-08-467-	Sequence 68, Applicati
39	43	61.4	1255	2	US-08-414-	Sequence 68, Applicati
40	43	61.4	1255	2	US-08-486-	Sequence 2, Applicatio
41	43	61.4	1255	2	US-08-625-	Sequence 2, Applicatio
42	42	60.0	158	2	US-08-828-	Sequence 68, Applicati
43	42	60.0	213	2	US-08-761-	Sequence 3, Applicatio
44	42	60.0	822	2	US-08-222-	Sequence 10, Applicati
45	42	60.0	3727	2	US-08-222-	Sequence 7, Applicatio

ALIGNMENTS

RESULT 1
ID PCT-US95-13795-2 STANDARD; PRT; 426 AA.
XX XXXXXX
AC
XX
DT

Sequence 2, Application PC/TUS9513795

Sequence 2, Application PC/TUS9513795

GENERAL INFORMATION:

APPLICANT: HOLIS, GREGORY F.

APPLICANT: PATEL, MAYUR D.

TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHRISTINE E. CARTY

STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13795

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: CARY, CHRISTINE E.

REGISTRATION NUMBER: 36,099

REFERENCE/DOCKET NUMBER: 19211Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-6734

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 426 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: Protein

SEQUENCE 426 AA; 47234 MW; 1032622 CN;

Query Match 71.4%; Score 50; DB 3; Length 426;
Best Local Similarity 63.6%; Pred. No. 3.08e+01;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 214 TSYLSPSPD 224
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QY 1 ASYLSTSSLD 11

RESULT 2
ID US-08-336-583-2 STANDARD; PRT; 426 AA.
XX xxxxxx
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DE Sequence 2, Application US/08336583
CC Sequence 2, Application US/08336583
CC Patent No. 5629415
CC GENERAL INFORMATION:
CC APPLICANT: HOLLI, GREGORY F.
CC APPLICANT: PATEL, MAYUR D.
CC TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CHRISTINE E. CARTY
CC STREET: 126 E. LINCOLN AVENUE
CC CITY: RAHWAY
CC STATE: NEW JERSEY
CC COUNTRY: USA
CC ZIP: 07065-0900
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/336,583
CC FILING DATE: 09-NOV-1994
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CARTY, CHRISTINE E.
CC REGISTRATION NUMBER: 36,099
CC REFERENCE/DOCKET NUMBER: 19211
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-6734
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 426 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 426 AA; 47234 MW; 1032622 CN;

Query Match 71.4%; Score 50; DB 1; Length 426;
Best Local Similarity 63.6%; Pred. No. 3.08e+01;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 214 TSYLSPSPD 224
:||||:||||
QY 1 ASYLSTSSLD 11

RESULT 3
ID US-08-457-245-5 STANDARD; PRT; 384 AA.
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AC
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XX
DT
XX

DE Sequence 5, Application US/08457245
XX Sequence 5, Application US/08457245
CC Patent No. 5573915
CC GENERAL INFORMATION:
CC APPLICANT: BARRY III, Clifton E.
CC APPLICANT: YUAN, YING
CC TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA INVOLVED
CC TITLE OF INVENTION: IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOLIC ACIDS IN
CC TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Hourie and Crew
CC STREET: Stewart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/457,245
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Chambers, Guy W.
CC REGISTRATION NUMBER: 30,617
CC REFERENCE/DOCKET NUMBER: 15280-216000
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 384 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: ORF2 protein
CC SEQUENCE 384 AA; 41963 MW; 701271 CN;

Query Match 70.0%; Score 49; DB 1; Length 384;
Best Local Similarity 54.5%; Pred. No. 4.00e+01;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

DB 235 SSTPLTKALD 245
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QY 1 ASYLSTSSLD 11

RESULT 4
ID PCT-US95-14692-2 STANDARD; PRT; 238 AA.
XX xxxxxx
AC
XX
XX
DT
XX

DE Sequence 2, Application PC/TUS9514692
CC Sequence 2, Application PC/TUS9514692
CC GENERAL INFORMATION:
CC APPLICANT: Telen, Roger Y.
CC APPLICANT: Helm, Roger
CC TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Robbins, Berliner & Carson
CC STREET: 201 North Figueroa Street, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90012

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/14692
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Spitals, John P.
CC REGISTRATION NUMBER: 29,215
CC REFERENCE/DOCKET NUMBER: 1279-178
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 977-1001
CC TELEFAX: (213) 977-1003
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 238 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 238 AA; 26886 MW; 291867 CN;
SQ

Query Match 68.6%; Score 48; DB 3; Length 238;
Best Local Similarity 70.0%; Pred. No. 5.18e+01;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 200 YLSTQSLSK 209
||| |
QY 3 YLSTSSSLDK 12

RESULT 5
ID US-08-588-201-2 STANDARD: PRT; 238 AA.
XX xxxxxx
DT
DE Sequence 2, Application US/08588201
XX Sequence 2, Application US/08588201
CC Patent No. 5874304
CC GENERAL INFORMATION:
CC APPLICANT: Zolotukhin, Sergei
CC APPLICANT: Hauswirth, William W.
CC APPLICANT: Muzyczka, Nicholas
CC TITLE OF INVENTION: Humanized Green Fluorescent Protein Genes
CC TITLE OF INVENTION: and Methods
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: TX
CC COUNTRY: USA
CC ZIP: 77210-4433
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/588,201
CC FILING DATE: Concurrently Herewith
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kitchell, Barbara S.
CC REGISTRATION NUMBER: 33,928
CC REFERENCE/DOCKET NUMBER: UFLA-039\KIT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-3100
CC

CC TELEFAX: (512) 474-7577
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 238 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC FEATURE:
CC NAME/KEY: Modified-site
CC LOCATION: 65
CC OTHER INFORMATION: /product= "OTHER"
CC OTHER INFORMATION: /note= "Xaa = Ser or Ther"
CC FEATURE:
CC NAME/KEY: Modified-site
CC LOCATION: 66
CC OTHER INFORMATION: /product= "OTHER"
CC OTHER INFORMATION: /note= "Xaa = Tyr or His"
CC SEQUENCE 238 AA; 26856 MW; 292586 CN;
SQ

Query Match 68.6%; Score 48; DB 2; Length 238;
Best Local Similarity 70.0%; Pred. No. 5.18e+01;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 200 YLSTQSLSK 209
||| |
QY 3 YLSTSSSLDK 12

RESULT 6
ID US-08-337-915A-2 STANDARD: PRT; 238 AA.
XX xxxxxx
DT
DE Sequence 2, Application US/08337915A
XX Sequence 2, Application US/08337915A
CC Patent No. 5625048
CC GENERAL INFORMATION:
CC APPLICANT: Tsien, Roger Y.
CC APPLICANT: Helm, Roger
CC TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Robbins, Berliner & Carson
CC STREET: 201 No. 5625048th Figueroa Street, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90012
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/337,915A
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Spitals, John P.
CC REGISTRATION NUMBER: 29,215
CC REFERENCE/DOCKET NUMBER: 1279-178
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 977-1001
CC TELEFAX: (213) 977-1003
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 238 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC

SQ **SEQUENCE** **238 AA; 26886 MW; 291867 CN;**

Query Match	68.68;	Score 48;	DB 1;	Length 238;
Best Local Similarity	70.08;	Pred. No. 5.18e+01;		
Matches	7;	Conservative	1;	Mismatches 2; Indels

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Db      200 YLSTQSAISK 205
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QY      3 YLSTSSSLDK 12
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RESULT	7	STANDARD;	PRT;	238 AA
ID	US-08-452-295-1			

AC XXXXXX

Sequence 1, Application US/08452295
Patent No. 5741668
GENERAL INFORMATION:

CC TITLE OF INVENTION: A BIOLUMINESCENT INDICATOR FOR GENE
CC TITLE OF INVENTION: EXPRESSION AND DETECTION OF MUTAGENESIS BASED UPON THE
CC TITLE OF INVENTION: EXPRESSION OF A GENE FOR A MODIFIED GREEN-FLUORESCENT
CC TITLE OF INVENTION: PROTEIN
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:

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CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:

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CC      NAME/KEY:  Protein
CC      LOCATION: one-of(1)
CC      OTHER INFORMATION: /note="Residue 1 Xaa -
CC      OTHER INFORMATION: Methionyl-alanine"
CC      SEQUENCE 238 AA; 26975 MW; 290556 CN;
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Query Match	68.68;	Score 48;	DB 1;	Length 238;
Best Local Similarity	70.08;	Pred. No. 5.18e+01;		
Matches	7;	Conservative	2;	Indels 0;
		Mismatches	2;	Gaps 0;

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Db      200 YLSTQSALSK 20
          ||| | : | |
Qy      3 YLSTSSSLDK 12
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RESULT	8	
ID	US-08-753-143-2	STANDARD; PRT; 238 AA

AC
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Sequence 2, Application US/08753143A

CC Sequence 2, Application US/08753143A
CC GENERAL INFORMATION:
CC APPLICANT: Tsien, Roger Y.
CC APPLICANT: Tsien, Roger Y.
CC TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
CC FILE REFERENCE: 07257/032003
CC CURRENT APPLICATION NUMBER: US/08/753,143A
CC CURRENT FILING DATE: 1996-11-20
CC NUMBER OF SEQ. ID NOS: 2
CC SOFTWARE: FASTSEQ for Windows Version 3.0
CC SEQ ID NO 2
CC LENGTH: 238

SQ SEQUENCE 238 AA; 26914 MW; 291547 CN;

Query Match	68.68;	Score 48;	DB 2;	Length 238;
Best Local Similarity	70.08;	Pred. No. 5.18e+01;		
Matches	7;	Conservative	2;	Indels 0;
				Gaps 0

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Db      200 YLSTQSAISK 209
        |||||:|
QY      3 YLSTSSSLDK 12
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RESULT	9	STANDARD;	PRT;	312 AA
ID	US-08-414-625-2			

AC XXXXXX

DE Sequence 2, Application US/08414625

CC Sequence 2, Application US/08414625
CC Patent No. 5563039

CC APPLICANT: Hsu, Hailing
CC TITLE OF INVENTION: INTRACELLULAR SIGNALING PROTEINS AND
CC TITLE OF INVENTION: METHODS OF USE
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:

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CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CHIPPED ADDRESSABLE DISK
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CC NAME: Osman, Richard A
CC REGISTRATION NUMBER: 36,627
CC REFERENCE/DOCKET NUMBER: A-60916/RAC

CC NAME: Osman, Richard A
CC REGISTRATION NUMBER: 36,627
CC REFERENCE/DOCKET NUMBER: A-60916/RAC

US-08-599-226-28.ra1

```

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 494-8700
CC TELEFAX: (415) 494-8771
CC TELEX: 910 277299
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 312 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 312 AA; 34247 MW; 431471 CN;
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Query Match 68.6%; Score 48; DB 1; Length 312;
Best Local Similarity 58.3%; Pred. No. 5,168+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0
Db 14 SAYLESSLDK 25
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OY 1 ASYLSTSSSLDK 12
RESULT. 10
ID US-08-367-227-2 STANDARD: PRT; 540 AA.
AC xxxxxx
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Sequence 2, Application US/08367227
DE
CC Sequence 2, Application US/08367227
CC Patent No. 5587304
CC GENERAL INFORMATION:
CC APPLICANT: BARRE, PIERRE
CC APPLICANT: DEQUIN, SYLVIE
CC APPLICANT: ANSAMAY, VIRGINIE
CC TITLE OF INVENTION: CLONING AND EXPRESSION OF THE GENE FOR
CC TITLE OF INVENTION: THE MALOLACTIC ENZYME OF LACTOCOCCUS LACTIS
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
CC STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
CC CITY: ARLINGTON
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22202
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/367,227
CC FILING DATE: 17-JAN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: FR PCT/FR94/00589
CC FILING DATE: 18-MAY-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: FR 93/06003
CC FILING DATE: 18-MAY-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: OBLON, NORMAN F
CC REGISTRATION NUMBER: 24,618
CC REFERENCE/DOCKET NUMBER: 384-42-0 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-413-3000
CC TELEFAX: 703-413-2220
CC TELEX: 248855 OPAT UR
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 540 amino acids
CC TYPE: amino acid
CC

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CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE   540 AA; 59350 MW; 1526476 CN;
Query Match          67.1%; Score 47; DB 1; Length 540;
Best Local Similarity 50.0%; Pred. No. 6.69e+01;
Matches              5; Conservative    3; Mismatches    2; Indels    0; Gaps    0;
Db      50 YLTKPSDLK 59
       11 : 1 1 1
       3 YLTSSSLDK 12
RESULT  11
ID      US-08-468-540B-2        STANDARD; PRT; 20 AA.
XX      XXXXXX
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DE      Sequence 2, Application US/08468540B
CC
CC      Sequence 2, Application US/08468540B
CC      Patent No. 5858980
CC      GENERAL INFORMATION:
CC      APPLICANT: Weiner, Howard
CC      APPLICANT: Hattler, David
CC      APPLICANT: Miller, Arlet
CC      APPLICANT: Al-Sabbagh, Ahmad
CC      TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
CC      USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
CC      NUMBER OF SEQUENCES: 25
CC      CORRESPONDENCE ADDRESSES:
CC      ADDRESSEE: Darby & Darby P.C.
CC      STREET: 805 Third Avenue
CC      CITY: New York
CC      STATE: NY
CC      COUNTRY: USA
CC      ZIP: 10022
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: DOS
CC      SOFTWARE: FastSeq for Windows Version 2.0
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/468,540B
CC      FILING DATE: 06-JUN-1995
CC      CLASSIFICATION: 514
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:
CC      FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Jacobs, Seth H
CC      REGISTRATION NUMBER: 32,140
CC      REFERENCE/DOCKET NUMBER:
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 212-527-7700
CC      TELEFAX:
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 20 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: No. 5858980e
SQ      SEQUENCE   20 AA; 2160 MW; 2047 CN;
Query Match          65.7%; Score 46; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 8.64e+01;
Matches              5; Conservative    5; Mismatches    1; Indels    0; Gaps    0;
Db      2 SKYLATASTD 12

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OY :||:|:|:|
1 ASYLSTSSLD 11

RESULT 12 STANDARD; PRT; 21 AA.

XX xxxxxx

DE Sequence 33, Application US/08787547

CC Sequence 33, Application US/08787547

CC Patent No. 5783567

CC GENERAL INFORMATION:

CC APPLICANT: Hedley, Mary Lynne

CC APPLICANT: Curley, Joanne M.

CC APPLICANT: Langer, Robert S.

CC TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY

CC TITLE OF INVENTION: OF NUCLEIC ACID

CC NUMBER OF SEQUENCES: 107

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Fish & Richardson, P.C.

CC STREET: 225 Franklin Street

CC CITY: Boston

CC STATE: MA

CC COUNTRY: US

CC ZIP: 02110-2804

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC COMPUTER: IBM Compatible

CC OPERATING SYSTEM: Windows95

CC SOFTWARE: FASTSEQ for Windows Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/787,547

CC FILING DATE: 22-JAN-1997

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER:

CC FILING DATE:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fraser, Janis K.

CC REGISTRATION NUMBER: 34,819

CC REFERENCE/DOCKET NUMBER: 08191/003001

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 617-542-5070

CC TELEFAX: 617-542-8906

CC TELEX: 200154

CC INFORMATION FOR SEQ ID NO: 33:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 21 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC SEQUENCE 21 AA; 2312 MW; 2012 CN;

Query Match 65.7%; Score 46; DB 2; Length 21;
Best Local Similarity 45.5%; Pred. No. 8.64e+01;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

DB 6 SKYLATASTMD 16

OY :||:|:|:|
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RESULT 13 STANDARD; PRT; 170 AA.

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AC xxxxxx

DT xxxxxx

XX xxxxxx

DE Sequence 1, Application US/08327357A

CC Sequence 1, Application US/08327357A

CC Patent No. 5817629

CC GENERAL INFORMATION:

CC APPLICANT: WARREN, Kenneth G.

CC APPLICANT: CATZ, Ingrid

CC TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC

CC TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN

CC TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS

CC NUMBER OF SEQUENCES: 1

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti

CC STREET: 1201 New York Avenue, N.W., Suite 1000

CC CITY: Washington

CC STATE: D.C.

CC COUNTRY: USA

CC ZIP: 20005

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/327,357A

CC FILING DATE: 21-OCT-1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/798,099

CC FILING DATE: 27-NOV-1991

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: CA 2,053,799-0

CC FILING DATE: 22-OCT-1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Ihnen, Jeffrey L.

CC REGISTRATION NUMBER: 28,957

CC REFERENCE/DOCKET NUMBER: 27052-115469

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 202-962-4810

CC TELEFAX: 202-962-8300

CC INFORMATION FOR SEQ ID NO: 1:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 170 amino acids

CC TYPE: amino acid

CC STRANDEDNESS:

CC MOLECULE TYPE: linear

CC ORIGINAL SOURCE:

CC ORGANISM: Homo sapiens

CC IMMEDIATE SOURCE:

CC CLONE: human myelin basic protein

CC SEQUENCE 170 AA; 18459 MW; 143992 CN;

Query Match 65.7%; Score 46; DB 2; Length 170;
Best Local Similarity 45.5%; Pred. No. 8.64e+01;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

DB 12 SKYLATASTMD 22

OY :||:|:|:|
1 ASYLSTSSLD 11

RESULT 14 STANDARD; PRT; 182 AA.

XX xxxxxx

AC 01-JAN-1900

DE Patent No. 5194425.

CC Patent No. 5194425

CC APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,

CC BRIAN R.
CC TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
CC AMELIORATING AUTOIMMUNITY
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/367,751
CC FILING DATE: 21-JUN-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 210,594
CC FILING DATE: 23-JUN-1988
CC SEQ ID NO: 4:
CC LENGTH: 168
CC SEQUENCE 182 AA: 19707 MW; 182144 CN;
SQ

Query Match 64.3%; Score 45; DB 4; Length 168;
Best Local Similarity 55.6%; Pred. No. 1.11e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 12 YLATASTD 20
11111111
3 YLSTSSSD 11

RESULT 15
ID US-08-706-292-2 STANDARD; PRT; 520 AA.
XX
AC xxxxxx
XX
DT
DE
XX
Sequence 2, Application US/08706292
CC
CC Patent No. 5705380
CC GENERAL INFORMATION:
CC APPLICANT: NORTH, Micheal
CC TITLE OF INVENTION: GENES ASSOCIATED WITH RETINAL
CC TITLE OF INVENTION: DYSTROPHIES
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
CC STREET: 4 Embarcadero Center, Suite 3400
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94111-4187
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/706,292
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: SHERWOOD, Pamela J.
CC REGISTRATION NUMBER: 36,677
CC REFERENCE/DOCKET NUMBER: A-63789/PJS
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-494-8700
CC TELEFAX: 415-494-8771
CC TELEX: 910 277299
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 520 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 520 AA: 58640 MW; 1375552 CN;
SQ

Query Match 64.3%; Score 45; DB 1; Length 520;

Best Local Similarity 60.0%; Pred. No. 1.11e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 308 YLSTSSSD 317
11111111
QY 3 YLSTSSSD 12

Search completed: Thu Sep 2 12:29:17 1999
Job time : 8 secs.

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 (TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Sep 2 12:26:51 1999; Maspar time 3.46 Seconds

Labular output not generated.

Title: >US-08-599-226-28
 Description: (1-12) from US08599226.pep
 Perfect Score: 70
 Sequence: 1 ASYLSTSSSLDK 12

Scoring table:
 PAM 150
 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 17.079; Variance 49.680; scale 0.344

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	70	100.0	12 27	W27587	Anti-TNF-alpha antibo	4.16e-01
2	64	91.4	12 27	W27586	Anti-TNF-alpha antibo	2.16e+00
3	63	90.0	12 27	W27589	Anti-TNF-alpha antibo	2.83e+00
4	63	90.0	12 27	W27588	Anti-TNF-alpha antibo	2.83e+00
5	60	85.7	12 27	W27593	Anti-TNF-alpha antibo	6.34e+00
6	58	82.9	12 27	W27594	Anti-TNF-alpha antibo	1.08e+01
7	57	81.4	12 27	W27563	Anti-TNF-alpha antibo	1.41e+01
8	57	81.4	12 27	W27592	Anti-TNF-alpha antibo	1.41e+01
9	57	81.4	12 27	W27591	Anti-TNF-alpha antibo	1.41e+01
10	57	81.4	12 27	W27569	Anti-TNF-alpha antibo	1.41e+01
11	55	78.6	12 27	W27590	Anti-TNF-alpha antibo	2.37e+01
12	52	74.3	12 27	W27593	Human tumour suppress	5.15e+01
13	50	71.4	12 27	W27567	Canine IgE heavy chain	8.57e+01
14	50	71.4	12 27	W27580	Arabidopsis phytochro	8.57e+01
15	49	70.0	12 27	W06968	M. tuberculosis ORF 2	1.10e+02
16	48	68.6	12 27	W52348	Engineered green fluo	1.42e+02

17	48	68.6	238 30	W52349	Engineered green fluo	1.42e+02
18	48	68.6	238 30	W52350	Engineered green fluo	1.42e+02
19	48	68.6	364 39	W95356	IL-1 alpha prolece-E	1.42e+02
20	48	68.6	544 38	W85029	Green fluorescent pro	1.42e+02
21	48	68.6	544 38	W85028	CDK2-green fluorescen	1.42e+02
22	48	68.6	554 31	W48661	Rg fusion protein seq	1.42e+02
23	48	68.6	604 38	W85016	Exk2-green fluorescen	1.42e+02
24	48	68.6	606 38	W85019	p38-green fluorescen	1.42e+02
25	48	68.6	624 38	W85010	p38-green fluorescen	1.42e+02
26	48	68.6	624 38	W85015	Exk1-green fluorescen	1.42e+02
27	48	68.6	633 38	W85009	Unk1-green fluorescen	1.42e+02
28	48	68.6	635 38	W85034	Green fluorescent pro	1.42e+02
29	48	68.6	718 38	W85024	Exk2-green fluorescen	1.42e+02
30	48	68.6	726 38	W85022	PKB-green fluorescen	1.42e+02
31	48	68.6	797 38	W85042	PKB-green fluorescen	1.42e+02
32	48	68.6	798 38	W85025	Snad4-green fluoresce	1.42e+02
33	48	68.6	806 38	W85013	Snad4-green fluoresce	1.42e+02
34	48	68.6	842 38	W85008	Gkx5-green fluorescen	1.42e+02
35	48	68.6	843 38	W85030	Green fluorescent pro	1.42e+02
36	48	68.6	853 38	W85031	Protein tyrosine phos	1.42e+02
37	48	68.6	865 38	W85027	Zap70-green fluoresce	1.42e+02
38	48	68.6	871 38	W85026	Green fluorescent pro	1.42e+02
39	48	68.6	916 38	W85023	Amino acid sequence o	1.42e+02
40	48	68.6	932 38	W85040	PKG-green fluorescen	1.42e+02
41	48	68.6	936 38	W85033	Ikkappa kinase alpha	1.42e+02
42	48	68.6	997 38	W85032	Green fluorescent pro	1.42e+02
43	48	68.6	1039 38	W85014	Stats-green fluoresce	1.42e+02
44	48	68.6	1045 38	W85050	Stats-green fluoresce	1.42e+02
45	48	68.6	1181 38	W85038	NPAT1-green fluoresce	1.42e+02

ALIGNMENTS

RESULT 1
 ID W27587 standard; peptide: 12 AA.
 AC W27587;
 DE 19-MAR-1998 (first entry)
 KW Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVIC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 KW Homo sapiens.
 OS WO9729131-A1.
 PN 14-AUG-1997.
 PD 10-FEB-1997; U02219.
 PF 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salteid JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 73; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 100.0%; Score 70; DB 27; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.16e-01;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 asylstssaid 12
 1 ASYLSTSSSIDK 12

RESULT 2
 ID W2586 standard; peptide: 12 AA.

AC W2586;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BAD1) BASF AG.
 PI Allen DV, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

Claim 20; Page 72; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis, Ab,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 91.4%; Score 64; DB 27; Length 12;
 Best Local Similarity 91.7%; Pred. No. 2.16e+00;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 asylstssaid 12
 1 ASYLSTSSSIDK 12

RESULT 3
 ID W2589 standard; peptide: 12 AA.

AC W2589;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BAD1) BASF AG.
 PI Allen DV, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

Claim 20; Page 73; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis, Ab,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 90.0%; Score 63; DB 27; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.83e+00;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 asylstssaid 11
 1 ASYLSTSSSID 11

RESULT 4
 ID W2588 standard; peptide: 12 AA.

AC W2588;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM heavy chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: 002219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 73; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 12 AA:
 SQ

Query Match 90.08; Score 63; DB 27; Length 12;
 Best Local Similarity 100.08; Pred. No. 2.83e+00;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 asylstssaid 11
 |||||
 1 ASYLSTSSSID 11

RESULT 5
 ID W27593 standard; peptide: 12 AA.
 AC W27593:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM heavy chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: 002219.

PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 75; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 12 AA:
 SQ

Query Match 85.78; Score 60; DB 27; Length 12;
 Best Local Similarity 81.88; Pred. No. 6.34e+00;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 asylstssaid 11
 |||||
 1 ASYLSTSSSID 11

RESULT 6
 ID W27594 standard; peptide: 12 AA.
 AC W27594:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM heavy chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: 002219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Disclosure; Page 75; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 determining region 3 (CDR3).
 CC

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 82.98; Score 58; DB 27; Length 12;
 Best Local Similarity 81.88; Pred. No. 1.08e+01;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 systassid 12
 |||||:|||||:
 QY 2 SYLSTSSLDK 12

RESULT 7
 ID W27563 standard; peptide: 12 AA.
 AC W27563;

DE Anti-TNF-alpha antibody heavy chain CDR3.
 DT 19-MAR-1998 (first entry)

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT Misc_difference 12
 FT /label- Tyr, Asn

W09729131-A1.

14-AUG-1997.

10-FEB-1997; U02219.

25-NOV-1996; US-031476.

09-FEB-1996; US-599226.

(BADI) BASF AG.

Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Seifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 9; Page 65; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, e.g. rheumatoid arthritis, allergy, multiple

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 81.48; Score 57; DB 27; Length 12;
 Best Local Similarity 90.08; Pred. No. 1.41e+01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 2 systassid 11
 |||||:|||||:
 QY 2 SYLSTSSLD 11

RESULT 8
 ID W27592 standard; peptide: 12 AA.
 AC W27592;

DE Anti-TNF-alpha antibody heavy chain CDR3.
 DT 19-MAR-1998 (first entry)

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW heavy chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.

W09729131-A1.

14-AUG-1997.

10-FEB-1997; U02219.

25-NOV-1996; US-031476.

09-FEB-1996; US-599226.

(BADI) BASF AG.

Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Seifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 74; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, e.g. rheumatoid arthritis, allergy, multiple

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA;

Query Match 81.48; Score 57; DB 27; Length 12;
 Best Local Similarity 81.88; Pred. No. 1.41e+01;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 asf1stssale 11
 11:|||||
 QY 1 ASYLSTSSSLD 11

RESULT 9
 ID W27591 standard; peptide: 12 AA.

AC W27591:
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 DE Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 heavy chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 Homo sapiens.

MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 Manovich JA, McGulness BT, Roberts AJ, Sakorats P,
 Salfield JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 76; 102pp. English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 Sequence 12 AA;

Query Match 81.4%; Score 57; DB 27; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1,41e+01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 asylstssal 10
 |||||||
 QY 1 ASYLSTSSSL 10

RESULT 10
 ID W27569 standard; protein: 121 AA.

AC W27569:
 DE Anti-TNF-alpha antibody heavy chain variable region.
 DE Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
 heavy chain; variable region; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 Homo sapiens.

OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 Manovich JA, McGulness BT, Roberts AJ, Sakorats P,
 Salfield JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 WPI: 97-415302/38.

DR N-PSDB: T88404.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 16; Page 76; 102pp. English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) heavy chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 Sequence 121 AA;

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 Sequence 121 AA;

Query Match 81.4%; Score 57; DB 27; Length 121;
 Best Local Similarity 90.0%; Pred. No. 1,41e+01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 100 sylstssald 109
 |||||||
 QY 2 SYLSTSSSLD 11

RESULT 11
 ID W27590 standard; peptide: 12 AA.

AC W27590:
 DE Anti-TNF-alpha antibody heavy chain CDR3.
 DE Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 heavy chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 Homo sapiens.

OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Manovicich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salefeld JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-413302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 74; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) heavy chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 12 AA:

Query Match 78.68; Score 55; DB 27; Length 12;
 Best Local Similarity 90.98; Pred. NO. 2.37e+01;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 asylstsfald 11
 11111111111111111111
 Qy 1 ASYLSTSSLD 11

RESULT 12
 ID W81867 standard; Protein: 2799 AA.
 AC W81867;
 DT 15-MAR-1999 (first entry)
 DE Human tumour suppressor EDD protein.
 KW EDD; E3 isolated by differential display; tumour suppressor gene;
 KW human; breast cancer; diagnosis.
 OS Homo sapiens.

TH Key Location/Qualifiers
 FT Peptide 1..10
 FT Peptide /note= "claimed peptide"
 FT Peptide 1..50
 FT Region /note= "claimed peptide"
 FT Region 186..266
 FT Region /note= "conserved region"
 FT Region 663..683
 FT Region /note= "conserved region"
 FT Region 809..843
 FT Region /note= "conserved region"
 FT Region 915..938
 FT Region /note= "conserved region"
 FT Region 1099..1345
 FT Region /note= "conserved region"
 FT Region 1383..1496
 FT Region /note= "conserved region"
 FT Region 2195..2242
 FT Region /note= "conserved region"
 FT Region 2271..2316
 FT Region /note= "conserved region"
 FT Region 2529..2799
 FT Peptide /note= "conserved region"
 FT Peptide 502..517
 FT Peptide /note= "putative nuclear localisation signal"
 FT Peptide 1222..1241

FT Region /note= "putative nuclear localisation signal"
 FT Region 2396..2445
 FT Peptide /note= "polyA-binding protein homology region"
 FT Peptide 2469..2474
 FT Domain /note= "peptide used to raise AbPEP1 antiserum"
 FT Domain 2529..2799
 FT /note= "HECT domain, includes conserved Cys-2768 residue"
 FT MISC_difference 43
 FT /note= "encoded by TTC"
 FT MISC_difference 44
 FT /note= "encoded by CAA"
 FT MISC_difference 336
 FT /note= "encoded by AAGC (frameshift)"
 FT MISC_difference 342
 FT /note= "encoded by ATG (frameshift)"
 FT MISC_difference 374
 FT /note= "encoded by ATG"
 FT MISC_difference 375
 FT /note= "encoded by ATG"
 FT MISC_difference 375
 FT /note= "no corresponding codon in nucleotide sequence"
 FT MISC_difference 440
 FT /note= "encoded by AAG"
 FT MISC_difference 898
 FT /note= "encoded by CCG"
 FT MISC_difference 899
 FT /note= "encoded by TTT"
 FT MISC_difference 900
 FT /note= "no corresponding codon in nucleotide sequence"
 FT MISC_difference 1213
 FT /note= "encoded by GCG"
 FT MISC_difference 1221
 FT /note= "encoded by TGG"
 FT MISC_difference 1722
 FT /note= "encoded by CTG"
 FT MISC_difference 1790
 FT /note= "encoded by AT (frameshift)"
 FT MISC_difference 1795
 FT /note= "encoded by AT (frameshift)"
 FT MISC_difference 2121
 FT /note= "encoded by AAG"
 FT MISC_difference 2123
 FT /note= "encoded by AAG"
 FT MISC_difference 2180
 FT /note= "encoded by CTT"
 FT MISC_difference 2270
 FT /note= "encoded by ATA"
 FT MISC_difference 2422
 FT /note= "encoded by GA (frameshift)"
 FT MISC_difference 2430
 FT /note= "encoded by TCT (frameshift)"
 FT MISC_difference 2623
 FT /note= "encoded by AAG"
 FT MISC_difference 2624
 FT /note= "encoded by AGA"
 FT MISC_difference 2638
 FT /note= "encoded by GAC"
 FT MISC_difference 2638
 FT /note= "encoded by GAC"
 PN W09848010-A1.
 PD 29-OCT-1998.
 PF 20-APR-1998; AU0280.
 PR 21-APR-1997; AU-006334.
 PA (GARV-) GARVAN INST MEDICAL RES.
 PI Callaghan MJ, Sutherland RL, Watts CKW;
 PI WPI: 98-609985/51.
 DR N-PSDB: V64871.
 PT E3 isolated by differential display (EDD) gene - used in method for
 PT determination of predisposition to a hyperproliferative disease
 PS Example: Fig 3C; 46pp; English.
 CC This is the amino acid of the protein encoded by the novel human
 CC EDD (E3 isolated by differential display) gene (see V64871). EDD
 CC is a p53-regulated tumour suppressor gene. EDD protein
 CC exhibits significant amino acid sequence identity with the HYD

CC T46163). Three ORFs have been found all within a 7.2 kb BamHI fragment
CC isolated from M. tuberculosis, and are believed to be related to the
CC biosynthesis of mycolic acids. The ORF 2 gene product has homology to
CC known enzymes involved in the oxidative/reductive interconversions of
CC a ketone and an alcohol. It is most homologous (30 percent identity
CC over 188 amino acids) to acetyl, beta-ketoadenyl reductase from
CC Streptomyces cinnamomeis which is involved in chain elongation in
CC polyketide biosynthesis. Cyclopropanation of mycolic acids distinguishes
CC pathogenic forms of mycobacterium from non-pathogenic forms. A method to
CC determine the ability of a cpd. to inhibit cyclopropanation of mycolic
CC acids in pathogenic mycobacterium is claimed.
SQ Sequence 384 AA;

Query Match 70.0%; Score 49; DB 20; Length 384;
Best Local Similarity 54.5%; Pred. No. 1.10e+02;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 235 seq1ptkaald 245

1 ASYLSRSSLD 11

Search completed: Thu Sep 2 12:27:09 1999
Job time : 18 secs.

 WIRENET (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:27:25 1999; Maspar time 3.26 Seconds
 Modular output not generated. 147.524 Million cell updates/sec

Title: >US-08-599-226-28
 Description: (1-12) from US08599226.pep
 Perfect Score: 70
 Sequence: 1 ASYLSTSSSLDK 12

Scoring table: GAP 150
 Gap 15

Searched: 122810 seqs, 40068593 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: PIR60
 1:PIR1 2:PIR2 3:PIR3 4:PIR4

Statistics: Mean 23.822; Variance 26.882; scale 0.886

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	51	72.9	471	2	C71439	hypothetical protein	2.87e+00
2	51	72.9	1001	2	H64593	type III restriction	2.87e+00
3	50	71.4	293	2	D70108	conserved hypothetical	4.75e+00
4	50	71.4	608	2	T02684	DNA-binding protein C	4.75e+00
5	50	71.4	619	2	A56519	CDG16 protein - human	4.75e+00
6	49	70.0	377	2	F71520	hypothetical protein	7.79e+00
7	49	70.0	650	2	F70974	probable acral protein	7.79e+00
8	49	70.0	684	2	G70744	hypothetical protein	7.79e+00
9	49	70.0	734	2	S4617	C50C3.11 protein - Ca	7.79e+00
10	48	68.6	203	2	F69381	flagellin (flaB1-1) h	1.27e+01
11	48	68.6	238	2	S48693	fluorescent protein -	1.27e+01
12	48	68.6	238	2	J01514	green fluorescent pro	1.27e+01
13	48	68.6	238	2	S51330	green fluorescent pro	1.27e+01
14	48	68.6	312	2	A56911	TRAPD protein - human	1.27e+01
15	47	67.1	524	2	J50746	cytochrome P450 1A1 -	2.05e+01
16	47	67.1	524	2	JX0189	cytochrome P450 1A1 -	2.05e+01
17	47	67.1	524	1	O4RTMC	unspecific monooxygen	2.05e+01
18	47	67.1	540	2	S38728	malolactic enzyme (EC	2.05e+01
19	47	67.1	661	2	B54078	methyl-accepting chem	2.05e+01
20	47	67.1	687	2	A41905	ferric vibriobactin r	2.05e+01
21	47	67.1	1160	2	A46423	transcription factor	2.05e+01
22	47	67.1	1655	2	S47446	nucleoporin Np188 - Y	2.05e+01
23	46	65.7	128	1	MBRTS	myelin basic protein	3.28e+01

24	46	65.7	132	2	H70759	hypothetical protein	3.28e+01
25	46	65.7	167	2	A37246	myelin basic protein	3.28e+01
26	46	65.7	171	2	MBR2B	myelin basic protein	3.28e+01
27	46	65.7	197	1	MBRUB	myelin basic protein	3.28e+01
28	46	65.7	221	2	S24328	glutathione peroxidase	3.28e+01
29	46	65.7	236	2	S60941	probable membrane pro	3.28e+01
30	46	65.7	301	2	S13095	P34 protein - Rickett	3.28e+01
31	46	65.7	328	1	MBMSB	goli-myelin basic pr	3.28e+01
32	46	65.7	351	2	S21345	retrovirus-related le	3.28e+01
33	46	65.7	357	1	Q0MSL	retrovirus-related le	3.28e+01
34	46	65.7	460	1	YKBYC	citrate (s1)-synthase	3.28e+01
35	46	65.7	471	2	S01052	flavonol 3-O-glucosyl	3.28e+01
36	46	65.7	471	2	S08325	flavonol 3-O-glucosyl	3.28e+01
37	46	65.7	471	2	S01037	flavonol 3-O-glucosyl	3.28e+01
38	46	65.7	564	2	S57124	CTP synthase (EC 6.3.	3.28e+01
39	46	65.7	842	2	S27533	histidine protein kin	3.28e+01
40	45	64.3	68	2	B55682	keratin 15, type I, c	5.21e+01
41	45	64.3	485	2	B37855	glucose-6-phosphate 1	5.21e+01
42	45	64.3	657	2	S51387	dnar-type molecular c	5.21e+01
43	45	64.3	832	2	S71788	P/CAF protein - human	5.21e+01
44	45	64.3	1328	2	S78457	exonuclease II - f1ss	5.21e+01
45	45	64.3	2351	2	G71415	hypothetical protein	5.21e+01

ALIGNMENTS

RESULT 1
 ENTRY C71439 #type complete
 TITLE hypothetical protein - Arabidopsis thaliana
 ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear cress

DATE #variety
 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change
 05-Dec-1998
 C71439
 A71400
 Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveen, M.; Stekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel, K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Gielens, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.; Leclercq, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.; Kavanagh, T.; Hempel, S.; Kotter, P.; Ertlin, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka, A.; Youklatou, E.; Milioni, D.; Hatzopoulos, P.; Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.; Moore, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Bens, V.; Reichen, S.; Anorge, W.; Cooke, R.; Berger, C.; Delenly, W.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klotterman, S.; Schueller, C.; Chaiwatiz, N.

#journal
 #title Nature (1998) 391:485-488
 Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana.

#accession C71439
 #status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA
 #residues 1-471 #label BNY
 #cross-references GB:297342; NID:g2245031; PID:e327038; PID:g2245065

GENETICS
 #map_position ACOP9-4G3845
 #length 471 #molecular-weight 52785 #checksum 7455

SUMMARY
 Query Match 72.9% Score 51; DB 2; Length 471;
 Best Local Similarity 63.6% Pred. No. 2.87e+00;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 19 ACYLTSSSLD 29
 1:|||||
 QY 1 ASYLSTSSSLD 11

```

RESULT 2
ENTRY   H64593      #type complete
TITLE   type III restriction enzyme R protein - Helicobacter pylori
        (strain 26695)
ORGANISM
        #formal_name Helicobacter pylori
        #formal_name Helicobacter pylori
DATE     09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
        10-Oct-1997
ACCESSIONS
REFERENCE H64593
        #authors Tombl, J.F.; White, O.; Kertlavage, A.R.; Clayton, R.A.;
        Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klein,
        H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
        J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
        Richardson, D.; Dodson, R.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.;
        McKenney, K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
        Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
        Fujii, C.; Bowman, C.; Wathey, L.; Wallin, E.; Hayes,
        W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser,
        C.M.; Venter, J.C.
        #journal Nature (1997) 388:539-547
        #title The complete genome sequence of the gastric pathogen
        Helicobacter pylori.
ACCESSION #cross-references M01D:97394467
REFERENCE H64593
        #status preliminary: nucleic acid sequence not shown;
        translation not shown
        ##molecule_type DNA
        ##residues 1-1001 ##label TOM
        ##cross-references GB:AE000572; GB:AE000511; NID:g2313703; PID:g2313710;
        TIGR:HP0592

GENETICS
#start_codon TTG
#length 1001 #molecular-weight 114809 #checksum 2681
SUMMARY
Query Match 72.9%; Score 51; DB 2; Length 1001;
Best Local Similarity 45.5%; Pred. No. 2.87e+00;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
DB 329 AYLSNATLEK 339
OY 2 SYLSTSSLDK 12

RESULT 3
ENTRY   D70108      #type complete
TITLE   conserved hypothetical protein BB0068 - Lyme disease
        spirochete
ORGANISM
        #formal_name Borrelia burgdorferi #common_name Lyme disease
        spirochete
DATE     13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change
        05-Jun-1998
ACCESSIONS
REFERENCE D70108
        #authors Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.;
        Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.;
        Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb,
        J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.;
        Kertlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
        Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman,
        J.; Utterback, T.; Wathey, L.; McDonald, L.; Atchich, P.;
        Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst,
        K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
        #journal Nature (1997) 390:580-586
        #title Genomic sequence of a Lyme disease spirochete, Borrelia
        burgdorferi.
ACCESSION #cross-references M01D:9805943
REFERENCE D70108
        #status preliminary: nucleic acid sequence not shown;
        translation not shown
        ##molecule_type DNA

#residues 1-293 ##label KLE
#cross-references GB:AE001120; GB:AE000783; NID:g2687951; PID:g2687956;
        TIGR:BB0068
#experimental_source strain B31
SUMMARY #length 293 #molecular-weight 33278 #checksum 5223
Query Match 71.4%; Score 50; DB 2; Length 293;
Best Local Similarity 60.0%; Pred. No. 4.75e+00;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 198 AYLSNATLE 207
OY 2 SYLSTSSLDK 11

RESULT 4
ENTRY   T02684      #type complete
TITLE   DNA-binding protein CCAL - Arabidopsis thaliana
        protein F19D11.11
ALTERNATE_NAMES
        #formal_name Arabidopsis thaliana #common_name mouse-ear
        cress
DATE     24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
        24-Mar-1999
ACCESSIONS
REFERENCE T02684
        #authors Rounsley, S.D.; Liu, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.;
        Mason, T.M.; Shen, M.; Ronning, C.M.; Fraser, C.M.;
        Somerville, C.R.; Venter, J.C.
        #submission submitted to the EMBL Data Library, September 1998
        #description Arabidopsis thaliana chromosome II BAC F19D11 genomic
        sequence.
ACCESSION T02684
        #status preliminary: translated from GB/EMBL/DDay
        ##molecule_type DNA
        ##residues 1-608 ##label ROT
        ##cross-references EMBL:AC005310; NID:g3510247; PID:g3510263

GENETICS
#map_position II
#introns 13/3; 51/1; 71/3; 136/3; 194/3; 488/3
#note F19D11.11
SUMMARY #length 608 #molecular-weight 66975 #checksum 7668
Query Match 71.4%; Score 50; DB 2; Length 608;
Best Local Similarity 60.0%; Pred. No. 4.75e+00;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 165 YLSAASSMK 174
OY 3 YLSTSSLDK 12

RESULT 5
ENTRY   A56519      #type complete
TITLE   CDC16 protein - human
        #formal_name Homo sapiens #common_name man
ORGANISM
        #formal_name Homo sapiens #sequence_revision 19-Oct-1995 #text_change
        17-Mar-1999
ACCESSIONS
REFERENCE A56519
        #authors Tugendreich, S.; Tomkiele, J.; Earnshaw, W.; Hleter, P.
        #journal Cell (1995) 81:261-268
        #title CDC27Hs colocalizes with CDC16Hs to the centrosome and
        mitotic spindle and is essential for the metaphase to
        anaphase transition.
        #cross-references M01D:95254635
        #accession A56519
        #status preliminary: nucleic acid sequence not shown;
        translation not shown
        ##molecule_type mRNA
        ##residues 1-619 ##label TUG
        ##cross-references GB:U18291; NID:g603230; PID:g603231
        CLASSIFICATION #superfamily tetratricopeptide repeat homology
        keywords mitosis
```



```

FEATURE
333-366          #domain tetratricopeptide repeat homology #label TT1\
367-400          #domain tetratricopeptide repeat homology #label TT2
SUMMARY          #length 619 #molecular-weight 71526 #checksum 6875

Query Match
Best Local Similarity 50.0%; Pred. No. 4,75e+00;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 321 YLSTSSSLDK 330
| | | | | | | |
QY 3 YLSTSSSLDK 12

RESULT 6
ENTRY          F71520 #type complete
TITLE          hypothetical protein yprs - Chlamydia trachomatis (serotype
                D, strain UW3/Cx)
ORGANISM       #formal_name Chlamydia trachomatis
                13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
                21-Nov-1998
ACCESSIONS     F71520
REFERENCE       A71570
AUTHORS        Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe,
                R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov,
                R.L.; Zhao, O.; Koonin, E.V.; Davis, R.W.
                Science (1998) 282:754-759
                Genome sequence of an obligate intracellular pathogen of
                humans: Chlamydia trachomatis.
                #cross-references MUID:99000809
                #accession F71520
                #status preliminary
                ##molecule_type DNA
                ##residues 1-377 ##label ANN
                ##cross-references GB:AE001312; GB:AE001273; NID:93328812; PID:93328818
                ##experimental_source serotype D, strain UW-3/Cx
GENETICS
#gene          yprs
SUMMARY        #length 377 #molecular-weight 41449 #checksum 9699

Query Match
Best Local Similarity 70.0%; Score 49; DB 2; Length 377;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 324 ASYLSSPSVE 334
| | | | | | | |
QY 1 ASYLSSPSVE 11

RESULT 7
ENTRY          F70974 #type complete
TITLE          probable acral protein - Mycobacterium tuberculosis (strain
                H37RV)
ORGANISM       #formal_name Mycobacterium tuberculosis
                17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                17-Jul-1998
ACCESSIONS     F70974
REFERENCE       A70500
AUTHORS        Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
                C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
                III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
                Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
                Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
                Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
                Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
                Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
                Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.;
                Taylor, K.; Whitehead, S.; Barrett, B.G.
                Nature (1998) 393:537-544.
                Deciphering the biology of Mycobacterium tuberculosis from
                the complete genome sequence.
                #cross-references MUID:98295987
                #accession F70974
                #status preliminary; nucleic acid sequence not shown;
                ##molecule_type DNA
                ##residues 1-684 ##label COL
                ##cross-references GB:Z77162; GB:AL123456; NID:93261606; PID:e255032;
                ##experimental_source strain H37RV
GENETICS
#gene          rv0492c
SUMMARY        #length 684 #molecular-weight 72252 #checksum 890

Query Match
Best Local Similarity 70.0%; Score 49; DB 2; Length 684;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 117 ASYLFGSLPR 128
| | | | | | | |
QY 1 ASYLFGSLPR 12

RESULT 9
ENTRY          S44617 #type complete
TITLE          C50C3.11 protein - Caenorhabditis elegans
ORGANISM       #formal_name Caenorhabditis elegans
                20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                09-Sep-1997
ACCESSIONS     S44617
REFERENCE       S44617
AUTHORS        Favallo, A.D.
                #cross-references MUID:98295987
                #accession F70974

```

```

#status          preliminary; nucleic acid sequence not shown;
                translation not shown
##molecule_type DNA
##residues       1-650 ##label COL
##cross-references GB:AL009198; GB:AL123456; NID:93242262; PID:e1203309;
                PID:g2661670
##experimental_source strain H37RV
GENETICS
#gene          acral
SUMMARY        #length 650 #molecular-weight 70939 #checksum 8551

Query Match
Best Local Similarity 54.5%; Pred. No. 7,79e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 501 SSYPTKALD 511
| | | | | | | |
QY 1 ASYLSTSSLD 11

RESULT 8
ENTRY          G70744 #type complete
TITLE          hypothetical protein rv0492c - Mycobacterium tuberculosis
                (strain H37RV)
ORGANISM       #formal_name Mycobacterium tuberculosis
                17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                17-Jul-1998
ACCESSIONS     G70744
REFERENCE       A70500
AUTHORS        Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
                C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
                III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
                Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
                Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
                Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
                Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
                Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
                Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.;
                Taylor, K.; Whitehead, S.; Barrett, B.G.
                Nature (1998) 393:537-544
                Deciphering the biology of Mycobacterium tuberculosis from
                the complete genome sequence.
                #cross-references MUID:98295987
                #accession G70744
                #status preliminary; nucleic acid sequence not shown;
                ##molecule_type DNA
                ##residues 1-684 ##label COL
                ##cross-references GB:Z77162; GB:AL123456; NID:93261606; PID:e255032;
                ##experimental_source strain H37RV
GENETICS
#gene          rv0492c
SUMMARY        #length 684 #molecular-weight 72252 #checksum 890

Query Match
Best Local Similarity 70.0%; Score 49; DB 2; Length 684;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 117 ASYLFGSLPR 128
| | | | | | | |
QY 1 ASYLFGSLPR 12

RESULT 9
ENTRY          S44617 #type complete
TITLE          C50C3.11 protein - Caenorhabditis elegans
ORGANISM       #formal_name Caenorhabditis elegans
                20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                09-Sep-1997
ACCESSIONS     S44617
REFERENCE       S44617
AUTHORS        Favallo, A.D.
                #cross-references MUID:98295987
                #accession F70974

```


DATE 07-May-1995 #sequence_revision 01-Sep-1995 #text_change
09-Sep-1997

ACCESSIONS S51330

REFERENCE Watkins, J.N.; Campbell, A.K.
#authors
#submissions submitted to the EMBL Data Library, January 1995
#accession S51330

#status Preliminary

#molecule_type mRNA

#residues 1-238 #label WAT

SUMMARY #cross-references EMBL:X83959; NID:9634008; PID:9634009
#length 238 #checksum 8475

Query Match 68.6%; Score 48; DB 2; Length 238;
Best Local Similarity 70.0%; Pred. No. 1.27e+01;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 200 YLSTOSLSLK 209
3 YLSTSSSLDK 12

RESULT 14

ENTRY A56911 #type complete
TITLE TRADD protein - human
ALTERNATE_NAMES TNF receptor 1-associated protein TRADD
ORGANISM #formal_name Homo sapiens #common_name man
DATE 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 17-Mar-1999

ACCESSIONS A56911
REFERENCE A56911

#authors Hsu, H.; Xiong, J.; Goeddel, D.V.
#journal Cell (1995) 81:495-504
#title The TNF receptor 1-associated protein TRADD signals cell death and NF-kappaB activation.
#cross-references MUID:95277836
#accession A56911

#status Preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-312 #label H5U
#cross-references GB:L41690

GENETICS GDB:TRADD
#gene
#cross-references GDB:1320395

KEYWORDS Apoptosis

SUMMARY #length 312 #molecular-weight 34247 #checksum 3573

Query Match 68.6%; Score 48; DB 2; Length 312;
Best Local Similarity 58.3%; Pred. No. 1.27e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 14 SAYLTVSSSLDK 25
1 ASYLSTSSSLDK 12

RESULT 15

ENTRY JS0746
TITLE cytochrome P450 1A1 - Chinese hamster
CONTAINS oxidoreductase (EC 1.-.-.-)
ORGANISM #formal_name Cricetus griseus #common_name Chinese hamster
DATE 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 05-Mar-1999

ACCESSIONS JS0746
REFERENCE JS0746

#authors Ohgaki, S.; Goda, T.; Ishizaki, K.; Morimoto, M.; Sakamoto, T.; Kanataki, T.; Shintaki, N.
#submissions submitted to JIPID, September 1992
#accession JS0746

#molecule_type mRNA
#residues 1-524 #label OHG
#cross-references DDBJ:D12977; NID:9220307; PID:9220308
#note this is a revision to the sequence from reference JX0189

#note the source is designated as golden hamster

CLASSIFICATION #superfamily human cytochrome P450 CYP2D6; cytochrome P450

KEYWORDS homology
chromoprotein; electron transfer; heme; iron; monooxygenase;
oxidoreductase; transmembrane protein

FEATURE 461
#binding site heme iron (Cys) (axial ligand) #status predicted

SUMMARY #length 524 #molecular-weight 59136 #checksum 4669

Query Match 67.1%; Score 47; DB 2; Length 524;
Best Local Similarity 50.0%; Pred. No. 2.05e+01;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 436 FLTSSGTLDK 445
3 YLSTSSSLDK 12

Search completed: Thu Sep 2 12:27:45 1999
Job time : 20 secs.

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protein - protein database search, using Smith-Waterman algorithm

Thu Sep 2 11:25:17 1999; MasPar time 4.46 Seconds

Output not generated.

~~>US-08-599-226-11~~

Score: 63

able:

179066 seqs, 54579741 residues

Listing first 45 summaries

1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mmc 8:sp_ornanelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 21.734; Variance 25.202; scale 0.862

13. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, as derived by analysis of the total score distribution.

SUMMARIES

Core	Query	Match	Length	DB	ID	Description	Pred. No.
56	88.9	337	2	034232	ORF40X1 PROTEIN.	7.36e-020	
56	88.9	337	2	087136	ORF19-17 PROTEIN.	7.36e-020	
50	79.4	360	5	044626	KLID12.1 PROTEIN.	1.86e+000	
48	76.2	131	8	035865	NADH DEHYDROGENASE SUB	5.18e+000	
48	76.2	450	2	050511	ZINC PROTEASE.	5.18e+000	
48	76.2	496	6	087348	LAIRK21 RESTRICTION EN	5.18e+000	
47	74.6	16	14	079455	LIGHT-CHAIN COMPLEMENTA	8.57e+000	
47	74.6	16	14	079461	LIGHT-CHAIN COMPLEMENTA	8.57e+000	
46	73.0	278	8	045792	PLASMIN PAD1, OPEN REA	1.41e+010	
46	73.0	322	5	045024	NAPHTHOX OX1 TRANSERI	1.41e+010	
46	73.0	333	6	028175	RETINAL PIGMENT EPTTTE	1.41e+010	
46	73.0	333	6	005661	RETINAL PIGMENT EPTTTE	1.41e+010	
45	71.4	264	1	059506	264AA LONG HYPOTHETICA	2.29e+010	
45	71.4	320	2	068847	SITE-SPECIFIC RECOMBIN	2.29e+010	
44	69.8	292	10	048821	POTATIVE SERINE PROTEIN	3.71e+010	
44	69.8	298	5	061731	NON-RECEPTOR PROTEIN-T	3.71e+010	
44	69.8	316	10	049814	BETA-CAROTENE HYDROXYL	3.71e+010	
44	69.8	329	2	P96645	YDHF PROTEIN.	3.71e+010	
44	69.8	396	5	044435	KR5B8-1.	3.71e+010	
44	69.8	448	5	002441	GDP-DISSOCIATION INHIB	3.71e+010	

(TM)

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protein - protein database search, using Smith-Waterman algorithm

Thu Sep 2 11:25:17 1999; MasPar time 4.46 Seconds
110.021 Million cell updates/sec

Output not generated.

>US-08-599-226-11
(1-9) from US0859226.pep

Score: 63
1 OKYNSAPYA 9

BLAST: PAM 150
Gap 15

179066 segs, 54579741 residues

Listing: Minimum Match 0%
Listing first 45 summaries

Summary 19
1:sp:archaea 2:sp:bacteria 3:sp:fungi 4:sp:human
5:sp:invertebrate 6:sp:mammal 7:sp:mhc 8:sp:organelle
9:sp:phage 10:sp:plant 11:sp:rodent 12:sp:unclassified
13:sp:vertebrate 14:sp:virus

Mean 21.734; Variance 25.202; scale 0.862

No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description	Pred. No.
55	88.9	337	2	034232	ORF40X1 PROTEIN.	7.36e-02
56	88.9	337	2	087136	ORF139-17 PROTEIN.	7.36e-02
57	89.4	560	5	044626	KLID12.1 PROTEIN.	1.86e+00
58	79.4	560	5	035865	NADH DEHYDROGENASE SUB	5.18e+00
59	76.2	131	8	035865	ZINC PROTEASE.	5.18e+00
60	76.2	450	2	050511	LIAR21 RESPIRCTION EN	5.18e+00
61	76.2	496	2	087348	LIGHT-CHAIN COMPLEMETA	8.57e+00
62	74.6	16	14	079461	LIGHT-CHAIN COMPLEMETA	8.57e+00
63	74.6	16	14	079461	LIGHT-CHAIN COMPLEMETA	8.57e+00
64	73.0	278	2	047792	PLASMAID PAD1, OPEN REA	1.41e+01
65	73.0	322	5	045024	AMPHIOXUS OXY TRANSFER	1.41e+01
66	73.0	533	6	028175	RETINAL PIGMENT EPTHE	1.41e+01
67	73.0	533	6	005661	RETINAL PIGMENT EPTHE	1.41e+01
68	71.4	264	1	059506	264A LONG HYPOHETICA	2.29e+01
69	71.4	320	2	068847	SITE-SPECIFIC RECOMBIN	2.29e+01
70	69.8	292	10	048821	POTATIVE SERINE PROTEI	3.71e+01
71	69.8	298	5	061731	NON-RECEPTOR PROTEIN-T	3.71e+01
72	69.8	316	10	049814	BETA-CAROTENE HYDROXYL	3.71e+01
73	69.8	329	2	044345	YDHD PROTEIN.	3.71e+01
74	69.8	396	5	044345	YDHD PROTEIN.	3.71e+01
75	69.8	448	5	002441	GDP-DISSOCIATION INHIB	3.71e+01

RESULT	ID	Score	DB	Length	Matches	Mismatches	Indels	Gaps
1	034232	88.9%	2	337	337	0	0	0
2	034232	88.9%	2	337	337	0	0	0
3	034232	88.9%	2	337	337	0	0	0
4	034232	88.9%	2	337	337	0	0	0
5	034232	88.9%	2	337	337	0	0	0
6	034232	88.9%	2	337	337	0	0	0
7	034232	88.9%	2	337	337	0	0	0
8	034232	88.9%	2	337	337	0	0	0
9	034232	88.9%	2	337	337	0	0	0
10	034232	88.9%	2	337	337	0	0	0
11	034232	88.9%	2	337	337	0	0	0
12	034232	88.9%	2	337	337	0	0	0
13	034232	88.9%	2	337	337	0	0	0
14	034232	88.9%	2	337	337	0	0	0
15	034232	88.9%	2	337	337	0	0	0
16	034232	88.9%	2	337	337	0	0	0
17	034232	88.9%	2	337	337	0	0	0
18	034232	88.9%	2	337	337	0	0	0
19	034232	88.9%	2	337	337	0	0	0
20	034232	88.9%	2	337	337	0	0	0
21	034232	88.9%	2	337	337	0	0	0

ALIGNMENTS

RESULT	ID	Score	DB	Length	Matches	Mismatches	Indels	Gaps
1	034232	88.9%	2	337	337	0	0	0
2	034232	88.9%	2	337	337	0	0	0
3	034232	88.9%	2	337	337	0	0	0
4	034232	88.9%	2	337	337	0	0	0
5	034232	88.9%	2	337	337	0	0	0
6	034232	88.9%	2	337	337	0	0	0
7	034232	88.9%	2	337	337	0	0	0
8	034232	88.9%	2	337	337	0	0	0
9	034232	88.9%	2	337	337	0	0	0
10	034232	88.9%	2	337	337	0	0	0
11	034232	88.9%	2	337	337	0	0	0
12	034232	88.9%	2	337	337	0	0	0
13	034232	88.9%	2	337	337	0	0	0
14	034232	88.9%	2	337	337	0	0	0
15	034232	88.9%	2	337	337	0	0	0
16	034232	88.9%	2	337	337	0	0	0
17	034232	88.9%	2	337	337	0	0	0
18	034232	88.9%	2	337	337	0	0	0
19	034232	88.9%	2	337	337	0	0	0
20	034232	88.9%	2	337	337	0	0	0
21	034232	88.9%	2	337	337	0	0	0
22	034232	88.9%	2	337	337	0	0	0
23	034232	88.9%	2	337	337	0	0	0
24	034232	88.9%	2	337	337	0	0	0
25	034232	88.9%	2	337	337	0	0	0
26	034232	88.9%	2	337	337	0	0	0
27	034232	88.9%	2	337	337	0	0	0
28	034232	88.9%	2	337	337	0	0	0
29	034232	88.9%	2	337	337	0	0	0
30	034232	88.9%	2	337	337	0	0	0
31	034232	88.9%	2	337	337	0	0	0
32	034232	88.9%	2	337	337	0	0	0
33	034232	88.9%	2	337	337	0	0	0
34	034232	88.9%	2	337	337	0	0	0
35	034232	88.9%	2	337	337	0	0	0
36	034232	88.9%	2	337	337	0	0	0
37	034232	88.9%	2	337	337	0	0	0
38	034232	88.9%	2	337	337	0	0	0
39	034232	88.9%	2	337	337	0	0	0
40	034232	88.9%	2	337	337	0	0	0
41	034232	88.9%	2	337	337	0	0	0
42	034232	88.9%	2	337	337	0	0	0
43	034232	88.9%	2	337	337	0	0	0
44	034232	88.9%	2	337	337	0	0	0
45	034232	88.9%	2	337	337	0	0	0

RT 0139 are closely related to those of *Vibrio cholerae* 022."
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AB012956; D1034567; -
 SQ SEQUENCE 337 AA; 40147 MW; 176846EB CRC32;

Query Match 88.9%; Score 56; DB 2; Length 337;
 Best Local Similarity 87.5%; Pred. No. 7,36e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 147 OKYSAFY 154
 |||:||||
 QY 1 OKYSAFY 8

RESULT 3 PRELIMINARY; PRT; 560 AA.
 ID 044626;
 AC 044626;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 GN K11D12.1 PROTEIN.
 GN K11D12.1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECCERNTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA HEKHAUS J., WOHLDMANN P., GILLAM B.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF039047; G2736445; -
 DR PROSITE; PS00028; ZINC_FINGER_C2H2; 1.
 KW ZINC-FINGER; METAL-BINDING; DNA-BINDING.
 SQ SEQUENCE 560 AA; 61136 MW; 5906EB7D CRC32;

Query Match 79.4%; Score 50; DB 5; Length 560;
 Best Local Similarity 75.0%; Pred. No. 1,86e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 81 OKYKAPY 88
 |||:||||
 QY 1 OKYKAPY 8

RESULT 4 PRELIMINARY; PRT; 131 AA.
 ID 035865;
 AC 035865;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE NADH DEHYDROGENASE SUBUNIT 5 (ND5) (FRAGMENT).

OS STRONGYLOCENTROTUS INTERMEDIUS.
 OG MITOCHONDRION.
 OC EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA; EUECHINOIDEA;
 OC ECHINACEA; ECHINOIDEA; STRONGYLOCENTROTIDAE; STRONGYLOCENTROTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91175684.
 RA THOMAS W.K., MA J., WILSON A.C.;
 RT "Shifting constraints on tRNA genes during mitochondrial DNA
 RT evolution in animals";
 RL NEW BIOL. 193-100(1989).
 DR EMBL; M27670; E18387; -
 KW MITOCHONDRION.
 FT NON_TER
 SQ SEQUENCE 131 AA; 14311 MW; E0B87988 CRC32;

Query Match 76.2%; Score 48; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 5,18e+00;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 60 KYNAGPA 67
 |||:||||
 QY 2 KYNAGPA 9

RESULT 5 PRELIMINARY; PRT; 450 AA.
 ID 050511;
 AC 050511;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ZINC PROTEASE.
 GN SC9B10.04.
 OS STREPTOMYCES COELICOLOR.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA OLIVER K., HARRIS D.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE; 97000351.
 RA REDENBACH M., KIESER H.M., DENAPATTE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb streptomycetes coelicolor A3(2) chromosome";
 RL MOL. MICROBIOL. 21:77-96(1996).
 DR EMBL; AL009204; E1202335; -
 KW PROTEASE.
 SQ SEQUENCE 450 AA; 49045 MW; 3E30B71A CRC32;

Query Match 76.2%; Score 48; DB 2; Length 450;
 Best Local Similarity 44.4%; Pred. No. 5,18e+00;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 147 ORYDNPY 155
 |||:||||
 QY 1 ORYDNPY 9

RESULT 6 PRELIMINARY; PRT; 496 AA.
 ID 087348;
 AC 087348;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE LIAKR21 RESTRICTION ENZYME.
 GN LIAKR21.
 OS LACTOCOCCUS LACTIS (STREPTOCOCCUS LACTIS).
 OG PLASMID PKR223.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC LACTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TWOMEY D.P., MCKAY L.L., O'SULLIVAN D.J.:
 RT "Molecular characterization of the Lactococcus lactis LIAKR21
 restriction-modification system and effect of an IS982 element
 positioned between the restriction and modification genes.";
 RL J. BACTERIOL. 180:0-0(1998).
 DR EMBL: AF051563; G3702799; -.
 KM PLASMID.
 SO SEQUENCE 496 AA; 58081 MW; A04BA2A9 CRC32;

Query Match 76.2%; Score 48; DB 2; Length 496;
 Best Local Similarity 62.5%; Pred. No. 5,18e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 33 EXOSTPY 40
 QY 1 QKYNAPY 8

RESULT 7
 ID 079455 PRELIMINARY; PRT; 16 AA.
 AC 079455;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE LIGHT-CHAIN COMPLEMENTARITY-DETERMINING REGION 3 MRNA
 DE (CLONE 14), PARTIAL CDS (FRAGMENT).
 OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
 OC VIRUSES; RETROVIRUSES; RETROVIRIDAE; LENTIVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BURTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
 RA LERNER R.A.:
 RT "A large array of human monoclonal antibodies to type 1 human
 immunodeficiency virus from combinatorial libraries of asymptomatic
 seropositive individuals.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
 RL EMBL: M80720; G327942; -.
 DR EMBL: M80720; G327942; -.
 FT NON_TER 1 16
 SEQUENCE 16 AA; 1883 MW; 5462C8DD CRC32;

Query Match 74.6%; Score 47; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8,57e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4 QKYNAPY 10
 QY 1 QKYNAPY 7
 RESULT 8
 ID 079461 PRELIMINARY; PRT; 16 AA.
 AC 079461;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE LIGHT-CHAIN COMPLEMENTARITY-DETERMINING REGION 3 MRNA
 DE (CLONE 31), PARTIAL CDS (FRAGMENT).
 OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
 OC VIRUSES; RETROVIRUSES; RETROVIRIDAE; LENTIVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 92052225.

RA BURTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
 RA LERNER R.A.:
 RT "A large array of human monoclonal antibodies to type 1 human
 immunodeficiency virus from combinatorial libraries of asymptomatic
 seropositive individuals.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
 RL EMBL: M80726; G327954; -.
 DR EMBL: M80726; G327954; -.
 FT NON_TER 1 16
 SEQUENCE 16 AA; 1883 MW; 5462C8DD CRC32;

Query Match 74.6%; Score 47; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8,57e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 4 QKYNAPY 10
 QY 1 QKYNAPY 7

RESULT 9
 ID 047792 PRELIMINARY; PRT; 278 AA.
 AC 047792;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PLASMID PAD1, OPEN READING FRAMES.
 OS ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS).
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; ENTEROCOCCACEAE;
 OC ENTEROCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-OG1X;
 RX MEDLINE: 97074879.
 RA HIRT H., WIRTH R., MUSCHOLL A.:
 RT "Comparative analysis of 18 sex pheromone plasmids from Enterococcus
 faecalis: detection of a new insertion element on pPD1 and
 RT implications for the evolution of this plasmid family.";
 RL MOL. GEN. GENET. 252:640-647(1996).
 DR EMBL: X96977; E236596; -.
 KM PLASMID.
 SO SEQUENCE 278 AA; 30520 MW; 67892F0F CRC32;

Query Match 73.0%; Score 46; DB 2; Length 278;
 Best Local Similarity 62.5%; Pred. No. 1,41e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 227 QKYNAPY 234
 QY 1 QKYNAPY 8

RESULT 10
 ID 045024 PRELIMINARY; PRT; 322 AA.
 AC 045024;
 DT 01-UTN-1998 (TREMBLREL. 06, CREATED)
 DT 01-UTN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE AMPHILOXUS OTX TRANSCRIPTION FACTOR.
 GN OTX.
 OS BRANCHIOSTOMA FLORIDAE (FLORIDA LANCELET) (AMPHIOXUS).
 OC EUBRANCHIOTA; METAZOA; CHORDATA; CEPHALOCHORDATA; BRANCHIOSTOMIDAE;
 OC BRANCHIOSTOMA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WILLIAMS N.A., HOLLAND P.W.H.:
 RL MOL. BIOL. EVOL. 0:0-0(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: AF043740; G2828716; -.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 KM HOMEBOX; DNA-BINDING; NUCLEAR PROTEIN.
 SO SEQUENCE 322 AA; 34715 MW; F0E80B18 CRC32;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 208 EKYNSAPY 215
 :||:||||
 QY 1 QKXNSAPY 8

RESULT 15
 ID 048821 PRELIMINARY; PRT; 292 AA.
 AC 048821;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE PUTATIVE SERINE PROTEINASE.
 GN T3L16.3.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHITES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRARALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 DE LA BASTIDE M., HAMEED A., GNOJ L., JENSEN K., SHODY N.,
 GOTTESMAN T., HABERMANN K., HUANG E.N., SCHUTZ K., KAPLAN N.,
 RA LODHI M., MARRA M., DEBHIA N., PARNELL L.D., MARTENSSEN R.,
 RA MCCOMBIE W.R.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AC003952; G2708739; -;
 SQ SEQUENCE 292 AA; 33189 MW; F69680E1 CRC32;

Query Match 69.88; Score 44; DB 10; Length 292;
 Best Local Similarity 62.58; Pred. No. 3.71e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 215 HHYSAPY 222
 :||:||||
 QY 1 QKXNSAPY 8

Search completed: Thu Sep 2 11:25:40 1999
 Job time : 23 secs.

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 WISEMAN (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:28:28 1999; MasPar time 4.43 Seconds
 Molecular output not generated. 147.702 Million cell updates/sec

Title: >US-08-599-226-28
 Description: (1-12) from US08593226.pep
 Perfect Score: 70
 Sequence: 1 ASYLSTSSSLDK 12

Scoring table:
 Gap 150
 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

splemb19
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mmc 8:sp_organelle
 9:sp_phage 10:sp_plant 11:sp_protein 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 23.357; Variance 26.922; scale 0.868

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	53	75.7	127	14	011696	NUCLEOPROTEIN (FRAGMENT)	1.29e+00
2	51	72.9	471	10	023552	HYPOHETICAL 52.8 KD P	3.58e+00
3	51	72.9	1001	2	025314	TYPE III RESTRICTION E	3.58e+00
4	50	71.4	237	3	001357	AMINOPEPTIDASE (FRAGMENT)	5.89e+00
5	50	71.4	293	3	051095	CONSERVED HYPOHETICAL	5.89e+00
6	50	71.4	460	3	002321	EXOCYTOLOHIDROLASE.	5.89e+00
7	50	71.4	608	10	P92973	CCAL.	5.89e+00
8	50	71.4	619	4	013042	CCAL.	5.89e+00
9	49	70.0	377	2	084397	HYPOHETICAL 41.4 KD P	9.65e+00
10	49	70.0	384	2	011197	HYPOHETICAL 41.9 KD P	9.65e+00
11	49	70.0	650	2	050417	MULTI-FUNCTIONAL ENZYME	9.65e+00
12	48	68.6	203	1	029208	FLAGELLIN (FLAB1-1).	1.57e+01
13	48	68.6	238	5	017105	GREEN FLUORESCENT PROT	1.57e+01
14	48	68.6	238	5	093125	GREEN FLUORESCENT PROT	1.57e+01
15	48	68.6	238	5	027903	GREEN FLUORESCENT PROT	1.57e+01
16	48	68.6	238	5	017104	GREEN FLUORESCENT PROT	1.57e+01
17	48	68.6	239	12	009206	GREEN FLUORESCENT PROT	1.57e+01
18	48	68.6	455	13	007426	KERATIN.	1.57e+01
19	48	68.6	649	3	060167	PROTEIN COMPLEX ASSEMB	1.57e+01
20	47	67.1	520	5	P91803	POTATIVE CYTOSOL AMINO	2.53e+01

RESULT	ID	PRELIMINARY	PRT	127 AA.	ALIGNMENTS
AC	011696				
DT	01-JUL-1997 (TREMBLREL. 04, CREATED)				
DT	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)				
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)				
DE	NUCLEOPROTEIN (FRAGMENT).				
OS	MEASLES VIRUS (SUBGENUS SCEROPSE PANENCEPHALITIS VIRUS).				
OC	VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;				
OC	PARAMYXOVIRIDAE; PARAMYXOVIRINAE; MORBILLIVIRUS.				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN-92-E;				
RX	MEDLINE: 97278133.				
RA	YAMAGUCHI S.;				
RT	*Identification of three lineages of wild measles virus by nucleotide				
RT	sequence analysis of N, P, M, F, and L genes in Japan.*;				
RL	J. MED. VIROL. 52:113-120(1997).				
DR	EMBL: D87487; D1020995; -.				
KM	NUCLEOPROTEIN.				
FT	NON_TER				
SQ	SEQUENCE 127 AA; 13950 MW; 42D75A2C CRC32;				

Query Match	75.7%	Score 53; DB 14; Length 127;
Best Local Similarity	63.6%	Pred. No. 1.29e+00;
Matches	7; Conservative	4; Mismatches 0; Indels 0; Gaps 0;
DB	66	AA:PTSTPLD 76
OY	1	ASYLSTSSSLD 11
RESULT	2	
ID	023552	PRELIMINARY; PRT; 471 AA.
AC	023552	
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	
DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)	
DE	HYPOHETICAL 52.8 KD PROTEIN.	
OS	ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).	
OC	EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMBRYOPHYTES; TRACHEOPHYTES;	
OC	EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMBRYOPHYTES; TRACHEOPHYTES;	
OC	CAPNARLES; BRASSICACEAE; ARABIDOPSIS.	
RN	[1]	

RP SEQUENCE FROM N.A.
 RA BEVAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T., TERRY N.,
 RA KREIS M., KAVANACH T., ENTIAN K.D., RIEGER M., JAMES R.,
 RA PUTODOMENICH P., HATZIOPOULOS P., OBERMAYER B., DUSTENHOF A.,
 RA JONES J., PALME K., ANSGORGE W., DELSENY M., BAUCROFT I., MEMES H.W.,
 RA SCHUELLER C., CHALMUTZIS N.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU ARABIDOPSIS SEQUENCING PROJECT. ESSA:
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 297342: E327038: -.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 471 AA; 52785 MW; 4EB8315 CRC32;

Query Match 72.9%; Score 51; DB 10; Length 471;
 Best Local Similarity 63.6%; Pred. No. 3.58e+00;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

19 AGLTSSDLD 29
 1 AYLSTSSLD 11

RESULT 3 PRELIMINARY; PRT; 1001 AA.
 ID 025314;
 AC 025314;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE TYPE III RESTRICTION ENZYME R PROTEIN (RES).
 GN HP0592.
 OS BACTERIA: PROTEOBACTERIA: EPSILON SUBDIVISION; HELICOBACTER GROUP;
 OC BACTERIA: PROTEOBACTERIA: EPSILON SUBDIVISION; HELICOBACTER GROUP;
 CC HELICOBACTER.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-26695;
 RX MEDLINE: 97394467.
 RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
 RA FLEISCHMANN R.D., KETCHUM K.A., KLEIN H.-P., GILL S., DOUGHERTY B.A.,
 RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
 RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
 RA KEMENY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
 RA BERG D.E., GOCAYNE J.D., UTTERBACK T., PETERSON J.D., KELLEY J.M.,
 RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., MATTHEY L., WALLIN E.,
 RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the gastric pathogen *Helicobacter pylori* (published extratum appears in Nature 1997 Sep 25:389(6649):412).";
 RL NATURE 388:539-547(1997).
 DR EMBL: AE000572; G2313710: -.
 DR TIGR: HP0592: -.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 1001 AA; 114809 MW; 32AC1C8 CRC32;

Query Match 72.9%; Score 51; DB 2; Length 1001;
 Best Local Similarity 45.5%; Pred. No. 3.58e+00;
 Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

DB 329 AYLNGATLKR 339
 2 SYLSTSSLDK 12

RESULT 4 PRELIMINARY; PRT; 237 AA.
 ID 001357;
 AC 001357;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
 DE AMINOPEPTIDASE (FRAGMENT).

OS LUMBRICUS RUBELLUS (HUMUS EARTHORM).
 CC EUKARYOTA: METAZOA: ANNELIDA: CLITELLATA; OLIGOCHAETA; HAPLOTAXIDA;
 OC LUMBRICINA; LUMBRICIDAE; LUMBRICUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STREZENBAUM S.R., MORGAN A.J., KILLE P.;
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: Y12106: E310486: -.
 KW AMINOPEPTIDASE 1
 FT NON_TER
 SQ SEQUENCE 237 AA; 25384 MW; 27FF054 CRC32;

Query Match 71.4%; Score 50; DB 5; Length 237;
 Best Local Similarity 50.0%; Pred. No. 5.89e+00;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

DB 186 AALFMASGLDK 197
 1 AYLSTSSLDK 12

RESULT 5 PRELIMINARY; PRT; 293 AA.
 ID 051095;
 AC 051095;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE BBO068.
 GN BBO068.
 OS BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).
 OC BACTERIA: SPIROCHAETALES; SPIROCHAETACEAE; BORRELIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35210 / B31;
 RX MEDLINE: 98065943.
 RA FRASER C.M., CASSENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
 RA LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GINN M.,
 RA DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
 RA PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALBERG S., HANSON M.,
 RA VAN VICT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
 RA UTTERBACK T., MATTHEY L., MCDONALD L., ARTTACH P., BOWMAN C.,
 RA GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
 RA SMITH H.O., VENTER J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*";
 RL NATURE 390:580-586(1997).
 DR EMBL: AE001120; G2687956: -.
 DR TIGR: BB0068: -.
 SQ SEQUENCE 293 AA; 33278 MW; 3FB9B9E2 CRC32;

Query Match 71.4%; Score 50; DB 2; Length 293;
 Best Local Similarity 60.0%; Pred. No. 5.89e+00;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 198 AYLSTPNSLE 207
 2 SYLSTSSLD 11

RESULT 6 PRELIMINARY; PRT; 460 AA.
 ID 002321;
 AC 002321;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE EXOCELLULOBIOLYDROLASE.
 GN CBH11.
 OS PHANEROCHAETE CHRYSOSPORIUM.
 CC EUKARYOTA: FUNGI: BASIDIOMYCOTA; HYMENOMYCETES; STEREALES;
 CC CORTICIACEAE; PHANEROCHAETE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95110131.

RA TEMPELARS C.A., BIRCH P.R., SIMS P.F., BRODA P.;
 RT "Isolation, characterization, and analysis of the expression of the
 RT chbII gene of *Phanerochaete chrysosporium*.";
 RL APPL. ENVIRON. MICROBIOL. 60:4387-4393(1994).
 DR EMBL: S76141: G913560; -;
 DR PROSITE: PS00562: CBD_FUNGAL; 1.
 DR PROSITE: PS00655: GLYCOSYL_HYDROL_F6_1; 1.
 DR PROSITE: PS00656: GLYCOSYL_HYDROL_F6_2; 1.
 DR PFAM: PF00734: CBD_fungal; 1.
 DR PFAM: PF01341: Glycosyl_hydr21; 1.
 DR HYDROLASE.
 RM HYDROLASE.
 SQ SEQUENCE 460 AA; 48444 MW; 608D00B4 CRC32;
 Query Match 71.4%; Score 50; DB 3; Length 460;
 Best Local Similarity 41.7%; Pred. No. 5.89e+00;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 161 GYTLASASALGR 172
 :|||::||:|
 1 ASYSTSSSLDK 12

RESULT 7
 ID P92973 PRELIMINARY; PRT; 608 AA.
 AC P92973;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE CCA1.
 GN CCA1 OR F19D11.11.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEONS; ROSIDAE;
 CC CAPRARIACE; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA WANG Z., KENIGSBUCH D., SUN L., HAREL E., ONG M.S., TOBIN E.M.;
 RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA ROUNSLEY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON T.M.,
 RA SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence.";
 RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U28422; G177443; -;
 DR PFAM: AC005310: G3510263; -;
 DR PFAM: PF00249: myb-DNA-binding; 1.
 DR MENDEL: 12930; ARATH; 2130.1.
 RM DNA-BINDING.
 SQ SEQUENCE 608 AA; 66975 MW; 581864BA CRC32;
 Query Match 71.4%; Score 50; DB 10; Length 608;
 Best Local Similarity 60.0%; Pred. No. 5.89e+00;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 165 YLSAASSMKN 174
 |||||::|:
 3 YLSTSSSLDK 12

RESULT 8
 ID Q13042 PRELIMINARY; PRT; 619 AA.
 AC Q13042;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE CDC16HS.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 95254635.
 RA TUGENDREICH S., TOMKIEL J., EARNSHAW W.C., HIETER P.A.;
 RT "CDC27hs colocalizes with CDC16hs to the centrosome and mitotic
 RT spindle and is essential for the metaphase to anaphase transition.";
 RL CELL 81:261-268(1995).
 DR EMBL: U18291: G603231; -;
 DR PFAM: PF00515: TPR; 1.
 DR SEQUENCE 619 AA; 71526 MW; AE745552 CRC32;
 Query Match 71.4%; Score 50; DB 4; Length 619;
 Best Local Similarity 50.0%; Pred. No. 5.89e+00;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 321 YLSKATLEK 330
 |||::|:
 3 YLSTSSSLDK 12

RESULT 9
 ID O84397 PRELIMINARY; PRT; 377 AA.
 AC O84397;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 41.4 KD PROTEIN.
 GN YPRS.
 OS CHLAMYDIA TRACHOMATIS.
 CC BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D/TW-3/CX;
 RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
 RA MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
 RA DAVIS R.W.;
 RT "Genome Sequence of an Obligate Intracellular Pathogen of Humans:
 RT Chlamydia trachomatis.";
 RL SCIENCE 0:0-0(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-D/TW-3/CX;
 RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
 RA MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
 RA DAVIS R.W.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AE001312; G3328818; -;
 RM HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 377 AA; 41449 MW; 2879B006 CRC32;
 Query Match 70.0%; Score 49; DB 2; Length 377;
 Best Local Similarity 63.6%; Pred. No. 9.65e+00;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 324 ASYLSSPSVE 334
 |||||::|:
 1 ASYLSSTSLDK 11

RESULT 10
 ID Q11197 PRELIMINARY; PRT; 384 AA.
 AC Q11197;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 41.9 KD PROTEIN IN CMA1 3' REGION (ORF2).
 OS MYCOBACTERIUM TUBERCULOSIS.
 CC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOTRITALES; CORINBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RA;
 RX MEDLINE: 95327699.

RA YUAN Y., LEE R.E., BESRA G.S., BELISLE J.T., BARRY C.E. III;
 RT "Identification of a gene involved in the biosynthesis of
 RT cyclopropenated mycolic acids in Mycobacterium tuberculosis";
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:6630-6634(1995).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC FAMILY (SDR).
 DR EMBL: U27357; G886103; -.
 DR PFM: PF00106; adh_short; 1.
 KW HYPOTHETICAL PROTEIN: OXIDOREDUCTASE.
 SQ SEQUENCE 384 AA; 41995 MW; 9FF8465A CRC32;
 Db 235 SYLPTKALD 245
 Qy 1 ASYLSTSSLD 11
 RESULT 11 PRELIMINARY: PRT: 650 AA.
 AC 050417;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MULTI-FUNCTIONAL ENZYME.
 GN MT0004.49.
 OS MYCOBACTERIUM TUBERCULOSIS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; CORINEBACTERIINAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA OLIVER K., SKELTON J., BADCOCK K., CHURCHER C.M., HARRIS D.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE: 96181548.
 RA PHILIP W.J., POULET S., EIGMEIER K., PASCOBELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 RT leprae";
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
 DR EMBL: AL009198; E1202309; -.
 SQ SEQUENCE 650 AA; 70939 MW; 1E552E85 CRC32;
 Db 501 SSYPTKALD 511
 Qy 1 ASYLSTSSLD 11
 Query Match 70.0%; Score 49; DB 2; Length 650;
 Best Local Similarity 54.5%; Pred. No. 9.65e+00;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 RESULT 12 PRELIMINARY: PRT: 203 AA.
 ID 029208;
 AC 029208;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE FLAGELLIN (FLA1-1).
 GN AF1054.
 OS ARCHAEoglobus fulgidus.

OC ARCHAEA; EURYARCHAEOTA; ARCHAEoglobales; ARCHAEoglobaceae;
 OC ARCHAEoglobus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE: 98049343.
 RA KLENN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
 RA KETCHUM K.A., DOBSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
 RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDIS N.C.,
 RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
 RA PETERSON S., REICH C.T., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L.,
 RA OVERBEER R., GOCCARNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
 RA SADDON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
 RA CATTON P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
 RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the hyperthermophilic,
 RT sulphate-reducing archaeon Archaeoglobus fulgidus";
 RL NATURE 390:364-370(1997).
 DR EMBL: AE001030; G2649535; -.
 DR TIGR: AF1054; -.
 KW HYPOTHETICAL PROTEIN,
 SQ SEQUENCE 203 AA; 21865 MW; 7597A80C CRC32;
 Db 115 STESSSSLDK 125
 Qy 2 SYLSTSSLDK 12
 Query Match 68.6%; Score 48; DB 1; Length 203;
 Best Local Similarity 81.8%; Pred. No. 1.57e+01;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 RESULT 13 PRELIMINARY: PRT: 238 AA.
 ID 017105;
 AC 017105;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 DE GREEN FLUORESCENT PROTEIN (FRAGMENT).
 GN GFP.
 OS AEQUOREA VICTORIA (JELLYFISH).
 OC EUKARYOTA; METAZOA; CNIDARIA; HYDROZOA; HYDROIDA; LEPTOMEDUSAE;
 OC CAMPANULINIDAE; AEQUOREA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WATKINS J.N., CAMPBELL A.K.;
 RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X83959; G634009; -.
 FT NON_TER 238
 SQ SEQUENCE 238 AA; 26950 MW; C550BDBE CRC32;
 Db 200 YLSTOSALSK 209
 Qy 3 YLSTSSLDK 12
 Query Match 68.6%; Score 48; DB 5; Length 238;
 Best Local Similarity 70.0%; Pred. No. 1.57e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 RESULT 14 PRELIMINARY: PRT: 238 AA.
 ID 093125;
 AC 093125;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GREEN FLUORESCENT PROTEIN MUTANT 3.
 GN GFP.
 OS AEQUOREA VICTORIA (JELLYFISH).
 OC EUKARYOTA; METAZOA; CNIDARIA; HYDROZOA; HYDROIDA; LEPTOMEDUSAE;
 OC CAMPANULINIDAE; AEQUOREA.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96305137.
 RA CORMACK B.P.; VALDIVIA R.H., FALKOW S.;
 RT "FACS-optimized mutants of the green fluorescent protein (GFP).";
 RL GENE 173:33-38(1996).
 DR EMBL: U73901; G1669868; -
 SQ SEQUENCE 238 AA; 26840 MW; EBBFE099 CRC32;

Query Match 68.6%; Score 48; DB 5; Length 238;
 Best Local Similarity 70.0%; Pred. No. 1.57e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 200 YLSTQSALS 209
 ||||| |:
 QY 3 YLSTSSSLDK 12

RESULT 15
 Q27903 PRELIMINARY; PRT; 238 AA.
 Q27903:

01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GREEN FLUORESCENT PROTEIN.
 GN GFP.
 OS Aequorea victoria (Jellyfish).
 CC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
 CC Campanulididae; Aequorea.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97299832.
 RA ROEMENDAL G.J.A.; MENDES O.; WOLBERT E.J.H.; DE ROER A.D.;
 RT "Enhanced expression in tobacco of the gene encoding green
 fluorescent protein by modification of its codon usage.";
 RL PLANT MOL. BIOL. 33:989-999(1997).
 DR EMBL: X96418; E228230; -
 SQ SEQUENCE 238 AA; 26884 MW; EFF6ABB6 CRC32;

Query Match 68.6%; Score 48; DB 5; Length 238;
 Best Local Similarity 70.0%; Pred. No. 1.57e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 200 YLSTQSALS 209
 ||||| |:
 QY 3 YLSTSSSLDK 12

Search completed: Thu Sep 2 12:28:51 1999
 Search time : 23 secs.

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 WIRENET
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March 1999 protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 12:28:02 1999; Maspar time 2.19 Seconds
 Tabular output not generated. 155.012 Million cell updates/sec

Title: >US-08-599-226-28
 Description: (1-12) from US08599226.pep
 Perfect Score: 70
 Sequence: 1 ASYLSTSSSLDK 12

Scoring table:
 PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 24.319; Variance 24.390; scale 0.997

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	49	70.0	311	1	PYDA_LACLC	2.83e+00
2	49	70.0	684	1	DHYROOROTATE DEHYDRO	2.83e+00
3	49	70.0	734	1	UN36_CAEEL	2.83e+00
4	48	68.6	238	1	GFP_AEQVI	4.83e+00
5	48	68.6	328	1	TRAD_HUMAN	4.83e+00
6	47	67.1	352	1	YDH3_SCHPO	8.17e+00
7	47	67.1	357	1	PMEF_PROMI	8.17e+00
8	47	67.1	524	1	CP11_MESAU	8.17e+00
9	47	67.1	524	1	CP11_MESAU	8.17e+00
10	47	67.1	540	1	MLES_LACLA	8.17e+00
11	47	67.1	621	1	YODA_CAEEL	8.17e+00
12	47	67.1	661	1	MCRA_BACSD	8.17e+00
13	47	67.1	687	1	VICRA_VIBCH	8.17e+00
14	47	67.1	1160	1	TFE3_YEAST	8.17e+00
15	47	67.1	1655	1	N188_YEAST	8.17e+00
16	46	65.7	127	1	MBP_RAT	1.37e+01
17	46	65.7	132	1	YMO7_MACTU	1.37e+01
18	46	65.7	167	1	MBP_PANTR	1.37e+01
19	46	65.7	171	1	MBP_PANTR	1.37e+01
20	46	65.7	194	1	MBP_MOUSE	1.37e+01
21	46	65.7	196	1	MBP_MOUSE	1.37e+01
22	46	65.7	221	1	GSHE_RAT	1.37e+01
23	46	65.7	301	1	P34_RICRI	1.37e+01

RESULT	ID	STANDARD	PRT	311 AA	ALIGNMENTS
24	46	65.7	379	1	YOIL_MOUSE
25	46	65.7	460	1	CIS2_YEAST
26	46	65.7	471	1	UPO2_MAIZE
27	46	65.7	471	1	UPO3_MAIZE
28	46	65.7	471	1	UPO4_MAIZE
29	46	65.7	577	1	PYRH_YEAST
30	46	65.7	842	1	PLEG_CAUCR
31	45	64.3	416	1	YELI_ECOLI
32	45	64.3	467	1	KICL_CARAU
33	45	64.3	584	1	G6PD_ZYMO
34	45	64.3	524	1	CP11_MOUSE
35	45	64.3	547	1	MERA_STAAU
36	45	64.3	555	1	DHAB_CITFR
37	45	64.3	533	1	YDGE_SCHPO
38	45	64.3	635	1	PUTATIVE FLAVOPROTEIN
39	45	64.3	671	1	CUT9_YEAST
40	45	64.3	722	1	YC06_KLEPN
41	45	64.3	753	1	YBHJ_ECOLI
42	45	64.3	949	1	HYSA_STRPN
43	45	64.3	1328	1	EXO2_SCHPO
44	44	62.9	116	1	YJ90_YEAST
45	44	62.9	817	1	YG4A_YEAST

RESULT 1
 ID PYDA_LACLC STANDARD: PRT: 311 AA.
 AC P54321;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE DIHYDROOROTATE DEHYDROGENASE A (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE A) (DHODASE A) (DHODA).
 GN PYDA.
 OS LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; LACTOCOCCUS.
 CC [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-MG1363;
 RX MEDLINE: 94292416.
 RA ANDERSEN P.S., JANSSEN P.J.G., HAMMER K.;
 RT "Two different dihydroorotate dehydrogenases in Lactococcus lactis.";
 RL J. BACTERIOL. 176:3975-3982(1994).
 CC [2]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RP MEDLINE: 97184689.
 RX ROWLAND P., NIELSEN F.S., JENSEN K.F., LARSEN S.;
 RT "The crystal structure of the flavin containing enzyme dihydroorotate dehydrogenase A from Lactococcus lactis.";
 RL STRUCTURE 5:239-252(1997).
 CC [3]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RP MEDLINE: 98318035.
 RX ROWLAND P., BORNERBERG O., NIELSEN F.S., JENSEN K.F., LARSEN S.;
 RT "The crystal structure of Lactococcus lactis dihydroorotate dehydrogenase A complexed with the enzyme reaction product throws light on its enzymatic function.";
 RL PROTEIN SCI. 7:1269-1279(1998).
 CC [4]
 RN CATALYTIC ACTIVITY: L-DIHYDROOROTATE + O(2) -> OROTATE + H(2)O(2).
 CC [5]
 RN CORRELATOR: PAD.
 CC [6]
 RN PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
 CC [7]
 RN SUBUNIT: HOMODIMER.
 CC [8]
 RN SUBCELLULAR LOCATION: INNER SIDE OF THE MEMBRANE (BY SIMILARITY).
 CC [9]
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CC      EMBL; X74206; G511015; -
DR      PDB; 1DOR; 21-APR-97.
DR      PDB; 2DOR; 12-APR-98.
DR      PROSITE; PS00911; DHODENASE_1; 1.
DR      PROSITE; PS00912; DHODENASE_2; 1.
DR      PFM; PF01180; DHODENASE; 1.
KW      PYRIMIDINE BIOSYNTHESIS; OXIDOREDUCTASE; FLAVOPROTEIN; FAD;
KW      3D-STRUCTURE.
FT      NP_BIND 243 251 FAD (NAD PART) (POTENTIAL).
SO      SEQUENCE 311 AA; 34210 MW; 8C236089 CRC32;

Query Match
Best Local Similarity 41.7%; Score 49; DB 1; Length 311;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db      38 GAYIRKSTLEK 49
      ::::|::|:|
      1 ASYLSTSSLDK 12

RESULT 2
ID      YV18_MYCTU STANDARD; PRT; 684 AA.
AC      011157;
DT      01-OCT-1996 (REL. 34, CREATED)
DT      01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      HYPOTHETICAL 57.3 KD PROTEIN GMC-TYPE OXIDOREDUCTASE CY20G9.18C.
DE      MTCY20G9.18C.
OS      MYCOBACTERIUM TUBERCULOSIS.
OC      BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC      ACTINOMYCETALES; CORINEBACTERIAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-H37RV;
RA      MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RA      SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDJ DATA BANKS.
CC      -1- COPACOR: FAD FLAVOPROTEIN (BY SIMILARITY)
CC      -1- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sdb.ch).
CC      -----
CC      EMBL; 277162; E255032; -
DR      PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
DR      PROSITE; PS00624; GMC_OXRED_2; 1.
KW      HYPOTHETICAL PROTEIN; OXIDOREDUCTASE; FLAVOPROTEIN; FAD.
SO      SEQUENCE 684 AA; 72253 MW; F4A65D1F CRC32;

Query Match
Best Local Similarity 58.3%; Score 49; DB 1; Length 684;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db      117 ASYLTTGRSLPR 128
      |||::|:|:|
      1 ASYLSTSSLDK 12

RESULT 3
ID      UN36_CAEEL STANDARD; PRT; 734 AA.
AC      P34374;
DT      01-FEB-1994 (REL. 28, CREATED)
DT      01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT      01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE      UNC-36 PROTEIN.
DE      UNC-36 OR UNC-72 OR C50C3.11.
GN      CAENORHABDITIS ELEGANS.
OS      EUTARICOTA; METAZOA; NEMATODA; SECERNENTERA; RHABDITIA; RHABDITIDA;

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OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERIMAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RC MEDLINE; 94150718.
RA WILSON R., AINSOUDH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BUTTON J., CONNELL M., COSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA FULTON L., GARDNER A., GREEN P., HAKINS T., HILLIER L., JIER M.,
RA JOHNSON L., JONES M., KERSHAW J., KIRSEN J., LAISSER N.,
RA LARRELLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA STULTON J., THIRRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA WATERSOHN R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA WORLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL NATURE 368:32-38(1994).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
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CC
CC EMBL; L14433; G389650; -.
DR PIR; S44617; S44617.
DR WORMPEP; C50C3.11; CE00117.
DR PF00092; vva; 1.
RW IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; VOLTAGE-GATED CHANNEL;
RW CALCIUM CHANNEL; GLYCOPROTEIN.
FT CARBOHYD 100 100 POTENTIAL.
FT CARBOHYD 140 140 POTENTIAL.
FT CARBOHYD 146 146 POTENTIAL.
FT CARBOHYD 302 302 POTENTIAL.
FT CARBOHYD 476 476 POTENTIAL.
FT CARBOHYD 514 514 POTENTIAL.
SQ SEQUENCE 734 AA; 85034 MW; 5470D9C8 CRC32;
-----
Query Match 70.0%; Score 49; DB 1; Length 734;
Best Local Similarity 58.3%; Pred. No. 2,836+00;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 11 ATYVSTSSFNK 22
Oy 1 ASYLTSSSLDK 12

RESULT 4
AC GFF AEQVI STANDARD; PRT; 238 AA.
AD P42212;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GREEN FLUORESCENT PROTEIN.
GN GFP.
OC AEQUOREA VICTORIA (JELLYFISH).
OC EUPAROTEA; METAZOA; CNIDARIA; HYDROZOA; HYDROIDA; LEFTONEDUSAE;
CC CAMPANULIDAE; AEQUOREA.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE; 92175527.
RA PRASHER D.C., ECKENRODE V.K., WARD W.W., PRENDERGAST F.G.,
RA COSMIDE M.J.;
RT "Primary structure of the Aequorea victoria green-fluorescent
RT protein."
RL GENE 111:229-233(1992).
RN [2]

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RP CHROMOPHORE.
 RX MEDLINE: 93192221.
 RA CODY C.M., PRASHER D.C., WESTLER W.M., PRENDERGAST F.G., WARD W.M.;
 RT "Chemical structure of the hexapeptide chromophore of the Aequorea
 RT green-fluorescent protein.";
 RL BIOCHEMISTRY 32:1212-1218(1993).
 [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE: 96355665.
 RA ORMO M., CUBITT A.B., KALLIO K., GROSS L.A., TS'EN R.Y.,
 RA REMINGTON S.J.;
 RT "Crystal structure of the Aequorea victoria green fluorescent
 RT protein.";
 RL SCIENCE 273:1392-1395(1996).
 [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE: 98294543.
 RA YANG F., MOSS L.G., PHILLIPS G.N. JR.;
 RT "The molecular structure of green fluorescent protein.";
 RT NAT. BIOTECHNOL. 14:1246-1251(1996).
 -1- FUNCTION: ENERGY-TRANSFER ACCEPTOR. FLUORESCES IN VIVO UPON
 RECEIVING ENERGY FROM THE CA(2+)-ACTIVATED PHOTOPROTEIN Aequorin.
 ABSORBS LIGHT MAXIMALLY AT 395 NM AND EXHIBITS A SMALLER
 PEAKS AT 509 NM WITH A SHOULDER AT 540 NM.
 -1- SUBUNIT: MONOMER.
 -1- TISSUE SPECIFICITY: PHOTOCYTES.
 -1- PTM: CONTAINS A COVALENTLY ATTACHED CHROMOPHORE, WHICH IS COMPOSED
 OF MODIFIED AMINO ACID RESIDUES. THE CHROMOPHORE IS FORMED UPON
 CYCLIZATION OF THE RESIDUES SER-DEHYDROXY-GLY.

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 CC
 DR EMBL: M62654; G155663; -
 DR EMBL: M62653; G155661; -
 DR PDB: 1GFL; 11-JAN-97.
 DR PDB: 1EMA; 08-NOV-96.
 DR PDB: 1EMB; 16-JUN-97.
 DR PDB: 1EMC; 20-AUG-97.
 DR PDB: 2EMD; 20-AUG-97.
 DR PDB: 1EMF; 20-AUG-97.
 DR PDB: 1EMK; 20-AUG-97.
 DR PDB: 1EML; 20-AUG-97.
 DR PDB: 1EMM; 20-AUG-97.
 DR PDB: 2EMN; 20-AUG-97.
 DR PDB: 2EMO; 20-AUG-97.
 DR PDB: 1BEP; 07-JUL-97.
 KM LUMINESCENCE; 3D-STRUCTURE.
 FT SITE 65 67
 FT VARIANT 100 100 F -> Y.
 FT VARIANT 108 108 T -> S.
 FT VARIANT 141 141 L -> M.
 FT VARIANT 219 219 V -> I.
 SQ SEQUENCE 238 AA; 26886 MW; EB9112B8 CRC32;
 Query Match 68.6%; Score 48; DB 1; Length 238;
 Best Local Similarity 70.0%; Pred. No. 4.83e+00;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

AC Q15628;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR RECEPTOR TYPE 1 ASSOCIATED PROTEIN (TNFR1
 DE ASSOCIATED PROTEIN) (FRAGMENT).
 GN TRADD.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CARNIVORIN; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX HSU H., XIONG J., GOEDDEL D.V.;
 RT "The TNF receptor 1-associated protein TRADD signals cell death and
 RT NF-kappa B activation.";
 RL CELL 81:495-504(1995).
 -1- FUNCTION: SPECIFICALLY INTERACTS WITH THE CYTOPLASMIC DOMAIN OF
 CC ACTIVATED TNFR1. INTERACTS WITH TRAFs (TRAF1 AND TRAF2), FADD AND
 CC RIP. ACTS AS AN ADAPTOR MOLECULE FOR TNFR1 MEDIATING ITS
 CC INTERACTION WITH FADD. OVEREXPRESSION OF TRADD LEADS TO TWO MAJOR
 CC TNF-INDUCED RESPONSES, APOPTOSIS AND ACTIVATION OF NF-KAPPA B.
 CC -1- DOMAIN: REQUIRES THE INTACT DEATH DOMAIN TO ASSOCIATE WITH TNFR1.
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL EXAMINED TISSUES.

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 CC
 DR EMBL: L41690; G808915; -
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW APOPTOSIS.
 FT NON_TER 1 1
 FT DOMAIN 195 305 DEATH DOMAIN.
 FT DOMAIN 208 214 POLY-PRO.
 SQ SEQUENCE 328 AA; 35791 MW; 5610BC9F CRC32;
 Query Match 68.6%; Score 48; DB 1; Length 328;
 Best Local Similarity 58.3%; Pred. No. 4.83e+00;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 30 SAYLEVSILDK 41
 OY 1 ASYLSTSSILDK 12

RESULT 6
 ID YD83_SCHPO STANDARD; PRT; 352 AA.
 AC Q92348;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHEICAL 39.7 KD PROTEIN C6G9.03C IN CHROMOSOME 1.
 GN SPAC6G9.03C.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
 OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 OC SCHIZOSACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., CONNOR R.E.;
 RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBI DATA BANKS.
 -1- SIMILARITY: SOME, TO YEAST YNL206C.

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DR EMBL: 281317; E27610. -
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 352 AA; 39679 MW; D92A9357 CRC32;

Query Match 67.18; Score 47; DB 1; Length 352;
Best Local Similarity 54.58; Pred. No. 8.17e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 303 SYLNEASSEN 313
|||:||||:
QY 2 SYLSTSSLDK 12

RESULT 7
PMFE_PROMI STANDARD; PRT; 357 AA.
P53532;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE MINOR FIMBRIAL SUBUNIT PMFE PRECURSOR.
PMFE.
PROTEUS MIRABILIS.
BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC PROTEUS.
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-H14320;
RX MEDLINE: 95047519.
RA MASSAD G., MOBLEY H.L.T.;
RT "Genetic organization and complete sequence of the Proteus mirabilis
RT pmf fimbria operon."
RT GENE 150:101-104(1994).
RL -1- SUBCELLULAR LOCATION: FIMBRIA.
CC -1- SUBCELLULAR LOCATION: FIMBRIA.
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DR EMBL: 235428; G515905. -
KW FIMBRIA: SIGNAL.
FT CHAIN 29 357 PUTATIVE MINOR FIMBRIAL SUBUNIT PMFE.
SQ SEQUENCE 357 AA; 38876 MW; D65527D9 CRC32;

Query Match 67.18; Score 47; DB 1; Length 357;
Best Local Similarity 41.78; Pred. No. 8.17e+00;
Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Db 283 SNYLTGSVDYR 294
:|||:||||:
QY 1 ASYLSTSSLDK 12

RESULT 8
CP11_MESAU STANDARD; PRT; 524 AA.
AC 000557; 064665;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CYTOCHROME P450 1A1 (EC 1.14.14.1) (CYPIA1) (P-450MC).
GN CYPIA1.
OS MESOCRICETUS AURATUS (GOLDEN HAMSTER).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; CRICETINAE; MESOCRICETUS.

RN [1]
SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RX MEDLINE: 92138673.
RA SAGAMI I., OHNACHI T., FUJII H., KIKUCHI H., WATANABE M.;
RT "Hamster cytochrome P-450 1A gene family, P-450IA1 and P-450IA2 in
RT lung and liver: cDNA cloning and sequence analysis."
RL J. BIOCHEM. 110:641-647(1991).

RN [2]
SEQUENCE FROM N.A.
RA OHGITA S., GODA T., ISHIZAKI K., MORIMOTO M., SAKAMOTO T.,
RA KAMETAKI T., SHINKIKI N.;
RT "Molecular cloning and expression of hamster cytochrome P450 1A1 and
RT cytochrome P450 reductase."
RL SUBMITTED (SEP-1992) TO EMBL/GENBANK/DDBI DATA BANKS.
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY 3-METHYLCHOLANTHRENE (3MC).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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DR EMBL: D10251; D1001565. -
DR EMBL: D12977; D1002853. -
DR EMBL: D10913; G398131. -
DR PIR: JX0189; JX0189.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR PFAM: PF00067; P450; 1.

KW MICROSOE; ENDOPLASMIC RETICULUM.
FT BINDING 461 461
FT CONFICIT 18 18 L -> V (IN G220317).
FT CONFICIT 521 521 H -> Y (IN G220317).
SQ SEQUENCE 524 AA; 59136 MW; 021B406D CRC32;

Query Match 67.18; Score 47; DB 1; Length 524;
Best Local Similarity 50.08; Pred. No. 8.17e+00;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 436 FLNMSGTLDK 445
:|||:||||:
QY 3 YLSTSSLDK 12

RESULT 9
CP11_RAT STANDARD; PRT; 524 AA.
AC P00185;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CYTOCHROME P450 1A1 (EC 1.14.14.1) (CYPIA1) (P450-C).
GN CYPIA1 OR CYPIA-1.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE: 84298082.
RA SOGANA K., GOTOH O., KANAJIRI K., FUJII-KURIYAMA Y.;
RT "Distinct organization of methylcholanthrene- and phenobarbital-
RT inducible cytochrome P-450 genes in the rat.";

```

RL  PROC. NATL. ACAD. SCI. U.S.A. 81:5066-5070(1984).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE: 84169583.
RA  YABUSAKI Y., SHINIZU M., MURAFAMI H., NAKAMURA K., OEDA K., OKAWA H.;
RT  "nucleotide sequence of a full-length cDNA coding for 3-
RT  methylcholanthrene-induced rat liver cytochrome P-450MC."
RL  NUCLEIC ACIDS RES. 12:2929-2938(1984).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE: 85147736.
RA  HIMES R.N., LEVY J.B., CONRAD R.D., IVERSEN P.L., SHEN M.-L.,
RA  REMI A.M., BRESNICK E.;
RT  "Gene structure and nucleotide sequence for rat cytochrome P-450C."
RL  ARCH. BIOCHEM. BIOPHYS. 237:465-476(1985).
CC  -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC  MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC  NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC  OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC  ACIDS, AND XENOBIOTICS.
CC  -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC  OXIDIZED FLAVOPROTEIN + H(2)O.
CC  -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC  -1- INDUCTION: BY 3-METHYLCOLANTHRENE (3MC).
CC  -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC  -----
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CC  entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC  or send an email to license@isb-sdb.ch).
CC  -----
DR  EMBL: X02246; G203761; -.
DR  EMBL: X00469; G56044; -.
DR  EMBL: M26129; G203755; -.
DR  PIR: A00185; O4RTMC.
DR  PIR: S45716; S45716.
DR  PROSITE: PS00086; CYTOCHROME_P450; 1.
DR  PFM: PF00067; P450; 1.
KW  OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE; HEME;
KW  MICROsome; ENDOPLASMIC RETICULUM.
FT  BINDING 461 461 HEME.
FT  CONFLICT 53 53 I -> M (IN REF. 2).
FT  CONFLICT 494 494 M -> S (IN REF. 3).
SQ  SEQUENCE 524 AA; 59393 MW; C1F3EE1E CRC32;

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RT      "Cloning sequence and expression of the gene encoding the malolactic
RT      enzyme from Lactococcus lactis.";
RL      FEBS LETT. 332:74-80(1993).
RN      [2]
RN      SEQUENCE FROM N.A.
RC      STRAIN-1L1441;
RX      MEDLINE: 94178715.
RA      DENAYROLLES M., AIGLE M., LONVANDU-PINEL A.;
RT      "Cloning and sequence analysis of the gene encoding Lactococcus
RT      lactis malolactic enzyme: relationships with malic enzymes.";
RL      FEBS MICROBIOL. LETT. 116:79-86(1994).
CC      -1- FUNCTION: KEY ENZYME IN THE DEGRADATION OF L-MALIC ACID BY LACTIC
CC      ACID BACTERIA.
CC      -1- CATALYTIC ACTIVITY: (S)-MALATE + NAD(+) -> LACTATE + CO(2) + NADH.
CC      -1- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X75982; G461324; -
DR      EMBL; X71897; G467569; ALT_INT.
DR      PROSITE; PS00331; MALIC_ENZYMES; 1.
DR      PFM; PF00390; malic; 1.
KV      OXIDOREDUCTASE; NAD.
FT      CONFLICT 44 44 V -> E (IN REF. 2).
FT      CONFLICT 128 128 S -> N (IN REF. 2).
FT      CONFLICT 452 452 H -> Y (IN REF. 2).
SQ      SEQUENCE 540 AA; 59434 MW; 50A4DD21 CRC32;
Query Match 67.1%; Score 47; DB 1; Length 540;
Best Local Similarity 50.0%; Pred. No. 8,17e+00;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 50 YLRKPSDLK 59
||:|:|:|
Oy 3 YLRSTSSLDK 12

RESULT 11
ID YODA CAEEL STANDARD; PRT; 621 AA.
AC 009268;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 69.5 KD PROTEIN C32D5.10 IN CHROMOSOME II.
GN C32D5.10.
OS CAENORABDITIS ELEGANS.
OC EUTEROTELA; METAFOA; NEMATODA; SEGERMENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORABDITIS.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MILLER N.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC      -----
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CC      -----
DR      EMBL; U23511; G746473; -
DR      WORMPEP; C32D5.10; CE01840.
DR      PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.

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DR PFAM: PF00097; zfc3hca4.1.
 DR HSSP: P28990; ICHC.
 KM HYPOTHEICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
 FT 2N.FING 41 81 C3HC4-TYPE.
 FT DOMAIN 462 468 POLY-ASP.
 FT DOMAIN 471 476 POLY-ASP.
 SQ SEQUENCE 621 AA; 69474 MW; 86CC80B4 CRC32;

Query Match 67.1%; Score 47; DB 1; Length 621;
 Best Local Similarity 50.0%; Pred. No. 8.17e+00;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 608 ASYLSTGSLDR 619
 OY 1 ASYLSTSSLDK 12

RESULT 12
 ID MCPA_BACSU STANDARD; PRT; 661 AA.
 P39214;

01-FEB-1995 (REL. 31, CREATED)
 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE METHYL-ACCEPTING CHEMOTAXIS PROTEIN MCPA (HI).
 GN MCPA.

OS BACILLUS SUBTILIS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC BACILLUS.

RP SEQUENCE FROM N.A.
 RC STRAIN-168 / 011085;
 RX MEDLINE: 94245722.

RA HANON D.W., ORDAL G.W.;
 RT "Cloning and characterization of genes encoding methyl-accepting
 J. BIOL. CHEM. 269:14038-14046(1994).
 RL J. BIOL. CHEM. 269:14038-14046(1994).
 CC -1- FUNCTION: RESPONSIBLE FOR DETECTING GLUCOSE AND ALPHA-METHYLDIOSIDE.

CC -1- FUNCTION: CHEMOTACTIC-SIGNAL TRANSDUCERS RESPOND TO CHANGES IN THE
 CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT.
 CC TRANSDUCE A SIGNAL FROM THE OUTSIDE TO THE INSIDE OF THE CELL, AND
 CC FACILITATE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL
 CC OF METHYLATION. ALL AMINO ACIDS SERVE AS ATTRACTANTS IN
 CC B. SUBTILIS, THEY APPEAR TO CAUSE AN INCREASE IN THE TURNOVER
 CC METHYL GROUPS, LEADING TO METHYLATION OF AN UNIDENTIFIED ACCEPTOR,
 CC WHILE REPELLENTS HAVE BEEN SHOWN TO CAUSE A DECREASE IN METHYL
 CC GROUP TURNOVER. THE METHYL GROUPS ARE ADDED BY A METHYLTRANSFERASE
 CC AND REMOVED BY A METHYLESTERASE.

CC -1- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
 CC -----
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 CC -----

DR EMBL: L29189; G459690; -;
 DR EMBL: 299119; E1185987; -;
 DR EMBL: 299120; E1184202; -;
 DR SUBTILIS; BG10861; MCPA.
 DR PFAM: PF00015; MCPA; signal; 1.
 DR PFAM: PF00672; DUF5; 1.

KM CHEMOTAXIS; TRANSDUCER; TRANSMEMBRANE; METHYLATION
 FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 17 37 POTENTIAL.
 FT DOMAIN 38 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 302 POTENTIAL.
 FT DOMAIN 303 661 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 370 370 METHYLATION (BY SIMILARITY).
 FT MOD_RES 594 594 DEMETHYLATION AND METHYLATION
 (BY SIMILARITY).

FT MOD_RES 629 629 METHYLATION (BY SIMILARITY).
 FT MOD_RES 636 636 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 661 AA; 72399 MW; 45AB82F9 CRC32;

Query Match 67.1%; Score 47; DB 1; Length 661;
 Best Local Similarity 63.6%; Pred. No. 8.17e+00;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 36 AYOSASSSLDR 46
 OY 2 YLSTSSSLDK 12

RESULT 13
 ID VIBU_VIBCH STANDARD; PRT; 687 AA.
 AC 000964;

DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE VIBRIOCHACTIN RECEPTOR PRECURSOR.
 GN VIBU.

OS VIBRIO CHOLERAE.
 OC BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
 CC [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-OGAMA 395;
 RX MEDLINE: 92276356.

RA BUTTERTON J.R., STORBERNER J.A., PAYNE S.M., CALDERWOOD S.B.;
 RT "Cloning, sequencing, and transcriptional regulation of vib, the
 gene encoding the ferric vibriobactin receptor of *Vibrio cholerae*."
 J. BACTERIOL. 174:3729-3738(1992).
 RL J. BACTERIOL. 174:3729-3738(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-OGAMA 395;
 RA LIAO W.J., CHOI M.H., BUTTERTON J.R.;
 RT SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL J. BACTERIOL. 174:3729-3738(1992).
 CC -1- FUNCTION: RECEPTOR FOR FERRIC VIBRIOBACTIN.

CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
 CC -----
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 CC -----

DR EMBL: AF030977; G2641147; -;
 DR PIR: A41905; A41905.

DR PFAM: PF00593; TonB_DoxC; 1.
 KM SIGNAL; RECEPTOR; OUTER MEMBRANE; IRON TRANSPORT.
 FT SIGNAL 1 37
 FT CHAIN 38 687 VIBRIOBACTIN RECEPTOR.
 SQ SEQUENCE 687 AA; 76413 MW; 525D3D49 CRC32;

Query Match 67.1%; Score 47; DB 1; Length 687;
 Best Local Similarity 66.7%; Pred. No. 8.17e+00;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 662 YLSTNTTID 670
 OY 3 YLSTSSSLDK 11

RESULT 14
 ID TFC3_YEAST STANDARD; PRT; 1160 AA.
 AC P34111;

DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE TRANSCRIPTION FACTOR TAD 138 KD SUBUNIT (TRITIC 138 KD SUBUNIT).
 GN TFC3 OR TSV15 OR VAL001C OR FUN24.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).

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OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCHAROMYCETALES;
OC SACCHAROMYCETACEAE; SACCHAROMYCES.
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-S288C;
RC MEDLINE: 93066269.
RX LEBEVEY O., CARLES C., CONESA C., SWANSON R.N., BOUET F., RIVA M.,
RA SENTENAC A.;
RT "TFC3: gene encoding the B-block binding subunit of the yeast
RL transcription factor TFC.";
RL PROC. NATL. ACAD. SCI. U.S.A. 89:10512-10516(1992).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE: 95028152.
RA CLARK M.W., KENG T., STORMS R.K., ZHONG W., FORTIN N., ZENG B.,
RA DELANEY S., OUELLETTE B.F.F., BARTON A.B., KABACK D.B., BUSSSEY H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RT the 42 kbp SP07-CEN1-CD15 region.";
RT YEAST 10:535-541(1994).
CC -1- FUNCTION: TFC3 MEDIATES TRNA AND 5S RNA GENE ACTIVATION BY
CC BINDING TO INTRAGENIC PROMOTER ELEMENTS. IT ASSEMBLES THE
CC INITIATION COMPLEX TFIIB-TFC3-TDNA. TFC3 IS ESSENTIAL FOR
CC CELL VIABILITY.
CC -1- SUBUNIT: COMPOSED OF OF AT LEAST FOUR DIFFERENT SUBUNITS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -----
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CC -----
DR EMBL: M98261; G170944; -
DR EMBL: L22015; G385245; -
DR PIR: A46423; A46423.
DR PIR: S40892; S40892.
DR PIR: S43444; S43444.
DR SGI: L0002287; TFC3.
KW TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN.
FT DNA BIND 1 68 HMG BOX.
FT DNA BIND 1037 1110 HMG BOX.
SQ SEQUENCE 1160 AA; 132108 MW; F8AF54E4 CRC32;

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Query Match 67.1%; Score 47; DB 1; Length 1160;
Best Local Similarity 33.3%; Pred. No. 8.17e+00;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

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DB 581 SKYMGSTTLDR 592
OY 1 ASYLSTSSSLDR 12

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RESULT 15
ID N188 YEAST STANDARD; PRT: 1655 AA.
AC P52593;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE NUCLEOPORIN NUP188 (NUCLEAR PORE PROTEIN NUP188).
GN NUP188 OR YML103C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCHAROMYCETALES;
OC SACCHAROMYCETACEAE; SACCHAROMYCES.
RN [1]
RN SEQUENCE FROM N.A.
RA ZABEL U., DOYE V., TEKOTTE H., WEPF R., HURT E.C.;
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RN SEQUENCE FROM N.A.
RA NEHRBASS U., ROUT M.P., MAGUIRE S., BLOBEL G., WOZNIAK R.W.;

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RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA DEVLIN K., CHURCHER C., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RN SEQUENCE OF 1187-1205 AND 1611-1629.
RX MEDLINE: 96095775.
RA HITCHISON J.D., ROUT M.P., MARELLI M., BLOBEL G., WOZNIAK R.W.;
RT "Two novel related yeast nucleoporins Nup170p and Nup157p:
RT complementation with the vertebrate homologue Nup155p and functional
RT interactions with the yeast nuclear pore-membrane protein Pom152p.";
RL J. CELL BIOL. 131:1133-1148(1995).
CC -1- FUNCTION: INTERACTS WITH THE CORE STRUCTURE OF THE NUCLEAR PORE
CC COMPLEX (NPC). MAY PROVIDE THE NECESSARY ASYMMETRY REQUIRED FOR
CC ANCHORING STRUCTURES SUCH AS CYTOPLASMIC FILAMENTS AND THE
CC NUCLEOPLASMIC CAGE.
CC -1- SUBUNIT: INTERACTS WITH NUP170 AND/OR POM152.
CC -1- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX.
CC -----
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CC -----
DR EMBL: X90580; E195137; -
DR EMBL: U47107; G119622; -
DR EMBL: X80835; G530341; -
DR SGI: L0003099; NUP188.
KW NUCLEAR PROTEIN; TRANSPORT.
SQ SEQUENCE 1655 AA; 188576 MW; E6ECB147 CRC32;

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Query Match 67.1%; Score 47; DB 1; Length 1655;
Best Local Similarity 58.3%; Pred. No. 8.17e+00;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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DB 673 SSYLNKSDLLDR 684
OY 1 ASYLSTSSSLDR 12

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Search completed: Thu Sep 2 12:28:11 1999
Job time : 9 secs.

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FT	DISULFID	422	437	BY SIMILARITY.
FT	DISULFID	600	605	BY SIMILARITY.
FT	DISULFID	738	830	BY SIMILARITY.
FT	CARBOHYD	410	410	POTENTIAL.
FT	CARBOHYD	417	417	POTENTIAL.
FT	CARBOHYD	428	428	POTENTIAL.
FT	CARBOHYD	636	636	POTENTIAL.
FT	CARBOHYD	691	691	POTENTIAL.
FT	CARBOHYD	720	720	POTENTIAL.
FT	CONFLICT	250	250	G -> S (IN REF. 2).
FT	CONFLICT	555	555	S -> T (IN REF. 2).
FT	CONFLICT	557	567	F -> Y (IN REF. 2).
SO	SEQUENCE	846 AA;	92745 MM;	AC82836D CRC32;
Query Match		76.2%;	Score 48;	DB 1;
Best Local Similarity		55.6%;	Pred. NO. 2.41e+00;	Length 846;
Matches	5;	Conservative	4;	Mismatches 0;
			Indels	0;
			Gaps	0;
Db	717 ERYNASSYA 725			
Oy	1 OKYNAPYA 9			
RESULT	3	STANDARD:	PRT:	1139 AA.
ID	PKC1_TRIRE			
AC	099014;			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DE	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)			
DE	PROTEIN KINASE C-LIKE (EC 2.7.1.1-).			
GN	PKC1.			
OS	TRICHODERMA RESEI (HYPOCREA JECORINA).			
OC	EURYARCTA; FUNGI; ASCOMYCOTA; EUROMYCETES; PYRENOMYCETES;			
OC	HYPOCREALES; HYPOCREACEAE; HYPOCREA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-QM814 / ROT C-30;			
RX	MEDLINE; 96158841.			
RA	MORAWETZ R., LEDENFELD T., MISCHAR H., MUHLBAUER M., GRUBER F.,			
RA	GOODNIGHT J., DE GRAAF L.H., VISSER J., MOSHINSKI J.F.,			
RA	KUBICEK C.P.;			
RT	"Cloning and characterisation of genes (pkc1 and pkc4) encoding			
RT	protein kinase C homologues from Trichoderma reesei and Aspergillus			
RT	niger.";			
RL	MOL. GEN. GENET. 250:17-28(1996).			
CC	-1- ENZYME REGULATION: STIMULATED ABOUT TWOFOLD BY PHOSPHOLIPIDS OR			
CC	PHOSPHO ESTERS.			
CC	-1- SIMILARITY: CONTAINS TWO COPIES OF THE ZINC-DEPENDENT PHOSPHO-			
CC	ESTER AND DAG BINDING DOMAIN.			
CC	-1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-			
CC	PROTEIN KINASES. BELONGS TO THE PKC FAMILY.			
CC	-----			
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CC	-----			
CC	EMBL; U10016; G501075; -.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP. 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST. 1.			
DR	PROSITE; PS00479; DAG_PE_BINDING_DOMAIN. 2.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM. 1.			
DR	PFAM; PF00069; PKinase. 1.			
DR	PFAM; PF00130; DAG_PE-Bind. 2.			
DR	PFAM; PF00433; PKinase_C. 1.			
DR	HSSP; 063450; 1A06.			
KM	TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING; ZINC;			
KM	PHOSBO-ESTER BINDING; DUPLICATION.			
FT	DOMAIN	455	502	PHOSBO-ESTER BINDING (BY
FT				SIMILARITY).

FT DOMAIN 523 572 PHORBOL-ESTER AND DAG BINDING (BY
SIMILARITY).
FT DOMAIN 814 1073 PROTEIN KINASE.
FT NP_BIND 820 828 APP (BY SIMILARITY).
FT BINDING 843 843 ATP (BY SIMILARITY).
FT ACT_SITE 939 939 BY SIMILARITY.
SQ SEQUENCE 1139 AA; 126055 MW; 2AF00B6 CRC32;

Query Match 74.68; Score 47; DB 1; Length 1139;
Best Local Similarity 66.78; Pred. No. 4.06e+00;
Matches 6; Conservative 1; Indels 0; Gaps 0;

Db 707 HKXPADYA 715
:||||:|
OY 1 OKYNSAPYA 9

RESULT 4
ID CO3_LAMJA STANDARD; PRT; 1673 AA.
AC 000685;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN] (FRAGMENT).
GN C3.
OS LAMPEIRA JAPONICA (JAPANESE LAMPREY).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CEPHALASPIDOMORPHI;
OC PETROMYZONTIFORMES; PETROMYZONTIDAE; LAMPEIRA.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RX MEDLINE: 92251197.
RA NONAKA M., TAKAHASHI M.;
RT *Complete complementary DNA sequence of the third component of
complement of lamprey. Implication for the evolution of thioester
containing proteins.
J. IMMUNOL. 148:3290-3295(1992).
-1- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
COMPLEMENT SYSTEM. AFTER ACTIVATION (C3b), IT CAN BIND COVALENTLY,
VIA ITS REACTIVE THIOESTER, TO CELL SURFACE CARBOHYDRATES OR
IMMUNE AGGREGATES. CYCLOSTOMATES C3 APPEARS TO REPRESENT THE
COMMON ANCESTOR OF MAMMALIAN C3 AND C4, SHOWING SIMILARITIES TO
BOTH PROTEINS.
-1- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
-1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
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or send an email to license@isb-sib.ch).
CC EMBL: D10087; G222888;
DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
DR PFAM: PF00207; AZM; 1.
DR HSSP: P01024; IC3D.
KM COMPLEMENT PATHWAY; PLASMA; INFLAMMATORY RESPONSE; GLYCOPROTEIN;
KW SIGNAL.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN <1 13 POTENTIAL.
FT CHAIN 14 1673 COMPLEMENT C3.
FT CHAIN 14 653 BETA CHAIN (BY SIMILARITY).
FT CHAIN 657 1375 ALPHA CHAIN (BY SIMILARITY).
FT CHAIN 1379 1673 GAMMA CHAIN (BY SIMILARITY).
FT PEPTIDE 657 732 C3A ANAPHYLATOXIN (BY SIMILARITY).
FT DOMAIN 678 713 ANAPHYLATOXIN-LIKE.
FT DISULFID 678 705 BY SIMILARITY.
FT DISULFID 679 712 BY SIMILARITY.
FT DISULFID 692 713 BY SIMILARITY.

FT THIOLEST 986 990 BY SIMILARITY.
SQ SEQUENCE 1673 AA; 187767 MW; D857446F CRC32;

Query Match 74.68; Score 47; DB 1; Length 1673;
Best Local Similarity 75.08; Pred. No. 4.06e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 443 OKYNSASY 450
|||||:
OY 1 OKYNSAPY 8

RESULT 5
ID RV3R_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BLA1).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86041852.
RA KLOBECK H.G., MEINDL A., COMBRIATO G., SOLOMON A., ZACHAU H.G.;
RT *Human immunoglobulin kappa light chain genes of subgroups II and
III.
J. NUCLEIC ACIDS RES. 13:6499-6513(1985).
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CC EMBL: Z00021; G33179; -
DR PIR: A01899; K3H041.
DR PFAM: PF00047; 15; 1.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BLA1).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 FRAMEWORK 2.
FT DOMAIN 55 69 FRAMEWORK 3.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 X1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128
SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;
Query Match 73.08; Score 46; DB 1; Length 128;
Best Local Similarity 44.48; Pred. No. 6.79e+00;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 109 OQSTSPYT 117
|:|:|:
OY 1 OKYNSAPYA 9

RESULT 6
ID ARGD_KLULA STANDARD; PRT; 423 AA.
AC O14433;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ACETYLMONITRINE AMINOTRANSFERASE PRECURSOR (EC 2.6.1.11) (AC0AT).
GN ARG8.
OS KLUYVEROMYCES LACTIS (YEAST).

```

CC EUKARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMETES; SACCCHAROMYCETALES;
CC SACCCHAROMYCETACEAE; KUYVEROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CK56-7A;
RX MEDLINE; 98205889.
RA JANSSEN A., CHEN X.J.;
RT "Cloning, sequencing and disruption of the ARG6 gene encoding
RT acetylornithine aminotransferase in the petite-negative yeast
RT Kuyveromyces lactis";
RL YEA5T 14:281-285(1998).
RL
CC -1- CATALYTIC ACTIVITY: N2-ACETYL-L-ORNITHINE + 2-OXOGLUTARATE -
CC N-ACETYL-L-GLUTAMATE 5-SEMIALDEHYDE + L-GLUTAMATE.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FOURTH STEP IN ARGININE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
-----
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CC
CC EMBL; U93209; G2511462; -
CC DR PROSITE; PS00600; AA:TRANSFER_CLASS_3; 1.
CC DR PFAM; PF00202; aminotran_3; 1.
CC DR HSSP; P04181; 10MT.
CC DR STRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE;
CC KW ARGININE BIOSYNTHESIS; TRANSIT PEPTIDE; MITOCHONDRION.
CC KM TRANSIT 1
CC FT CHAIN ? 423 MITOCHONDRION (POTENTIAL).
CC FT BINDING 276 276 ACETYLORNITHINE AMINOTRANSFERASE.
CC FT SEQUENCE 423 AA; 46627 MM; EBA8A5B8 CRC32; PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC
CC SQ
CC
CC Query Match 73.0%; Score 46; DB 1; Length 423;
CC Best Local Similarity 55.6%; Pred. 6; 79e+00;
CC Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CC
CC DB 21 OKYQATYA 29
CC ||| : ||
CC QY 1 OKYNSAPYA 9
CC
CC RESULT 7
CC YMS5_CAEEL STANDARD; PRT; 1385 AA.
CC
CC RC P34501;
CC DT 01-FEB-1994 (REL. 28, CREATED)
CC DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
CC DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CC DE HYPOTHEETICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III.
CC K03H1.5.
CC OS CAENORHABDITIS ELEGANS.
CC CC EUKARYOTA: METAZOA; NEMATODA; SECCERNENTERA; RHABDITIA: RHABDITIA;
CC RHABDITINAE; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
CC [1]
CC RN SEQUENCE FROM N.A.
CC RP STRAIN-BRISTOL N2;
CC RX MEDLINE; 94150718.
CC RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
CC BOWFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
CC CRAXTON M., DEAR S., DU Z., DREBIN R., FAVELLO A., FRASER A.,
CC FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M.,
CC JOHNSON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
CC LAURELLE P., LIGHTING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
CC PARSONS J., PERCY C., REKEN L., ROOPEA A., SANDERS D., SHOWNKEEN R.,
CC SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
CC SUSTON J., THIERRY-MIES J., THOMAS K., VADDIN M., VAUGHAN K.,
CC WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
CC WOHLDMAN P.;

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RT      "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT      elegans".
RL      NATURE 368:32-38(1994).
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; 229560; E134784; -.
DR      PIR; S41028; S41028.
DR      MORPEP; K03H1.5; CEO3459.
DR      PIRAM; PF00084; ussh1.1.
KW      HYPOTHETICAL PROTEIN.
SQ      SEQUENCE 1385 AA; 159181 MW; A21334063 CRC32;

Query Match      73.0%; Score 46; DB 1; Length 1385;
Best Local Similarity 50.0%; Pred. No. 6,796+00;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db      797 HRYGAPY 804
OY      1 OKYNSAPY 8

RESULT      8
ID      KVIV.HUMAN      STANDARD:      PRT:      108 AA.
AC      P04430.
DT      13-AUG-1987 (REL. 05, CREATED)
DT      13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE      01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE      IG KAPPA CHAIN V-I REGION (BAN).
DE      OS HOMO SAPIENS (HUMAN).
DE      EUKARYOTA; METAOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN      [1]
RP      SEQUENCE.
RX      MEDLINE; 86174817.
RA      DWULFE F.E., O'CONNOR T.P., BENSON M.D.;
RL      "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL      MOL. IMMUNOL. 23:73-78(1986).
DR      PIR; A01878; KIHUBN.
DR      HSSP; PF00047; 19; 1.
DR      IMMUNOGLOBULIN V REGION; AMYLOID.
KW      DOMAIN
FT      DOMAIN 1 23 FRAMEWORK 1.
FT      DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN 3 49 FRAMEWORK 2.
FT      DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN 5 57 FRAMEWORK 3.
FT      DOMAIN 6 88 COMPLEMENTARITY-DETERMINING 3.
FT      DOMAIN 7 97 FRAMEWORK 4.
FT      DISULFID 98 107 BY SIMILARITY.
FT      NON_TER 23 88
FT      SEQUENCE 108 AA; 11840 MW; 0D44DB0A CRC32;

Query Match      71.4%; Score 45; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 1,136+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db      89 OQYNSPYT 97
OY      1 OKYNSAPYA 9

RESULT      9
ID      KVIA.HUMAN      STANDARD:      PRT:      114 AA.
AC      P01625.
DT      21-JUL-1986 (REL. 01, CREATED)
DT      01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

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ID EXA3_MOUSE STANDARD; PRT; 510 AA.
AC P97480; P97768; 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DE EYES ABSENT HOMOLOG 3.
GN EYA3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE-EMBRYO;
RA MEDLINE: 97202104.
RA ZIMMERMAN J.E., BUI Q.T., STEINGRIMSSON E., NAGLE D.L., FU W.,
RA BONINI A., SPINNER N.B., COPELAND N.G., JENKINS N.A., BUCAN M.,
RA BONINI N.M.;
RT "Cloning and characterization of two vertebrate homologs of the
RT Drosophila eyes absent gene";
RT GENOME RES. 7:128-141(1997).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE-EMBRYO;
RX MEDLINE: 97158722.
RX XU P.-X., WOO I., HER H., BEIER D.R., MAAS R.L.;
RT "Mouse Eya homologues of the Drosophila eyes absent gene require Pax6
RT for expression in lens and nasal placode";
RT DEVELOPMENT 124:219-231(1997).
RL
CC -1- FUNCTION: MAY BE INVOLVED IN DEVELOPMENT OF THE EYE. MAY PLAY A
CC ROLE IN MEDIATING THE INDUCTION AND DIFFERENTIATION OF CRANIAL
CC PLACODES.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN, ISOFORMS 1 AND 2,
CC MAY BE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE
CC IS THAT OF ISOFORM 1.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRANCHIAL ARCHES, CNS AND
CC DEVELOPING EYE.
CC -1- SIMILARITY: TO DROSOPHILA EYES ABSENT.
CC -----
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CC -----
RR EMBL: U81604; G1816533; -
RR EMBL: U61112; G1850335; -
RR MCD: MG1:109339; EYA3.
RR DEVELOPMENTAL PROTEIN; MULTIGENE FAMILY; ALTERNATIVE SPLICING.
RR VARSPLIC 1 105 MOEPRQETLSQVNNPDASDEKPEPTSSIASNLSMESEIMCT
RR DYPBRSDYTSQWNSAKPAHILSVSEETYPGOTGYOT
RR LOOSAPYAVYPOANTQGTGLPFA -> MILPHCILOT
RR (IN ISOFORM 2).
FT FT CONFLICT 272 272 A -> V (IN REF. 2).
FT FT SEQUENCE 510 AA; 55945 MW; 84087104 CRC32;
SQ
Query Match 69.8%; Score 44; DB 1; Length 510;
Best Local Similarity 55.6%; Pred. No. 1.85e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DE DELTA-ISOMERASE) (TYROSINASE-RELATED PROTEIN 2) (TRP-2) (TRP2) (SLATY
DE LOCUS PROTEIN).
DE DCT OR TYRP2 OR TYRP-2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92164640.
RA JACKSON I.J., CHAMBERS D.M., TSUKAMOTO K., COPELAND N.G.,
RA GILBERT D.J., JENKINS N.A., HEARING V.J.;
RT "A second tyrosinase-related protein, TRP-2, maps to and is mutated
RT at the mouse slaty locus";
RL EMBO J. 11:527-536(1992).
[2]
RP SEQUENCE OF 1-98 FROM N.A., AND VARIANTS SLATY-2J AND SLATY-LT.
RC STRAIN-129/SV;
RX MEDLINE: 96079089.
RA BUDD P.S., JACKSON I.J.;
RT "Structure of the mouse tyrosinase-related protein-2/dopachrome
RT tautomerase (Tyrp2/Dct) gene and sequence of two novel slaty
RT alleles";
RL GENOMICS 29:35-43(1995).
[3]
RN CHARACTERIZATION.
RX MEDLINE: 92164639.
RX TSUKAMOTO K., JACKSON I.J., URABE K., MONTAGUE P.M., HEARING V.J.;
RT "A second tyrosinase-related protein, TRP-2, is a melanogenic enzyme
RT termed Dopachrome tautomerase";
RL EMBO J. 11:519-526(1992).
[4]
RN ZINC-BINDING.
RX MEDLINE: 95071460.
RX SOLANO F., MARTINEZ-LIARTE J.H., JIMENEZ-CERVANTES C.,
RA GARCIA-BORRON J.C., LOZANO J.A.;
RT "Dopachrome tautomerase is a zinc-containing enzyme";
RL BIOCHEM. BIOPHYS. RES. COMMON. 204:1243-1250(1994).
[5]
RN ZINC-BINDING.
RX MEDLINE: 96152526.
RX SOLANO F., MARTINEZ-LIARTE J.H., JIMENEZ-CERVANTES C.,
RA GARCIA-BORRON J.C., JARA J.R., LOZANO J.A.;
RT "Molecular mechanism for catalysis by a new zinc-enzyme, dopachrome
RT tautomerase";
RL BIOCHEM. J. 313:447-453(1996).
CC -1- CATALYTIC ACTIVITY: L-DOPACHROME -> 5,6-DIHYDROXYINDOLE-2-
CC CARBOXYLATE.
CC -1- COFACTOR: CONTAINS TWO ZINC ATOMS.
CC -1- PATHWAY: MELANIN BIOSYNTHESIS.
CC -1- SUBUNIT: TYROSINASE, TRP-1 AND TRP-2 MAY FORM A MULTIZYME
CC COMPLEX.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MELANOSOMAL.
CC -1- TISSUE SPECIFICITY: MELANOCYTES AND RETINAL PIGMENTED EPITHELIUM.
CC -1- DISEASE: THE SLATY MUTATION IN TYRP2 LEADS TO A DECREASE OF DT
CC ACTIVITY AND A CONSEQUENT CHANGE IN THE PIGMENTATION OF THE MICE
CC TO A DARK GREY/BROWN EUMELANIN. THE SLATY-2J MUTATION HAS A
CC SIMILAR PHENOTYPE. THE SLATY-LT (LIGHT) MUTATION HAS A MORE SEVERE
CC EFFECT AND IS SEMIDOMINANT. ITS PHENOTYPE MAY BE A RESULT OF THE
CC FAILURE OF THE ENZYME TO BE CORRECTLY TARGETED TO ITS NORMAL
CC LOCATION ON THE INNER FACE OF THE MELANOSOMAL MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC -----
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CC -----
RR EMBL: X63349; G55066; -
RR EMBL: X85126; G854335; -
RR PIR: S19243; S19243.

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN-CB/20;
 RX MEDLINE; 97172972.
 RA ABDELHAK S., KALATZIS V., HEILIG R., COMPAIN S., SAMSON D.,
 RA VINCENT C., WEIL D., CRUAUD C., SAHLY I., LEBOVICI M.,
 RA BITNER-GLINDZIC M., FRANCIS M., LACOMBE D., VIGNERON J.,
 RA CHARACHON R., BOVEN K., BEDBEDER P., VAN REGEMORTER N.,
 RA WEISSENBACH J., PETIT C.;
 RT "A human homologue of the Drosophila eyes absent gene underlies
 RT branchio-oto-renal (BOR) syndrome and identifies a novel gene
 RT family.";
 RL NAT. GENET. 15:157-164(1997).
 CC -1- FUNCTION: MAY BE INVOLVED IN DEVELOPMENT OF THE EYE. MAY PLAY A
 CC ROLE IN MEDIATING THE INDUCTION AND DIFFERENTIATION OF CRANIAL
 CC PLACODES.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN, ISOFORMS 1 AND 2,
 CC MAY BE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE
 CC IS THAT OF ISOFORM 1.
 CC -1- TISSUE SPECIFICITY: EXTENSIVELY EXPRESSED IN CRANIAL PLACODES,
 CC BRANCHIAL ARCHES, CNS AND DEVELOPING EYE AND NOSE.
 CC -1- SIMILARITY: TO DROSOPHILA EYES ABSENT.
 CC -----
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 CC -----
 DR EMBL; U61110; G1850331; -.
 DR EMBL; Y10263; E290307; -.
 DR MGD; MGI:109344; EYAL.
 KW DEVELOPMENTAL PROTEIN; MULTIGENE FAMILY; ALTERNATIVE SPLICING.
 FT VARSPLIC 1 41 MEMOLTPSPHRLSGSSSPGPKLDSHINSTMTNGTE
 FT VARSPLIC 140 144 MISSING (IN ISOFORM 2).
 FT VARSPLIC 349 360 GILHLFPMDYG -> RDPTYSVLGR (IN ISOFORM
 FT 2).
 FT CONFLICT 117 117 M -> V (IN REF. 2).
 FT CONFLICT 163 163 L -> F (IN REF. 2).
 FT CONFLICT 324 325 LL -> FI (IN REF. 2).
 FT CONFLICT 405 405 R -> T (IN REF. 2).
 FT CONFLICT 450 450 K -> N (IN REF. 2).
 FT CONFLICT 505 505 S -> I (IN REF. 2).
 FT CONFLICT 535 535 S -> G (IN REF. 2).
 FT CONFLICT 539 539 R -> G (IN REF. 2).
 FT CONFLICT 548 548 V -> L (IN REF. 2).
 FT CONFLICT 551 552 LL -> VV (IN REF. 2).
 FT CONFLICT 559 559 E -> K (IN REF. 2).
 SQ SEQUENCE 591 AA; 64494 MW; A9F14613 CRC32;

Query Match 69.8%; Score 44; DB 1; Length 591;
 Best Local Similarity 71.4%; Pred. No. 1.85e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 229 YNNSPPY 235
 |||:|:
 QY 3 YNSAPYA 9

Search completed: Thu Sep 2 11:25:00 1999
 Job time : 9 secs.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Title: >US-08-599-226-11

Scoring table:

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Post-processing: Minimum Match 08
Listing first 45 summaries
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Statistics: Mean 14.794; Variance 45.658; scale 0.324

SUMMARIES

[illegible]

CC INFORMATION FOR SEQ ID NO: 84:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11532 MW; 65513 CN;
Query Match 74.6%; Score 47; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.75e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 87 OKYNSAP 93
QY 1 OKYNSAP 7
RESULT 7
ID PCT-US95-08743-82 STANDARD; PRT; 107 AA.
xxxxxx
DE Sequence 82, Application PC/TUS9508743
XX Sequence 82, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 82:
CC SEQUENCE CHARACTERISTICS:
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CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11570 MW; 65513 CN;
Query Match 74.6%; Score 47; DB 3; Length 107;
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QY 1 OKYNSAP 7
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XX Sequence 84, Application US/08899575
CC Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R

CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
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CC FILING DATE: 24-JUL-1997
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CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Filling, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 84:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
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CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170

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CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
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CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
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CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
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CC Query Match 74.6%; Score 47; DB 2; Length 107;
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CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8

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CC	NAME:	Fitting, Thomas
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CC	GENERAL INFORMATION:	
CC	APPLICANT:	Burton, Dennis R
CC	APPLICANT:	Barbas, Carlos F
CC	APPLICANT:	Lerner, Richard A
CC	TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES	
CC	TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS	
CC	NUMBER OF SEQUENCES:	170
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: The Scripps Research Institute, Office of	
CC	ADDRESSEE: Patent Counsel	
CC	STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,	
CC	STREET: Mail Drop TPC8	
CC	CITY:	La Jolla
CC	STATE:	CA
CC	COUNTRY:	USA
CC	ZIP:	92037
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CC	FILING DATE:	30-SEP-1993
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CC	APPLICATION NUMBER:	US 07/954,148
CC	FILING DATE:	30-SEP-1992
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CC	NAME:	Fitting, Thomas
CC	REGISTRATION NUMBER:	34,163
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CC	APPLICANT:	Burton, Dennis R
CC	APPLICANT:	Barbas, Carlos F
CC	APPLICANT:	Lerner, Richard A
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CC	TITLE OF INVENTION:	TO HUMAN IMMUNODEFICIENCY VIRUS
CC	NUMBER OF SEQUENCES:	170
CC	CORRESPONDENCE ADDRESSES:	
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CC	ADDRESSEE:	Patent Counsel
CC	STREET:	10666 NO. 5652138th Torrey Pines Road, Suite 220,
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CC	FILING DATE:	30-SEP-1992
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Fitting, Thomas
CC	REGISTRATION NUMBER:	34,163
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CC	NAME: Fitting, Thomas
CC	REGISTRATION NUMBER: 34,163
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CC	TELEFAX: 619-554-6312
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CC	GENERAL INFORMATION:
CC	APPLICANT: Genentech, Inc.
CC	TITLE OF INVENTION: Immunoglobulin Variants
CC	NUMBER OF SEQUENCES: 40
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Genentech, Inc.
CC	STREET: 460 Point San Bruno Blvd
CC	CITY: South San Francisco
CC	STATE: California
CC	COUNTRY: USA
CC	ZIP: 94080
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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CC	APPLICATION NUMBER: PCT/US93/07832
CC	FILING DATE: 19930820
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CC	APPLICATION NUMBER: 07/715272
CC	FILING DATE: 14-JUN-1991
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CC	APPLICATION NUMBER: PCT/US92/05126
CC	FILING DATE: 15-JUN-1992
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: 07/934373
CC	FILING DATE: 21-AUG-1992
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME:
CC	REGISTRATION NUMBER:

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CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE:
CC TELEFAX: 415/952-9881
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CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 109 AA; 11850 MW; 69772 CN;

Db Query Match 74.6%; Score 47; DB 3; Length 109;
OY Best Local Similarity 66.7%; Pred No. 5.75e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0

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DX
DY
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XX Patent No. 5821337
CC GENERAL INFORMATION:
CC APPLICANT: Paul J. Carter
CC APPLICANT: Leonard G. Presta
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 1 DNA Way
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
CC COMPUTER: IBM PC compatible
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CC CURRENT APPLICATION DATA:
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CC FILING DATE: 15-JUN-1992
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CC FILING DATE: 14-JUN-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER: 40,378
CC REFERENCE/DOCKET NUMBER: P0709P2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 650/225-1994
CC TELEFAX: 650/952-9881
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CC	GENERAL INFORMATION:			
CC	APPLICANT: B ylk, Claes Olof; Eriksson, Ulf; Peterson, Per A.			
CC	TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which			
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CC	TITLE OF INVENTION: Therefor, And Uses Thereof			
CC	NUMBER OF SEQUENCES: 6			
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CC	ADDRESSEE: Felte & Lynch			
CC	STREET: 805 Third Avenue			
CC	CITY: New York City			
CC	STATE: New York			
CC	COUNTRY: USA			
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CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Kohli, Vineet			
CC	REGISTRATION NUMBER: 37,003			
CC	REFERENCE/DOCKET NUMBER: LUD 5280.3			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (212) 688-9200			
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Search completed: Thu Sep 2 11:26:05 1999
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 WISE RELEASE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Msearch.p protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:23:44 1999; Maspar time 3.56 Seconds
 53.828 Million cell updates/sec

 Molecular output not generated.

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Scoring table: PAM 150

Gap 15

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

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a-geneseqs
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 19:part19 20:part20 21:part21 22:part22 23:part23
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Statistics: Mean 15.775; Variance 47.273; scale 0.334

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

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5	58	92.1	9 27	W27571	Anti-TNF-alpha antilo	7.21e+00
6	57	90.5	9 27	W27573	Anti-TNF-alpha antilo	9.38e+00
7	57	90.5	9 27	W27582	Anti-TNF-alpha antilo	9.38e+00
8	56	88.9	9 27	W27578	Anti-TNF-alpha antilo	1.22e+01
9	56	88.9	9 27	W27575	Anti-TNF-alpha antilo	1.22e+01
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12	54	85.7	9 27	W27580	Anti-TNF-alpha antilo	2.06e+01
13	53	84.1	9 27	W27583	Anti-TNF-alpha antilo	2.67e+01
14	53	84.1	9 27	W27584	Anti-TNF-alpha antilo	2.67e+01
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19	49	77.8	107 10	R54308	Anti-HIV gp120 immuno	1.22e+02
20	47	74.6	107 10	R54305	Anti-HIV gp120 immuno	1.22e+02
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27	46	73.0	107 28	W31726	Alpha light chain anti	1.57e+02
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40	45	71.4	155 26	W32483	Kappa light chain var	2.01e+02
41	45	71.4	342 26	W32482	Growth factor TRLH (C	2.01e+02
42	44	69.8	495 26	W32480	Growth factor CTAB-T	2.01e+02
43	44	69.8	749 21	W14053	TIM01 mutant protein.	2.57e+02
44	44	69.8	1389 21	W14051	TIM protein splice va	2.57e+02
45	44	69.8	2270 14	R71010	Human neuronal calcin	2.57e+02

ALIGNMENTS

RESULT 1
 ID W27570 standard; peptide; 9 AA.
 AC W27570;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Seifeld JG, Schoenhaut D, Vaughan TV, White M, Willon AJ;
 PI WPI; 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 67; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L292 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerostis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 100.0%; Score 63; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.90e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysapya 9
 |||||||
 Qy 1 OKNSAPYA 9

RESULT 2
 W2574 standard; peptide; 9 AA.

AC W2574:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Markovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 69; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 96.8%; Score 61; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3.25e+00;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 qkysapya 9
 |||||||
 Qy 1 OKNSAPYA 9

RESULT 3
 W2576 standard; peptide; 9 AA.

ID W2576:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Markovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 69; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 93.7%; Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.35e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysapya 8
 |||||||
 Qy 1 OKNSAPYA 8

RESULT 4
 W2577 standard; peptide; 9 AA.

ID W2577:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM peridontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PI Salfield JG, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
 WPI: 97-415302/38.
 PS High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, peridontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 SQ Sequence 9 AA:
 Query Match 93.7%: Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%: Pred. No. 5.53e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 qkynsapy 8
 |||||
 1 OKYNSAPY 8

PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, peridontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 SQ Sequence 9 AA:
 Query Match 92.1%: Score 58; DB 27; Length 9;
 Best Local Similarity 88.9%: Pred. No. 7.21e+00;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 qkynsapy 9
 |||||
 1 OKYNSAPYA 9

RESULT 5
 ID W2571 standard; peptide: 9 AA.
 AC W2571:
 DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM peridontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PI Salfield JG, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

RESULT 6
 ID W2573 standard; peptide: 9 AA.
 AC W2573:
 DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM peridontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PI Salfield JG, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption diseases,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA.

Query Match 90.5%; Score 57; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 9.39e+00;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
| | | | |
OY 1 QKNSAPYA 9

RESULT 7
ID W2582 standard: peptide; 9 AA.

AC W2582;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain: complementarity determining region 3; inhibition;
KW treatment: sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PR 25-NOV-1996: US-031476.
PS 09-FEB-1996: US-599226.
PT (BADT) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 71; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption diseases,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA.

Query Match 90.5%; Score 57; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 9.39e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
| | | | |
OY 1 QKNSAPYA 9

RESULT 8
ID W2575 standard: peptide; 9 AA.

AC W2575;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain: complementarity determining region 3; inhibition;
KW treatment: sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PR 25-NOV-1996: US-031476.
PS 09-FEB-1996: US-599226.
PT (BADT) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 69; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA.

Query Match 88.9%; Score 56; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.22e+01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
| | | | |
OY 1 QKNSAPYA 9

RESULT 9

W2578 standard: peptide: 9 AA.

AC W2578;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha: TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN W09729131-A1.

PD 14-AUG-1997.

PE 10-FEB-1997; U02219.

PR 25-NOV-1996; US-031476.

PR 09-FEB-1996; US-599226.

PA (BAD1) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Milton AJ;

PI MPI: 97-415302/38

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 70; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Kof rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

CC Sequence 9 AA.

Query Match 88.9%; Score 56; DB 27; Length 9;

Best Local Similarity 77.8%; Pred. No. 1.22e+01;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkytsapyt 9

| | | | |

QY 1 QKYSAPYA 9

RESULT 10

W2585 standard: peptide: 9 AA.

AC W2585;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha: TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN W09729131-A1.

PD 14-AUG-1997.

PE 10-FEB-1997; U02219.

PR 25-NOV-1996; US-031476.

PR 09-FEB-1996; US-599226.

PA (BAD1) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Milton AJ;

PI MPI: 97-415302/38

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 72; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Kof rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

CC Sequence 9 AA.

Query Match 87.3%; Score 55; DB 27; Length 9;

Best Local Similarity 77.8%; Pred. No. 1.59e+01;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkytsapya 9

| | | | |

QY 1 QKYSAPYA 9

RESULT 11

W2579 standard: peptide: 9 AA.

AC W2579;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha: TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN W09729131-A1.

PD 14-AUG-1997.

PE 10-FEB-1997; U02219.

PR 25-NOV-1996; US-031476.

PR 09-FEB-1996; US-599226.

PA (BAD1) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PT Claim 20: Page 70: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, allergy, multiple
 CC spondylitis, osteoarthritis, gouty arthritis, rheumatoid
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 85.7%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.06e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynary 8
 1 OKVNSAPY 8

1 n 5

RESULT 12
 ID W27580 standard; peptide: 9 AA.
 AC W27580;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Menkovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 71: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 85.7%; Score 54; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.06e+01;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsaays 9
 1 OKVNSAPYA 9

RESULT 13
 ID W27583 standard; peptide: 9 AA.
 AC W27583;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Menkovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 72: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 84.1%; Score 53; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.67e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkysappt 9
 ||| |||
 1 OKYNSAPYA 9

RESULT 14
 ID W27568 standard; peptide: 9 AA.
 AC W27584;

DE 19-MAR-1998 (first entry)
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Menkovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI; 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS Claim 20; Page 72; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 84.1%; Score 53; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.67e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkynrpyt 9
 ||| |||
 1 OKYNSAPYA 9

RESULT 15
 ID W27568 standard; Protein: 107 AA.
 AC W27568;

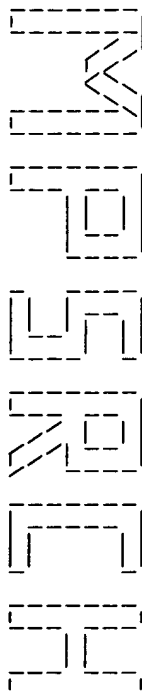
DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody;
 KW light chain; variable region; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Menkovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI; 97-415302/38.
 DR N-PDB; T88403.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS Claim 15; Page 75; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 107 AA;

Query Match 84.1%; Score 53; DB 27; Length 107;
 Best Local Similarity 66.7%; Pred. No. 2.67e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 89 qkynrpyt 97
 ||| |||
 1 OKYNSAPYA 9

Search completed: Thu Sep 2 11:24:03 1999
 Job time : 19 secs.

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(TM)

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Search on: Thu Sep 2 11:24:20 1999; Maspar time 3.07 Seconds

Protein - protein database search, using Smith-Waterman algorithm

117.515 Million cell updates/sec

Output not generated.

Title: >US-08-599-226-11
Description: (1-9) from US08599226.pep
Perfect Score: 63
Sequence: 1 OKNSAPYA 9

Scoring table: PAM 150
Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: disco
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 22.058; Variance 27.104; scale 0.814

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	48	76.2	500	2	S64220	hypothetical protein
2	48	76.2	846	2	S12005	neurotactin - fruit f
3	48	76.2	846	2	S13795	neurotactin - fruit f
4	47	74.6	91	2	S67940	ig kappa chain V reg1
5	47	74.6	92	2	S37513	ig kappa chain V reg1
6	47	74.6	95	2	PH0863	ig kappa chain V reg1
7	47	74.6	107	2	S40366	ig kappa chain V-J re
8	47	74.6	109	2	A30608	ig kappa chain V-J re
9	47	74.6	109	2	H30601	ig kappa chain V-J re
10	47	74.6	1139	2	S61918	protein kinase C (EC
11	47	74.6	1673	2	I50806	complement component
12	46	73.0	128	1	K3H041	ig kappa chain precu
13	46	73.0	278	1	S72385	hypothetical protein
14	46	73.0	533	2	A47143	retinal pigment mero
15	46	73.0	1409	2	S41028	hypothetical protein
16	45	71.4	106	2	A49138	iga kappa rheumatoid
17	45	71.4	107	2	A28195	ig kappa chain V reg1
18	45	71.4	108	2	PL0204	anti-DNA autoantibody
19	45	71.4	108	1	K1H0BN	ig kappa chain V-I re
20	45	71.4	114	1	K4H0BN	ig kappa chain V-I re
21	45	71.4	129	1	S40369	ig kappa chain - huma
22	45	71.4	216	2	JE0241	ig kappa chain Am37 p
23	45	71.4	264	2	D71197	hypothetical protein

24	45	71.4	376	2	S73941	oligopeptide transpor
25	44	69.8	292	2	T00829	homeodomain transcrip
26	44	69.8	329	2	A69776	transposon-related pr
27	44	69.8	376	2	S55149	hypothetical protein
28	44	69.8	517	2	S19243	tyrosinase-related pr
29	44	69.8	615	1	ABCHS	serum albumin precurs
30	44	69.8	790	2	S27458	SMY2 protein - yeast
31	44	69.8	947	1	PXBYP2	H+-transporting ATPas
32	44	69.8	1010	1	PX2P2P	H+-transporting ATPas
33	44	69.8	1144	2	A36968	p1-like adhesin precu
34	44	69.8	1203	2	S27545	pullulanase - Thermoa
35	44	69.8	1260	2	S28407	guanine nucleotide-ex
36	44	69.8	1290	2	A56493	leucocyte common anti
37	44	69.8	1388	2	A57655	tim (timeless) protei
38	44	69.8	1897	1	TDHUK	leucocyte antigen-rel
39	44	69.8	1898	2	S46216	leucocyte antigen-rel
40	44	69.8	2251	2	B54972	voltage-dependent cal
41	44	69.8	2259	2	S29236	calcium channel prote
42	44	69.8	2270	2	A54972	voltage-dependent cal
43	44	68.3	279	1	SNF5K	multicatalytic endope
44	43	68.3	473	2	A54494	knob-associated histi
45	43	68.3	657	2	A29454	knob-associated histi

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE S64220 #type complete
hypothetical protein YGL202w - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein G1253
ORGANISM #formal name Saccharomyces cerevisiae
DATE 17-May-1996 #sequence_revision 17-May-1996 #text_change 06-Feb-1998

ACCESSIONS S64220
REFERENCE S64218
#authors Bjournson, A.J.; McReynolds, A.D.K.; Wright, L.F.
#submission submitted to the Protein Sequence Database, May 1996
#accession S64220
#molecule_type DNA
#residues 1-500 #label BJO
#cross-references EMBL:Z72724; NID:G1322833; PID:E243502; PID:G1322834;
MIPS:YGL202w

GENETICS
#experimental_source strain S288C
#gene SCD:ARO8
#cross-references SCD:S0003170; MIPS:YGL202w

SUMMARY
#map_position 71
#length 500 #molecular_weight 56177 #checksum 3537

Query Match 76.2%; Score 48; DB 2; Length 500;
Best Local Similarity 85.7%; Pred. No. 7.08e+00;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 415 KINSAPY 421
QY 2 KINSAPY 8

RESULT 2
ENTRY 2
TITLE S12005 #type complete
neurotactin - fruit fly (Drosophila sp.)
ORGANISM #formal name Drosophila sp.
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1998

ACCESSIONS S12005
REFERENCE S12005
#authors de la Escalera, S.; Bockamp, E.O.; Moya, F.; Piovant, M.; Jimenez, F.
#journal EMBO J. (1990) 9:3593-3601
#title Characterization and gene cloning of neurotactin, a Drosophila transmembrane protein related to cholinesterases.

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#cross-references MUID:91006059
#accession S12005
##status Preliminary
##molecule-type mRNA
##residues 1-846 ##label ESC
##cross-references EMBL:X5837; NID:98287; PID:98288
GENETICS
#gene FlyBase:Nrt
##cross-references FlyBase:FBgn0004108
KEYWORDS phosphoprotein; transmembrane protein
SUMMARY #length 846 #molecular-weight 92805 #checksum 5987

Query Match 76.2% Score 48; DB 2; Length 846;
Best Local Similarity 55.6% Pred. No. 7.08e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 717 EKNASSYA 725
QY 1 QKNSAPYA 9

RESULT 3
ENTRY S13795 #type complete
TITLE neurotactin - fruit fly (Drosophila melanogaster)
ORGANISM #format_name Drosophila melanogaster
DATE 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
24-Sep-1998
ACCESSIONS S13795
REFERENCE S13795
#authors Hortsch, M.; Patel, N.H.; Bieker, A.J.; Traquine, Z.R.;
Goodman, C.S.
#journal Development (1990) 110:1327-1340
#title Drosophila neurotactin, a surface glycoprotein with homology
to serine esterases, is dynamically expressed during
embryogenesis.
#cross-references MUID:91301057
#accession S13795
##status Preliminary
##molecule-type mRNA
##residues 1-846 ##label HOR
##cross-references EMBL:X54999; NID:98289; PID:98290
GENETICS
#gene FlyBase:Nrt
##cross-references FlyBase:FBgn0004108
KEYWORDS phosphoprotein; transmembrane protein
SUMMARY #length 846 #molecular-weight 92745 #checksum 4655

Query Match 76.2% Score 48; DB 2; Length 846;
Best Local Similarity 55.6% Pred. No. 7.08e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 717 EKNASSYA 725
QY 1 QKNSAPYA 9

RESULT 4
ENTRY S67940 #type fragment
TITLE Ig kappa chain V region, subgroup III (clone MH52) - human
(fragment)
ORGANISM #format_name Homo sapiens #common_name man
DATE 19-Mar-1997 #sequence_revision 09-May-1997 #text_change
20-Mar-1998
ACCESSIONS S67940
REFERENCE S67940
#authors Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith,
B.R.
#journal Autoimmunity (1992) 12:135-141
#title Cloning of a human autoimmune response: preparation and
sequencing of a human anti-thyroglobulin autoantibody using
a combinatorial approach.
#cross-references MUID:92314301
#accession S67940

```

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#status      preliminary
#molecule_type  mRNA
#residues    1-91 ##label HEX
#cross-references  EMBL:X73852
CLASSIFICATION  #superfamily Immunoglobulin V region; Immunoglobulin homology
SUMMARY        #length 91 #checksum 3259

Query Match      74.6%  Score 47;  DB 2;  Length 91;
Best Local Similarity 55.6%  Pred. No. 1.13e+01;
Matches 5;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;

Db      71  QOYGSPYT 79
| | | | |
Oy      1  QKNSAPYA 9

RESULT 5
ENTRY      S37513      #type fragment
TITLE      Ig kappa chain V region (V-kappa 3) - human (fragment)
ORGANISM   Homo sapiens #common_name man
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
            08-Sep-1997
ACCESSIONS S37513
REFERENCE   S37501
#authors    Klein, U.; Kuipers, R.; Rajewsky, K.
#submission Human IgM(+)IgD(+) cells, the major B cell subset in the
#description peripheral blood, expresses V(kappa) genes with no or
            little somatic mutation throughout life.
#accession  S37513
#status     preliminary
#molecule_type  mRNA
#residues    1-92 ##label KLE
#cross-references  EMBL:Z26599; NID:g405668; PID:g405669
CLASSIFICATION  #superfamily Immunoglobulin V region; Immunoglobulin homology
KEYWORDS     heterotrimer; immunoglobulin
SUMMARY      #length 92 #checksum 6096

Query Match      74.6%  Score 47;  DB 2;  Length 92;
Best Local Similarity 55.6%  Pred. No. 1.13e+01;
Matches 5;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;

Db      73  QOYGSPYT 81
| | | | |
Oy      1  QKNSAPYA 9

RESULT 6
ENTRY      PH0863      #type fragment
TITLE      Ig kappa chain V region (anti-DNA, IIT-2R) - human (fragment)
ORGANISM   Homo sapiens #common_name man
DATE       09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
            09-May-1997
ACCESSIONS PH0863
REFERENCE   PH0862
#authors    Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosssein, C.;
            Smith, A.; Diamond, B.
#journal    J. Exp. Med. (1991) 174:1639-1652
#title      Molecular characteristics of antibodies bearing an
            anti-DNA-associated idiotype.
#cross-references  MIMD:9207875
#accession  PH0863
#molecule_type  DNA
#residues    1-95 ##label MAN
COMMENT     This antibody is produced by Epstein-Barr virus-transformed B cell
            that bears the 3i idiotype expressed on anti-DNA antibody.
CLASSIFICATION  #superfamily Immunoglobulin V region; Immunoglobulin homology
KEYWORDS     heterotrimer; immunoglobulin
FEATURE      1-23      #region framework 1\
            24-34      #region complementarity-determining 1\
            35-49      #region framework 2\
            50-56      #region complementarity-determining 2\

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57-88 #region framework 3\
89-95 #region complementarity-determining 3
SUMMARY #length 95 #checksum 6652

Query Match 74.6%; Score 47; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.13e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 OKYNSAP 95
1 OKYNSAP 7

*two only of 9 minor
variants of seq ID 11*

RESULT 7
ENTRY S40366 #type complete
TITLE Ig kappa chain V-J region - human
ORANISM #formal_name Homo sapiens #common_name man
DATE 19-May-1994 #sequence_revision 26-May-1995 #text_change 20-Mar-1998

ACCESSIONS
#status S40366 preliminary; translation not shown
#molecule_type mRNA
#residues 1-107 ##label KLE
#cross-references EMBL:X72476; NID:G441420; PID:G441421
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 107 #molecular_weight 11556 #checksum 91449

Query Match 74.6%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.13e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 OKYNSAP 107
1 OKYNSAP 7

RESULT 8
ENTRY A30608 #type fragment
TITLE Ig kappa chain V-III region (Son) - human (fragment)
ORANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS
#status A30608
#molecule_type protein
#residues 1-109 ##label GON
#cross-references WVID:89215279
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6031

Query Match 74.6%; Score 47; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 1.13e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 90 QOYGSPT 98
1 OKYNSAP 9

RESULT 9
ENTRY H30601 #type fragment
TITLE Ig kappa chain V-III region (Gar and Fio) - human (fragment)
ORANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS
#status H30601
#molecule_type protein
#residues 1-109 ##label GON1
#cross-references WVID:89215279
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5951

Query Match 74.6%; Score 47; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 1.13e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 90 QOYGSPT 98
1 OKYNSAP 9

RESULT 10
ENTRY S61918 #type complete
TITLE protein kinase C (EC 2.7.1.1) PKC1 - fungus (Trichoderma reesei)
ORANISM #formal_name Trichoderma reesei
DATE 23-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

ACCESSIONS
#status S61918
#molecule_type protein
#residues 1-1139 ##label MOR
#cross-references EMBL:U10016; NID:G501074; PID:G501075
CLASSIFICATION #superfamily yeast protein kinase C; protein kinase C
KEYWORDS ATP; duplication; phospholipid binding; phosphotransferase;
serine/threonine-specific protein kinase; zinc

GENETICS
#gene PKC1
#introns 139/1; 228/1; 555/1; 917/2; 984/3; 1120/1
#superfamily yeast protein kinase C; protein kinase C
#zinc-binding repeat homology; protein kinase homology
ATP; duplication; phospholipid binding; phosphotransferase;
serine/threonine-specific protein kinase; zinc

FEATURE
455-502 #domain protein kinase C zinc-binding repeat homology
523-572 #domain protein kinase C zinc-binding repeat homology
812-1073 #domain protein kinase homology #label KIN

820-828 #region protein kinase ATP-binding motif
SUMMARY #length 1139 #molecular-weight 126055 #checksum 3417

Query Match 74.6%; Score 47; DB 2; Length 1139;
Best Local Similarity 66.7%; Pred. No. 1.13e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 707 HKYNPADYA 715
: : : : :
QY 1 OKYNSAPYA 9

RESULT 11
ENTRY #type fragment
TITLE complement component C3 - Japanese lamprey (fragment)
ORGANISM #formal_name Lampetra japonica #common_name Japanese lamprey
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Aug-1998

ACCESSIONS 150806
REFERENCE 150806
#authors Noma, M.; Takahashi, M.
#journal J. Immunol. (1992) 148:3290-3295
#title Complete complementary DNA sequence of the third component of complement of lamprey; implication for the evolution of thioester containing protein.

#cross-references MUID:92251197
#accession 150806
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-1673 #label NON
CLASSIFICATION #superfamily alpha-2-macroglobulin
SUMMARY #length 1673 #checksum 8983

Query Match 74.6%; Score 47; DB 2; Length 1673;
Best Local Similarity 75.0%; Pred. No. 1.13e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 443 OKYASASY 450
: : : : :
QY 1 OKYNSAPY 8

RESULT 12
ENTRY #type complete
TITLE Ig kappa chain precursor V-III region (IARC/BL41) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997

ACCESSIONS A01899
REFERENCE A93588
#authors Klobbeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zechau, H.G.
#journal Nucleic Acids Res. (1985) 13:6499-6513
#title Human immunoglobulin kappa light chain genes of subgroups II and III.

#cross-references MUID:86041852
#accession A01899
#molecule_type DNA
#residues 1-128 #label KLO
GENETICS #note the sequence was determined from the differentiated gene

GENETICS GDB:IGKV3
#gene #cross-references GDB:136266
#map_position 2p12-2p11
#introns 17/1
COMPLEX An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-20
21-128
21-43
44-54
55-69
70-76
77-108
109-117
118-128
43-108
SUMMARY #length 128 #molecular-weight 14070 #checksum 5944

Query Match 73.0%; Score 46; DB 1; Length 128;
Best Local Similarity 44.4%; Pred. No. 1.8e+01;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 109 QOYSTSPYT 117
: : : : :
QY 1 OKYNSAPYA 9

RESULT 13
ENTRY #type complete
TITLE hypothetical protein 9 - Enterococcus faecalis plasmid PAD1
ORGANISM #formal_name Enterococcus faecalis
DATE 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Jun-1998

ACCESSIONS S72385
REFERENCE S72385
#authors Hirt, H.; Wirth, R.; Muscholl, A.
#journal Mol. Gen. Genet. (1996) 252:640-647
#title Comparative analysis of 18 sex pheromone plasmids from Enterococcus faecalis: detection of a new insertion element on pPDI and implications for the evolution of this plasmid family.

#cross-references MUID:97074879
#accession S72385
#status Nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-278 #label HIR
#cross-references EMBL:X96977; NID:q1279406; PID:e236596; PID:q1279411
#experimental_source strain OG1X
#note the nucleotide sequence was submitted to the EMBL Data Library, February 1996

GENETICS
#genome plasmid pADI
SUMMARY #length 278 #molecular-weight 30520 #checksum 877

Query Match 73.0%; Score 46; DB 2; Length 278;
Best Local Similarity 62.5%; Pred. No. 1.81e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 227 OKYGNAPF 234
: : : : :
QY 1 OKYNSAPY 8

RESULT 14
ENTRY #type complete
TITLE retinal pigment microsomal protein RPE65, epithelium-specific - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 10-Sep-1997

ACCESSIONS A47143; A48017; S28503
REFERENCE A47143
#authors Hamel, C.P.; Tsilou, E.; Pfeiffer, B.A.; Hooks, J.J.; Detrick, B.; Redmond, T.M.
#journal J. Biol. Chem. (1993) 268:15751-15757

```

#title      Molecular cloning and expression of RPE65, a novel retinal
            pigment epithelium-specific microsomal protein that is
            post-transcriptionally regulated in vitro.
#cross-references MIMD:93340181
#accession   A47143
#status      preliminary
#molecule_type mRNA
#residues    1-533 #label HAM
#cross-references GB:L1356; NID:g163656; PID:g163657
REFERENCE    A48017
#authors     Bayk, C.O.; Levy, F.; Hellman, U.; Wernstedt, C.; Eriksson,
            U.
#journal     J. Biol. Chem. (1993) 268:20540-20546
#title       The retinal pigment epithelial membrane receptor for plasma
            retinol-binding protein. Isolation and cDNA cloning of the
            63-kDa protein
#cross-references MIMD:93388633
#accession   A48017
#status      preliminary
#molecule_type mRNA
#residues    1-340,'L',342-533 #label BA2
#cross-references EMBL:X66277; NID:g563; PID:g564
KEYWORDS     membrane protein
SUMMARY      #length 533 #molecular-weight 60944 #checksum 3885

Db      424 OKYGRPYT 432
        ||| : ||:
        QY      1 OKYNSAPYA 9

RESULT  15
ENTRY    S41028 #type complete
TITLE    hypothetical protein K03H1.4 - Caenorhabditis elegans
ORGANISM 06-Jan-1995 #formal_name Caenorhabditis elegans
DATE      06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change

ACCESSIONS S41028
REFERENCE   S41024
#authors    Smith, M.; Ainscough, R.
#submission submitted to the EMBL Data Library, January 1994
#accession  S41028
#status      preliminary
#molecule_type DNA
#residues    1-1409 #label SMI
#cross-references EMBL:229560
JETICS
#introns    44/3: 189/3; 223/3: 319/3: 340/3: 375/2: 493/3; 517/3; 591/2;
            662/3; 852/2; 928/1; 988/1; 1104/1; 1202/1; 1324/2
SUMMARY      #length 1409 #molecular-weight 161796 #checksum 2817

Query Match      73.0%; Score 46; DB 2; Length 1409;
Best Local Similarity 50.0%; Pred. No. 1.81e+01;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db      821 HRYGAPY 828
        :| :|||
        QY      1 OKYNSAPY 8

Search completed: Thu Sep 2 11:24:34 1999
Job time : 14 secs.

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 W2571 (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:27:10 1999; Maspar time 9.93 Seconds
 19,280 Million cell updates/sec

Modular output not generated.

Title: >US-08-599-226-12
 Description: (1-9) from US08599226.pep
 Perfect Score: 68
 Sequence: 1 OKYNAPYA 9

Scoring table: PAM 150
 Gap 15

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

a.geneseq15
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 16.581; Variance 48.098; scale 0.345

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	68	100.0	9	27	W2571	Anti-TNF-alpha antibo
2	66	97.1	9	27	W2571	Anti-TNF-alpha antibo
3	65	95.6	9	27	W2585	Anti-TNF-alpha antibo
4	64	94.1	9	27	W2579	Anti-TNF-alpha antibo
5	63	92.6	9	27	W2584	Anti-TNF-alpha antibo
6	63	92.6	9	27	W2584	Anti-TNF-alpha antibo
7	61	89.7	9	27	W2582	Anti-TNF-alpha antibo
8	61	89.7	9	27	W2582	Anti-TNF-alpha antibo
9	58	85.3	9	27	W2570	Anti-TNF-alpha antibo
10	56	82.4	9	27	W2574	Anti-TNF-alpha antibo
11	54	79.4	9	27	W2577	Anti-TNF-alpha antibo
12	54	79.4	9	27	W2576	Anti-TNF-alpha antibo
13	52	76.5	9	27	W2573	Anti-TNF-alpha antibo
14	52	76.5	9	27	W2582	Anti-TNF-alpha antibo
15	52	76.5	9	27	W2582	Anti-TNF-alpha antibo
16	51	75.0	9	27	W2578	Anti-TNF-alpha antibo

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
17	50	73.5	263	4	R22957	Human proteasome comp
18	50	73.5	269	1	R22666	Protein used to raise
19	49	72.1	9	27	W2580	Anti-TNF-alpha antibo
20	48	70.6	287	7	W2583	Anti-TNF-alpha antibo
21	48	70.6	287	7	R34030	Anti-TNF-alpha antibo
22	48	70.6	287	11	R59920	Human fc-alpha-R.
23	48	70.6	520	1	P94617	Neutral protease enco
24	48	70.6	521	3	P51009	Sequence of neutral P
25	47	69.1	1737	22	W19669	ATM mutant 5178del1142
26	47	69.1	1737	22	W19669	ATM mutant 5178del1142
27	47	69.1	1851	22	W19666	ATM mutant 5539del111
28	47	69.1	2415	22	W19686	ATM mutant 7240del14
29	47	69.1	2598	22	W19656	ATM mutant 7789del1139
30	47	69.1	2652	22	W19655	ATM mutant 7883del15
31	47	69.1	2713	22	W19654	ATM mutant C8140T
32	47	69.1	2759	22	W19652	ATM mutant 8269del1403
33	47	69.1	2766	22	W19651	ATM mutant 8283del17C
34	47	69.1	2932	22	W19675	ATM mutant G8307A
35	47	69.1	2987	22	W19649	ATM mutant 8467del1372
36	47	69.1	2987	22	W19649	ATM mutant 8467del1372
37	47	69.1	2988	22	W19691	ATM mutant 3403del1174
38	47	69.1	3005	22	W19648	ATM mutant 9001del1AG
39	47	69.1	3005	22	W19653	ATM mutant 8269del1153
40	47	69.1	3046	22	W19690	ATM mutant C9140T
41	47	69.1	3054	22	W19702	ATM mutant 7278del16
42	47	69.1	3055	22	W19693	ATM mutant 8578del13
43	47	69.1	3056	22	W37133	Ataxia-telangiectasia
44	47	69.1	3056	23	W19733	Cell cycle checkpoint
45	47	69.1	3085	22	W19701	ATM mutant G9170C

ALIGNMENTS

RESULT 1
 ID W2571 standard; peptide: 9 AA.
 AC W2571:
 DE 19-MAR-1998 (first entry)
 KW Human; tumor necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 Saltefeld JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumor necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption diseases,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 100.0%; Score 68; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.40e-01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpya 9
 1 OKYNRPPYA 9

RESULT 2
 W2575 standard; peptide: 9 AA.

DT 19-MAR-1998 (first entry)
 AC W2575:
 KW Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity; e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 69; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 97.1%; Score 66; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 9.42e-01;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 qkynrpyt 9
 1 OKYNRPPYA 9

RESULT 3
 W2585 standard; peptide: 9 AA.

DT 19-MAR-1998 (first entry)
 AC W2585:
 KW Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity; e.g. to treat autoimmune diseases and cancer
 Claim 20: Page 72; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 95.6%; Score 65; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.24e+00;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpya 9
 1 OKYNRPPYA 9

RESULT 4
 W2579 standard; peptide: 9 AA.

DT 19-MAR-1998 (first entry)
 AC W2579:
 KW Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PI (BADI) BASF AG. *WNT*
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Manukovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
 WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity; e.g. to treat autoimmune diseases and cancer
 CC Claim 20; Page 70; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 CC Sequence 9 AA:
 SQ

Query Match 94.1% Score 64; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gkyurapy 8
 |||||
 1 OKYNRAPHY 8

RESULT 5
 ID W27584 standard; peptide; 9 AA.
 AC W27584;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; 002219.

PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226. *WNT*
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Manukovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
 DR WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity; e.g. to treat autoimmune diseases and cancer
 CC Claim 20; Page 72; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 CC Sequence 9 AA:
 SQ

Query Match 92.6% Score 63; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.15e+00;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 gkyurpyt 9
 |||||
 1 OKYNRAPHY 9

RESULT 6
 ID W27568 standard; Protein; 107 AA.
 AC W27568;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
 KM light chain; variable region; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226. *WNT*
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Manukovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
 DR WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity; e.g. to treat autoimmune diseases and cancer
 CC Claim 15; Page 75; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 107 AA;

Query Match 92.6%; Score 63; DB 27; Length 107;
 Best Local Similarity 77.8%; Pred. No. 2.15e+00;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 89 grynrapyt 97
 1 QKYNRAPYA 9

RESULT 7
 ID W25752 standard; peptide: 9 AA.

AC W25752;
 DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

FT Key Location/Qualifiers

FT MISC-difference 9 /label=Thr, Ala

FT PN M09729131-A1.

FT 14-AUG-1997.

FT 10-FEB-1997; U02219.

FT 25-NOV-1996; US-031476.

FT 09-FEB-1996; US-599226.

FT (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;

DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 9; Page 64; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 89.7%; Score 61; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 3.71e+00;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 grynrapyt 8
 1 QKYNRAPYA 8

RESULT 8
 ID W25772 standard; peptide: 9 AA.

AC W25772;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

FT Key Location/Qualifiers

FT PN M09729131-A1.

FT 14-AUG-1997.

FT 10-FEB-1997; U02219.

FT 25-NOV-1996; US-031476.

FT 09-FEB-1996; US-599226.

FT (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,

PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;

DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 68; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 89.7%; Score 61; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3.71e+00;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
| | | | |
OY 1 QKYNRAPYA 9

RESULT 9
ID W27570 standard; peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
AC W27570;
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

Homo sapiens.
MO9729131-A1.

PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PR 25-NOV-1996: US-031476.
PW 09-FEB-1996: US-599226.

Handwritten: 100

PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20: Page 67; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).

CC Sequence 9 AA:

Query Match 85.3%; Score 58; DB 27; Length 9;
Best Local Similarity 88.9%; Pred. No. 8.33e+00;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
| | | | |
OY 1 QKYNRAPYA 9

RESULT 10
ID W27574 standard; peptide; 9 AA.

AC W27574;
DE Anti-TNF-alpha antibody light chain CDR3.

KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

Homo sapiens.
MO9729131-A1.

PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PR 25-NOV-1996: US-031476.
PW 09-FEB-1996: US-599226.

Handwritten: 100

PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20: Page 69; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).

CC Sequence 9 AA:

Query Match 82.4%; Score 56; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.42e+01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
| | | | |
OY 1 QKYNRAPYA 9

RESULT 11
ID W27577 standard; peptide; 9 AA.

AC W27577;
DE Anti-TNF-alpha antibody light chain CDR3.

KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

Homo sapiens.
MO9729131-A1.

PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PW 09-FEB-1996: US-031476.

PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20: Page 69; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ,
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 79.4%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.41e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkynasy 8
 1 QKYNRPY 8

RESULT 12
 ID W27576 standard; peptide: 9 AA.
 AC W27576: (first entry)
 DT 19-MAR-1998
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PE 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ,
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 69: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 79.4%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.41e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkynasy 8
 1 QKYNRPY 8

RESULT 13
 ID W27573 standard; peptide: 9 AA.
 AC W27573:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PE 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ,
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 76.58; Score 52; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 4.06e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkyssapyt 9
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 QY 1 QKYNRAPYA 9

RESULT 14
 ID W27582 standard; peptide: 9 AA.

AC W27582;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-559226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kolff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 76.58; Score 52; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 4.06e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 gkyssapyt 9
 |||: |||:
 QY 1 QKYNRAPYA 9

RESULT 15
 ID R75006 standard; Protein: 360 AA.

AC R75006;
 DT 01-NOV-1995 (first entry)
 DE Tomato S-adenosyl-methionine-decarboxylase.
 KW SAM-decarboxylase; transgenic plant; senescence;
 KW fruit ripening.
 OS Lycopersicon esculentum.
 PN WD9514092-A.
 PD 26-MAY-1995.
 PE 17-NOV-1994: G02532.
 PR 18-NOV-1993; GB-023771.
 PA (ZENE) ZENECA LTD.
 PI Fray RG, Grierson D, Wallace AD;
 DR WPI: 95-200382/26.
 DR N-PSDB; Q90508.
 PT New S-adenosyl methionine-decarboxylase DNA - used to transform
 PT plants to modify senescence and fruit-ripening characteristics.
 PS Disclosure; Page 25-26; 34pp; English.
 CC DNA encoding SAM-decarboxylase is used to transform plants.
 CC Modifying SAM-decarboxylase (SAM) gene expression in transgenic
 CC plants modifies senescence or fruit-ripening characteristics.
 CC Increased SAMD levels reduce ethene production by the plant, and
 CC decreased SAMD levels increase ethene production by the plant.
 SQ Sequence 360 AA;

Query Match 76.58; Score 52; DB 13; Length 360;
 Best Local Similarity 62.5%; Pred. No. 4.06e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 332 gkfttpty 339
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 QY 1 QKYNRAPY 8

Search completed: Thu Sep 2 11:27:25 1999
 Job time : 15 secs.

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WORLDWIDE
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 11:29:20 1999; Maspar time 1.36 Seconds
67.062 Million cell updates/sec
Module output not generated.

Title: >US-08-599-226-12
Description: (1-9) from US08599226.pep
Perfect Score: 68
Sequence: 1 OKYNAPYA 9

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 15.564; Variance 46.387; scale 0.336

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	50	73.5	269	1	US-08-202-	Sequence 4, Applicatio	3.12e+01
2	48	70.6	287	4	5198342-2	Patent No. 5198342.	5.19e+01
3	48	70.6	287	1	US-07-971-	Sequence 2, Applicatio	5.19e+01
4	47	69.1	1708	1	US-08-493-	Sequence 2, Applicatio	6.69e+01
5	47	69.1	1708	2	US-08-508-	Sequence 2, Applicatio	6.69e+01
6	47	69.1	3056	2	US-08-508-	Sequence 8, Applicatio	6.69e+01
7	47	69.1	3056	2	US-08-629-	Sequence 3, Applicatio	6.69e+01
8	46	67.6	246	2	US-08-604-	Sequence 3, Applicatio	8.60e+01
9	46	67.6	466	2	US-08-604-	Sequence 3, Applicatio	8.60e+01
10	46	67.6	507	3	PCT-US95-0	Sequence 2, Applicatio	8.60e+01
11	46	67.6	507	3	PCT-US95-0	Sequence 2, Applicatio	8.60e+01
12	46	67.6	718	1	US-08-444-	Sequence 4, Applicatio	8.60e+01
13	46	67.6	718	1	US-08-444-	Sequence 4, Applicatio	8.60e+01
14	44	64.7	33	2	US-08-824-	Sequence 12, Applicati	1.41e+02
15	44	64.7	107	2	US-08-824-	Sequence 12, Applicati	1.41e+02
16	44	64.7	107	3	PCT-US95-0	Sequence 87, Applicati	1.41e+02
17	44	64.7	107	3	PCT-US95-0	Sequence 87, Applicati	1.41e+02
18	44	64.7	107	1	US-08-899-	Sequence 87, Applicati	1.41e+02
19	43	63.2	52	2	US-08-162-	Sequence 43, Applicati	1.81e+02
20	43	63.2	109	3	PCT-US93-0	Sequence 23, Applicati	1.81e+02
21	43	63.2	109	2	US-08-162-	Sequence 23, Applicati	1.81e+02
22	43	63.2	324	2	US-08-484-	Sequence 22, Applicati	1.81e+02
23	43	63.2	442	2	US-08-363-	Sequence 11, Applicati	1.81e+02

RESULT	ID	Sequence	STANDARD	PRT	269 AA.
1	US-08-202-857-4	Sequence 4, Application US/08202857			
2	US-08-202-857-4	Sequence 4, Application US/08202857			
3	US-08-202-857-4	Sequence 4, Application US/08202857			
4	US-08-202-857-4	Sequence 4, Application US/08202857			
5	US-08-202-857-4	Sequence 4, Application US/08202857			
6	US-08-202-857-4	Sequence 4, Application US/08202857			
7	US-08-202-857-4	Sequence 4, Application US/08202857			
8	US-08-202-857-4	Sequence 4, Application US/08202857			
9	US-08-202-857-4	Sequence 4, Application US/08202857			
10	US-08-202-857-4	Sequence 4, Application US/08202857			
11	US-08-202-857-4	Sequence 4, Application US/08202857			
12	US-08-202-857-4	Sequence 4, Application US/08202857			
13	US-08-202-857-4	Sequence 4, Application US/08202857			
14	US-08-202-857-4	Sequence 4, Application US/08202857			
15	US-08-202-857-4	Sequence 4, Application US/08202857			
16	US-08-202-857-4	Sequence 4, Application US/08202857			
17	US-08-202-857-4	Sequence 4, Application US/08202857			
18	US-08-202-857-4	Sequence 4, Application US/08202857			
19	US-08-202-857-4	Sequence 4, Application US/08202857			
20	US-08-202-857-4	Sequence 4, Application US/08202857			
21	US-08-202-857-4	Sequence 4, Application US/08202857			
22	US-08-202-857-4	Sequence 4, Application US/08202857			
23	US-08-202-857-4	Sequence 4, Application US/08202857			
24	US-08-202-857-4	Sequence 4, Application US/08202857			
25	US-08-202-857-4	Sequence 4, Application US/08202857			
26	US-08-202-857-4	Sequence 4, Application US/08202857			
27	US-08-202-857-4	Sequence 4, Application US/08202857			
28	US-08-202-857-4	Sequence 4, Application US/08202857			
29	US-08-202-857-4	Sequence 4, Application US/08202857			
30	US-08-202-857-4	Sequence 4, Application US/08202857			
31	US-08-202-857-4	Sequence 4, Application US/08202857			
32	US-08-202-857-4	Sequence 4, Application US/08202857			
33	US-08-202-857-4	Sequence 4, Application US/08202857			
34	US-08-202-857-4	Sequence 4, Application US/08202857			
35	US-08-202-857-4	Sequence 4, Application US/08202857			
36	US-08-202-857-4	Sequence 4, Application US/08202857			
37	US-08-202-857-4	Sequence 4, Application US/08202857			
38	US-08-202-857-4	Sequence 4, Application US/08202857			
39	US-08-202-857-4	Sequence 4, Application US/08202857			
40	US-08-202-857-4	Sequence 4, Application US/08202857			
41	US-08-202-857-4	Sequence 4, Application US/08202857			
42	US-08-202-857-4	Sequence 4, Application US/08202857			
43	US-08-202-857-4	Sequence 4, Application US/08202857			
44	US-08-202-857-4	Sequence 4, Application US/08202857			
45	US-08-202-857-4	Sequence 4, Application US/08202857			

Sequence 4, Application US/08202857

Patent No. 5635345

GENERAL INFORMATION:

APPLICANT: Scherrer, Klaus

APPLICANT: Bureau, Jean-Paul

TITLE OF INVENTION: Diagnostic Method

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: PRO-SOMA SARL C/O AKZO PHARMA

STREET: 1330-A PICCARD DRIVE

CITY: ROCKVILLE

STATE: MARYLAND

COUNTRY: USA

ZIP: 20850-4377

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202,857

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/860,492

FILING DATE: 11-JUNE-1992

APPLICATION NUMBER: PCT/EP91/01945

FILING DATE: 10-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: BOBROWICZ, DONNA

REGISTRATION NUMBER: 32,196

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-258-5200

TELEFAX: 301-977-1403

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: human
SQ SEQUENCE 269 AA; 30227 MW; 341084 CN;
Query Match 73.5%; Score 50; DB 1; Length 269;
Best Local Similarity 55.6%; Pred. No. 3.12e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 127 ORYXRRPYG 135
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OY 1 OKYNRAPIYA 9
RESULT 2
ID 5198342-2 STANDARD: PRT; 311 AA.
XX xxxxxx
XX 01-JAN-1900
DE Patent No. 5198342.
XX
CC Patent No. 5198342
CC APPLICANT: MALISZEWSKI, CHARLES R.
CC TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/548, 059
CC FILING DATE: 05-JUL-1990
CC SEQ ID NO: 2:
CC LENGTH: 287
SQ SEQUENCE 311 AA; 34908 MW; 558002 CN;
Query Match 70.6%; Score 48; DB 4; Length 287;
Best Local Similarity 83.3%; Pred. No. 5.19e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSPY 202
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OY 3 YNRAPY 8
RESULT 3
ID US-07-971-092-2 STANDARD: PRT; 287 AA.
XX xxxxxx
DE Sequence 2, Application US/07971092
XX
CC Sequence 2, Application US/07971092
CC Patent No. 5328987
CC GENERAL INFORMATION:
CC APPLICANT: Maliszewski, Charles R.
CC TITLE OF INVENTION: Huiga Fc Receptor
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex
CC STREET: 51 University
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/971,092
CC FILING DATE: 19921104
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Perkins, Patricia A.
CC REGISTRATION NUMBER: 34693
CC REFERENCE/DOCKET NUMBER: 2603
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 287 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 287 AA; 32265 MW; 435416 CN;
Query Match 70.6%; Score 48; DB 1; Length 287;
Best Local Similarity 83.3%; Pred. No. 5.19e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSPY 202
|:|:|:
OY 3 YNRAPY 8
RESULT 4
ID US-08-493-092-2 STANDARD: PRT; 1708 AA.
XX xxxxxx
XX
DE Sequence 2, Application US/08493092
XX
CC Sequence 2, Application US/08493092
CC Patent No. 5728807
CC GENERAL INFORMATION:
CC APPLICANT: Shilon, Yosef
CC APPLICANT: Tagile, Danilo A.
CC APPLICANT: Collins, Francis S.
CC TITLE OF INVENTION: Ataxia-Telanglectasia Gene
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reising, Ethlington, Bernard & Perry
CC STREET: P.O. Box 4390
CC CITY: Troy
CC STATE: Michigan
CC COUNTRY: US
CC ZIP: 48099
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/493,092
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kohn, Kenneth I.
CC REGISTRATION NUMBER: 30,955
CC REFERENCE/DOCKET NUMBER: P-310 (TAV)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (810) 689-3500
CC TELEFAX: (810) 689-4071
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1708 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 1708 AA; 195977 MW; 14824289 CN;
Query Match 69.1%; Score 47; DB 1; Length 1708;

Best Local Similarity 50.08; Pred. No. 6.69e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 234 KYSRGPPS 241
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QY 2 KYNRAPYA 9

RESULT 5
ID US-08-508-836A-2 STANDARD; PRT: 1708 AA.
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AC xxxxxx

Sequence 2, Application US/08508836A

Sequence 2, Application US/08508836A
Patent No. 5777093

GENERAL INFORMATION:

APPLICANT: Shiloh, Yosef

APPLICANT: Tagle, Danilo A.

APPLICANT: Collins, Francis S.

TITLE OF INVENTION: Ataxia-Telangiectasia Gene

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Relising, Ethlington, Barnard & Perry

STREET: P. O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: US

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/508, 836A

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-313 (TAU)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (810) 689-3500

TELEFAX: (810) 689-4071

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1708 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE 1708 AA; 195977 MW; 14824289 CN;

Query Match 69.18; Score 47; DB 2; Length 1708;

Best Local Similarity 50.08; Pred. No. 6.69e+01;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 234 KYSRGPPS 241
||:|:|:|:
QY 2 KYNRAPYA 9
RESULT 6
ID US-08-508-836A-8 STANDARD; PRT: 3056 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 8, Application US/08508836A

XX Sequence 8, Application US/08508836A
CC Patent No. 5777093
CC
CC GENERAL INFORMATION:

APPLICANT: Shiloh, Yosef

APPLICANT: Tagle, Danilo A.

APPLICANT: Collins, Francis S.

TITLE OF INVENTION: Ataxia-Telangiectasia Gene

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Relising, Ethlington, Barnard & Perry

STREET: P. O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: US

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/508, 836A

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-313 (TAU)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (810) 689-3500

TELEFAX: (810) 689-4071

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 3056 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE 3056 AA; 350651 MW; 47948122 CN;

Query Match 69.18; Score 47; DB 2; Length 3056;

Best Local Similarity 50.08; Pred. No. 6.69e+01;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1582 KYSRGPPS 1589
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QY 2 KYNRAPYA 9
RESULT 7
ID US-08-629-001A-3 STANDARD; PRT: 3056 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 3, Application US/08629001A
XX
CC Sequence 3, Application US/08629001A
CC Patent No. 5858661
CC
CC GENERAL INFORMATION:
CC APPLICANT: Shiloh, Yosef
CC APPLICANT: Tagle, Danilo A.
CC APPLICANT: Collins, Francis S.
CC TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE AND ITS
CC NUMBER OF SEQUENCES: 139
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kohn & Associates
CC STREET: 30500 No. 5858661thwestern Hwy.
CC CITY: Farmington Hills
CC STATE: Michigan
CC COUNTRY: US
CC ZIP: 48334
CC
CC COMPUTER READABLE FORM:

CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	Patentin Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/629,001A
CC	FILING DATE:	
CC	CLASSIFICATION:	435
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Kohn, Kenneth I.
CC	REGISTRATION NUMBER:	30,955
CC	REFERENCE/DOCKET NUMBER:	2290,00032
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	(810) 539-5050
CC	TELEFAX:	(810) 539-5055
CC	INFORMATION FOR SEQ ID NO:	3:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	3056 amino acids
CC	TYPE:	amino acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	protein
CC	ORIGINAL SOURCE:	
CC	ORGANISM:	Homo sapiens
SO	SEQUENCE	3056 AA; 350651 MW; 47948122 CN;
DB	Query Match	69.1%; Score 47; DB 2; Length 3056;
	Best Local Similarity	50.0%;
	Matches	4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Oy	1582 KYSRGPFS 1589	
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Oy	2 KYNRAPYA 9	
XX	xxxxxx	
DE	Sequence 3, Application US/08604989A	
CC	Sequence 3, Application US/08604989A	
CC	Patent No. 5834208	
CC	GENERAL INFORMATION:	
CC	APPLICANT:	Sakano, S.
CC	TITLE OF INVENTION:	No. 5834208el Tyrosine Kinase
CC	NUMBER OF SEQUENCES:	11
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	Pennie & Edmonds LLP
CC	STREET:	1155 Avenue of the Americas
CC	CITY:	New York
CC	STATE:	New York
CC	COUNTRY:	USA
CC	ZIP:	10036-2711
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Diskette
CC	COMPUTER:	IBM Compatible
CC	OPERATING SYSTEM:	DOS
CC	SOFTWARE:	FASTSEQ Version 2.0
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/604,989A
CC	FILING DATE:	February 23, 1996
CC	CLASSIFICATION:	435
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Charles E. Miller
CC	REGISTRATION NUMBER:	24,576
CC	REFERENCE/DOCKET NUMBER:	1920-026
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	(212) 790-9090
CC	TELEFAX:	(212) 869-8864/9741

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CC      TELEX: 66141 PENNIE
CC      INFORMATION FOR SEQ ID NO: 3:
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 246 amino acids
CC          TYPE: amino acid
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      ORIGINAL SOURCE:
CC          ORGANISM: human
CC          STRAIN: UT-7
CC      SEQUENCE 246 AA; 27425 MW; 326654 CN;
CC
CC      Query Match 67.6%; Score 46; DB 2; Length 246;
CC      Best Local Similarity 71.4%; Pred. No. 8.60e+01;
CC      Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC
Db      188 YGRAYP 194
Cc      | |||:
Cc      3 YNRAVYA 9
Cc
Cc      RESULT 9 STANDARD; PRT; 466 AA.
Cc      ID US-08-604-989A-4
Cc      AC xxxxxx
Cc      DX
Cc      XX
Cc      DE Sequence 4, Application US/08604989A
Cc      XX
Cc      CC Sequence 4, Application US/08604989A
Cc      CC Patent No. 5834208
Cc      CC GENERAL INFORMATION:
Cc      CC APPLICANT: Sakano, S.
Cc      CC TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
Cc      CC NUMBER OF SEQUENCES: 11
Cc      CC CORRESPONDENCE ADDRESS:
Cc      CC ADDRESSEE: Pennie & Edmonds LLP
Cc      CC STREET: 1155 Avenue of the Americas
Cc      CC CITY: New York
Cc      CC STATE: New York
Cc      CC COUNTRY: USA
Cc      CC ZIP: 10036-2711
Cc      CC COMPUTER READABLE FORM:
Cc      CC MEDIUM TYPE: Diskette
Cc      CC COMPUTER: IBM Compatible
Cc      CC OPERATING SYSTEM: DOS
Cc      CC SOFTWARE: FastSeq Version 2.0
Cc      CC CURRENT APPLICATION DATA:
Cc      CC APPLICATION NUMBER: US/08/604,989A
Cc      CC FILING DATE: February 23, 1996
Cc      CC CLASSIFICATION: 435
Cc      CC ATTORNEY/AGENT INFORMATION:
Cc      CC NAME: Charles E. Miller
Cc      CC REGISTRATION NUMBER: 24,576
Cc      CC REFERENCE/DOCKET NUMBER: 1920-026
Cc      CC TELECOMMUNICATION INFORMATION:
Cc      CC TELEPHONE: (212) 790-9090
Cc      CC TELEFAX: (212) 869-8864/9741
Cc      CC TELEX: 66141 PENNIE
Cc      CC INFORMATION FOR SEQ ID NO: 4:
Cc      CC SEQUENCE CHARACTERISTICS:
Cc      CC LENGTH: 466 amino acids
Cc      CC TYPE: amino acid
Cc      CC TOPOLOGY: linear
Cc      CC MOLECULE TYPE: protein
Cc      CC ORIGINAL SOURCE:
Cc      CC ORGANISM: human
Cc      CC STRAIN: UT-7
Cc      CC SEQUENCE 466 AA; 51898 MW; 1114727 CN;
Cc
Cc      Query Match 67.6%; Score 46; DB 2; Length 466;
Cc      Best Local Similarity 71.4%; Pred. No. 8.60e+01;

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Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 379 YGRAPY 385
QY 3 YNRAPYA 9

RESULT 10
ID PCT-US95-05008-2 STANDARD; PRT; 507 AA.

AC xxxxxx

Sequence 2, Application PC/TUS9505008

GENERAL INFORMATION:
APPLICANT: Sugen, Inc.

APPLICANT: 515 Galveston Drive

APPLICANT: Redwood City, California 94063-4720

APPLICANT: United States of America

APPLICANT: Wissenschaften E.V.

APPLICANT: München 80539

APPLICANT: Germany

TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05008

FILING DATE: 24-APR-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/232,545

FILING DATE: 22-APR-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-074

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212)869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: Protein

SEQUENCE 507 AA; 56469 MW; 1316735 CN;

Query Match 67.6%; Score 46; DB 3; Length 507;

Best Local Similarity 71.4%; Pred. No. 8.60e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 420 YGRAPY 426
QY 3 YNRAPYA 9

RESULT 11
ID US-08-604-989A-5 STANDARD; PRT; 507 AA.

AC xxxxxx

Sequence 5, Application US/08604989A

GENERAL INFORMATION:
Patent No. 5834208

APPLICANT: Sakano, S.

TITLE OF INVENTION: No. 5834208e1 Tyrosine Kinase

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604,989A

FILING DATE: February 23, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Charles E. Miller

REGISTRATION NUMBER: 24,576

REFERENCE/DOCKET NUMBER: 1920-026

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

ORIGINAL SOURCE:

ORGANISM: human

STRAIN: DT-7

SEQUENCE 507 AA; 56491 MW; 1317560 CN;

Query Match 67.6%; Score 46; DB 2; Length 507;

Best Local Similarity 71.4%; Pred. No. 8.60e+01;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 420 YGRAPY 426
QY 3 YNRAPYA 9

RESULT 12
ID US-08-444-792-4 STANDARD; PRT; 718 AA.

AC xxxxxx

Sequence 4, Application US/08444792

GENERAL INFORMATION:

Sequence 4, Application US/08444792

Patent No. 5726037

GENERAL INFORMATION:

CC APPLICANT: Bodary, Sarah C.
CC APPLICANT: Gorman, Cornelia M.
CC APPLICANT: Mclean, John W.
CC APPLICANT: Napier, Mary A.
CC TITLE OF INVENTION: METHOD FOR PREPARING WATER SOLUBLE
CC TITLE OF INVENTION: POLYPEPTIDES
CC NUMBER OF SEQUENCES: 18
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WinPatIn (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/444,792
CC FILING DATE: 19-May-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/380227
CC FILING DATE: 30-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/218878
CC FILING DATE: 28-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/821337
CC FILING DATE: 13-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/444490
CC FILING DATE: 01-DEC-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/290224
CC FILING DATE: 22-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER: 00,000
CC REFERENCE/DOCKET NUMBER: P0552P1C3D4
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-1994
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 718 amino acids
CC TYPE: Amino Acid
CC TOPOLOGY: Linear
CC SEQUENCE 718 AA; 79240 MW; 2616883 CN;
SO
Query Match 67.6%; Score 46; DB 1; Length 718;
Best Local Similarity 57.1%; Pred. No. 8.60e+01;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 645 KEDREPY 651
QY 2 KYNRAPY 8
RESULT 13
ID US-08-445-042-4 STANDARD; PRT; 718 AA.
XX xxxxxx
AC
DT
XX
XX
DE Sequence 4, Application US/08445042
CC
CC Sequence 4, Application US/08445042
CC Patent No. 5726290

CC GENERAL INFORMATION:
CC APPLICANT: Bodary, Sarah C.
CC APPLICANT: Gorman, Cornelia M.
CC APPLICANT: Mclean, John W.
CC APPLICANT: Napier, Mary A.
CC TITLE OF INVENTION: METHOD FOR PREPARING WATER SOLUBLE
CC TITLE OF INVENTION: POLYPEPTIDES
CC NUMBER OF SEQUENCES: 18
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WinPatIn (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/445,042
CC FILING DATE: 19-May-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/380227
CC FILING DATE: 30-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/218878
CC FILING DATE: 28-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/821337
CC FILING DATE: 13-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/444490
CC FILING DATE: 01-DEC-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/290224
CC FILING DATE: 22-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER: 00,000
CC REFERENCE/DOCKET NUMBER: P0552P1C3D1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-1994
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 718 amino acids
CC TYPE: Amino Acid
CC TOPOLOGY: Linear
CC SEQUENCE 718 AA; 79240 MW; 2616883 CN;
SO
Query Match 67.6%; Score 46; DB 1; Length 718;
Best Local Similarity 57.1%; Pred. No. 8.60e+01;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 645 KEDREPY 651
QY 2 KYNRAPY 8
RESULT 14
ID US-08-724-194-12 STANDARD; PRT; 33 AA.
XX xxxxxx
AC
DT
XX
XX
DE Sequence 12, Application US/08724194
CC
CC Sequence 12, Application US/08724194

CC Patent No. 5824875
CC GENERAL INFORMATION:
CC APPLICANT: RANU, RAJINDER S.
CC TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
CC TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
CC TITLE OF INVENTION: IN GERANIUMS
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SANTANGELO LAW OFFICES PC
CC STREET: 315 WEST OAK STREET, STE 701
CC CITY: FORT COLLINS
CC STATE: CO
CC COUNTRY: USA
CC ZIP: 80521
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/724,194
CC FILING DATE: 01-OCT-1996
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: SANTANGELO, LUKE
CC REGISTRATION NUMBER: 31,997
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (970) 224-3100
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 33 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 33 AA: 3822 MW; 5035 CN;
SQ
DB Query Match 64.7%; Score 44; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.41e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 8 YDRDPY 13
QY 3 YNRAPY 8
RESULT 15
US-08-899-575-87 STANDARD; PRT; 107 AA.
xxxxxx
DE Sequence 87, Application US/08899575
XX Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
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DB Query Match 64.7%; Score 44; DB 2; Length 107;
Best Local Similarity 44.4%; Pred. No. 1.41e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
DB 88 OQYHSSPYT 96
QY 1 QKYNRAPYA 9

Search completed: Thu Sep 2 11:29:27 1999
Job time : 7 secs.

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 WIREZEH (TM)

Release 3.1A John F. Collins, Bloccomputing Research Unit.
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MSrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:27:42 1999; Maspar time 3.06 Seconds
 117.904 Million cell updates/sec
 Molecular output not generated.

Title: >US-08-599-226-12
 Description: (1-9) from US08599226.pep
 Perfect Score: 68
 Sequence: 1 QKYNRAVYA 9

Scoring table: PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: p1r60
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 22.885; Variance 29.282; scale 0.782

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	54	79.4	1260	2	S28407	guanine nucleotide-ex	1.02e+00
2	53	77.9	279	1	SNRFSK	multicatalytic endope	1.64e+00
3	53	77.9	521	2	I39956	neutral proteinase (E	1.64e+00
4	52	76.5	360	2	S28047	TUBB3 protein - potat	2.63e+00
5	52	76.5	360	2	S52662	S-adenosylmethionine	2.63e+00
6	50	73.5	263	1	SNRRC2	multicatalytic endope	6.65e+00
7	50	73.5	269	2	JC1445	multicatalytic endope	6.65e+00
8	50	73.5	689	2	S45901	probable membrane pro	6.65e+00
9	49	72.1	342	2	H71258	protein tp33 precursor	1.05e+01
10	49	72.1	421	2	JC5323	anthranilate synthase	1.05e+01
11	49	72.1	490	2	E71486	probable s/t protein	1.05e+01
12	48	70.6	615	1	ABCHS	serum albumin precurs	1.05e+01
13	48	70.6	239	2	G02630	Fcalphabab - human	1.64e+01
14	48	70.6	287	2	JH0332	IGA (Fc) receptor, my	1.64e+01
15	48	70.6	367	2	S49009	fork head protein 2 -	1.64e+01
16	48	70.6	370	2	S49008	fork head protein 2 -	1.64e+01
17	48	70.6	419	3	JE0389	catabolite repressor	1.64e+01
18	48	70.6	488	1	RKPFLE	ribulose-bisphosphate	1.64e+01
19	48	70.6	488	1	RKPFLE	ribulose-bisphosphate	1.64e+01
20	48	70.6	491	1	JC1390	cyclin A - fruit fly	1.64e+01
21	48	70.6	521	1	HYBSN	bacillolysin (EC 3.4.	1.64e+01
22	48	70.6	790	2	S77032	ABC-type transport pr	1.64e+01
23	47	69.1	321	2	B71854	type II DNA modificat	2.55e+01

24	47	69.1	361	2	T01934	adenosylmethionine de	2.55e+01
25	47	69.1	1708	2	A43100	atxiva telanglectasia	2.55e+01
26	46	67.6	89	2	C47759	retrovirus-related re	3.93e+01
27	46	67.6	210	2	B25599	repB protein - Strept	3.93e+01
28	46	67.6	210	2	S05981	repB protein - Strept	3.93e+01
29	46	67.6	241	2	B55945	endothelial cell prot	3.93e+01
30	46	67.6	465	2	I48926	protein-tyrosine kina	3.93e+01
31	46	67.6	465	2	I58397	gene lsk protein - hu	3.93e+01
32	46	67.6	467	2	I56579	non-receptor protein	3.93e+01
33	46	67.6	505	2	I59296	protein-tyrosine kina	3.93e+01
34	46	67.6	507	2	A55625	protein-tyrosine kina	3.93e+01
35	46	67.6	516	2	S40996	hypothetical protein	3.93e+01
36	46	67.6	527	2	A49865	protein-tyrosine kina	3.93e+01
37	46	67.6	788	2	A26547	platelet glycoprotein	3.93e+01
38	46	67.6	903	2	T00358	hypothetical protein	3.93e+01
39	46	67.6	1013	2	S65195	probable membrane pro	3.93e+01
40	46	67.6	4957	2	T03435	ALR protein - human	3.93e+01
41	46	67.6	5262	2	T03454	ALR protein - human	3.93e+01
42	46	66.2	239	2	S61204	NEF protein - simian	6.03e+01
43	46	66.2	244	2	S61205	NEF protein - simian	6.03e+01
44	45	66.2	244	2	S61208	NEF protein - simian	6.03e+01
45	45	66.2	926	2	A54142	nucleoporin NUP107 -	6.03e+01

ALIGNMENTS

RESULT	ENTRY	1	#type complete
TITLE	S28407		guanine nucleotide-exchange activator CDC25 homolog - mouse
ORGANISM			Formal_name Mus musculus #common_name house mouse
DATE	17-Apr-1993		#sequence_revision 17-Apr-1993 #text_change 10-Sep-1997

ACCESSIONS	#authors	#journal	#title
S28407	Cen, H.; Papageorge, A.G.; Zippel, R.; Lowy, D.R.; Zhang, K.	EMBO J. (1992) 11:4007-4015	Isolation of multiple mouse cDNAs with coding homology to Saccharomyces cerevisiae CDC25: identification of a region related to Bcr, Vav, Dbl and CDC24.

REFERENCE	#cross-references	#status	#molecule-type	#residues
S28407	not compared with conceptual translation		1-1260	#label CEN

REFERENCE	#cross-references	#status	#molecule-type	#residues
S22693	not compared with conceptual translation		1-1260	#label CEN

REFERENCE	#cross-references	#status	#molecule-type	#residues
M46199	EMBL:X59868; NID:950357; PID:950358		789-1260	#label MAR

REFERENCE	#cross-references	#status	#molecule-type	#residues
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CLASSIFICATION	#superfamily	#residues	#experimental-source	#note
homology; CDC24 homology; pleckstrin repeat homology	superfamily CDC25-type guanine nucleotide exchange activator	1029-1030, 'D', 1032-1224	NCBI backbone (NCBI:111101, NCBI:111102)	sequence extracted from NCBI backbone (NCBI:111101, NCBI:111102)

FEATURE
242-428 #domain CDC24 homology #label CD24\
1021-1257 #domain CDC25-type guanine nucleotide exchange activator
homology #label SOS

SUMMARY #length 1260 #molecular-weight 143900 #checksum 9725

Query Match 79.4%; Score 54; DB 2; Length 1260;
Best Local Similarity 62.5%; Pred. No. 1.02e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1058 EXTERPRY 1065
1 1 1 1 1 1
1 OKYNRAPY 8

RESULT 2

ENTRY SNFE5K #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) 35k chain
- fruit fly (Drosophila melanogaster)
19S cylinder particle 35k chain; multicatalytic proteinase
35k chain; prosome 35k chain; proteasome 35k chain
#formal_name Drosophila melanogaster
ORGANISM 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
DATE 05-Sep-1997
ACCESSIONS S23450; S05507; A38761
REFERENCE S23450
#authors Frenzel, S.; Troxell, M.; Haass, C.; Pesold-Hurt, B.;
Glaetzer, K.H.; Klotzel, P.M.
#journal Eur. J. Biochem. (1992) 205:1043-1051
#title Molecular characterization of the genomic regions of the
Drosophila alpha-type subunit proteasome genes PROS-Dm28.1
and PROS-Dm35.
#cross-references MVID:92249308
#accession S23450
#molecule-type DNA
#residues 1-279 ##label FREN
#cross-references EMBL:X62285; NID:98387; PID:98388
#experimental_source strain Canton S
REFERENCE S05507
#authors Haass, C.; Pesold-Hurt, B.; Multhaup, G.; Beyreuther, K.;
Klotzel, P.M.
#journal EMBO J. (1989) 8:2373-2379
#title The PROS-35 gene encodes the 35 kd protein subunit of
Drosophila melanogaster proteasome.
#cross-references MVID:9005444
#accession S05507
#molecule-type mRNA
#residues 1-279 ##label HAA
#cross-references EMBL:X15497; NID:98381; PID:98382
#accession A38761
#molecule-type protein
#residues 4-18;194-206 ##label HAA2

GENETICS
#gene PROS-35
#cross-references FlyBase:FBgn0003151
#map_position 89f-90A
#introns 1/3; 211/3
CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9
KEYWORDS hydrolase; phosphoprotein; proteinase
SUMMARY #length 279 #molecular-weight 31058 #checksum 365

Query Match 77.9%; Score 53; DB 1; Length 279;
Best Local Similarity 55.6%; Pred. No. 1.64e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 121 QKYNRAPY 129
1 1 1 1 1 1
1 OKYNRAPY 9

RESULT 3

ENTRY I39956 #type complete
TITLE neutral proteinase (EC 3.4.24.-) - Bacillus amyloliquefaciens

ORGANISM #formal_name Bacillus amyloliquefaciens
DATE 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
18-Mar-1997

ACCESSIONS I39956
REFERENCE I39956

#authors Shimada, H.; Honjo, M.; Mita, I.; Nakayama, A.; Akao, A.;
Manabe, K.; Furutani, Y.
#journal J. Biotechnol. (1985) 2:75-85
#title The nucleotide sequence and some properties of the neutral
protease gene of Bacillus amyloliquefaciens.
#accession I39956
#status preliminary; translated from GB/EMBL/DBJ
#molecule-type DNA
#residues 1-521 ##label RES
#cross-references GB:M36723; NID:g143352; PID:g143353

GENETICS
#start_codon GTC
CLASSIFICATION #superfamily thermolysin
KEYWORDS hydrolase; metalloproteinase
SUMMARY #length 521 #molecular-weight 56725 #checksum 6816

Query Match 77.9%; Score 53; DB 2; Length 521;
Best Local Similarity 75.0%; Pred. No. 1.64e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 308 OKYNRNSY 315
1 1 1 1 1 1
1 OKYNRAPY 8

RESULT 4

ENTRY S28047 #type complete
TITLE TUB13 protein - potato
#formal_name Solanum tuberosum #common_name potato
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
09-Sep-1997
ACCESSIONS S28047
REFERENCE S28046
#authors Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie,
L.A.; Pearce, S.R.; Flavell, A.J.
#journal Plant Mol. Biol. (1992) 20:641-651
#title Expression and sequence analysis of cDNAs induced during the
early stages of tuberisation in different organs of the
potato plant (Solanum tuberosum L.).
#accession S28047
#molecule-type mRNA
#residues 1-360 ##label TAY
#cross-references EMBL:Z11680; NID:921484; PID:921485

GENETICS
#gene TUB13
SUMMARY #length 360 #molecular-weight 39726 #checksum 7941

Query Match 76.5%; Score 52; DB 2; Length 360;
Best Local Similarity 62.5%; Pred. No. 2.63e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 332 QKFTTPY 339
1 1 1 1 1 1
1 OKYNRAPY 8

RESULT 5

ENTRY S52662 #type complete
TITLE S-adenosylmethionine decarboxylase (SAMDC) - potato
#formal_name Solanum tuberosum #common_name potato
DATE 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
21-Jul-1995
ACCESSIONS S52662
REFERENCE S52662
#authors Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.;
Burgh, L.R.; Davies, H.V.; Stark, W.J.R.; Kumar, A.
#journal Plant Mol. Biol. (1994) 26:327-338
#title Characterisation of the S-adenosylmethionine decarboxylase

8-269 long splice form #status predicted #label MATL\N
#product multicatalytic endopeptidase complex chain C2,
short splice form #status predicted #label MATS\N
230 #binding site phosphate (Tyr) (covalent) #status
predicted

SUMMARY #length 269 #molecular-weight 30239 #checksum 5946

Query Match 73.5%; Score 50; DB 2; Length 269;
Best Local Similarity 55.6%; Pred. NO. 6.65e+00;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 127 ORGNRPPY 135
1:1:1:1:1:
QY 1 QKYNRAPYA 9

RESULT 8
ENTRY S45901 #type complete
TITLE probable membrane protein YBR043c - yeast (Saccharomyces
cerevisiae)
#FERNATE_NAMES hypothetical protein YBR0413
#ORGANISM #formal_name Saccharomyces cerevisiae
DATE 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change
04-Sep-1998

ACCESSIONS S45901
REFERENCE S45893
#authors Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.;
Urrestarazu, A.; Vissers, S.
#submission submitted to the Protein Sequence Database, August 1994
#accession S45901

#molecule_type DNA
#residues 1-689 #label AND
##cross-references EMBL:Z35912; NID:g536267; PID:g536268; MIPS:YBR043c
##experimental_source strain S288C

GENETICS
#map_position 2R
CLASSIFICATION #superfamily yeast probable membrane protein YBR043c
KEYWORDS transmembrane protein

FEATURE
108-124 #domain transmembrane #status predicted #label TM1\
140-161 #domain transmembrane #status predicted #label TM2\
177-193 #domain transmembrane #status predicted #label TM3\
239-256 #domain transmembrane #status predicted #label TM4\
265-287 #domain transmembrane #status predicted #label TM5\
476-493 #domain transmembrane #status predicted #label TM6\
513-529 #domain transmembrane #status predicted #label TM7\
555-579 #domain transmembrane #status predicted #label TM8\
587-603 #domain transmembrane #status predicted #label TM9\
629-645 #domain transmembrane #status predicted #label TM10\
648-670 #domain transmembrane #status predicted #label TM11
SUMMARY #length 689 #molecular-weight 77300 #checksum 8706

Query Match 73.5%; Score 50; DB 2; Length 689;
Best Local Similarity 71.4%; Pred. NO. 6.65e+00;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 500 KYSRPPY 506
1:1:1:1:1:
QY 2 KYNRAPY 8

RESULT 9
ENTRY H71258 #type complete
TITLE protein tp33 precursor - syphilis spirochete
#formal_name Treponema pallidum subsp. pallidum #common_name
#ORGANISM syphilis spirochete
DATE 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
17-Mar-1999

ACCESSIONS H71258; S19825; S18232
REFERENCE A71250
#authors Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.;
Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayton,
R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,

M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
D.; Howell, J.K.; Chidambaram, M.; Uteerapack, T.; McDonald,
L.; Artlach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Watthey,
L.; Weidman, J.; Smith, H.O.; Venter, J.C.
#journal Science (1998) 281:375-388
#title Complete genome sequence of Treponema pallidum, the syphilis
spirochete.

#cross-references MIMD:98332770
#accession H71258

##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-342 #label COL
##cross-references GB:AE001264; GB:AE000520; NID:g3323278; PID:g3323279
##experimental_source strain Nichols

REFERENCE S19825
#authors Blanco, D.
#submission submitted to the EMBL Data Library, August 1991
#accession S19825
##molecule_type DNA
##residues 1-9,'S',11-16,'A',18-28 #label BLA1
##cross-references EMBL:X61228; GB:S84879; NID:g48228; PID:g48229
S18230

REFERENCE S18230
#authors Blanco, D.R.; Giladi, M.; Champion, C.I.; Haake, D.A.;
Chikami, G.K.; Miller, J.N.; Lovett, M.A.
#journal Mol. Microbiol. (1991) 5:2405-2415
#title Identification of Treponema pallidum subspecies pallidum
genes encoding signal peptides and membrane-spanning
sequences using a novel alkaline phosphatase expression
vector.

#cross-references MIMD:92167806
#accession S18232
##status not compared with conceptual translation
##molecule_type DNA
##residues 1-16,'A',18-28 #label BLA2
##cross-references EMBL:X61228; GB:S84879; NID:g48228

GENETICS
#gene Tp33; TP0957
FEATURE
1-17

SUMMARY #domain signal sequence #status predicted #label SIG
#length 342 #molecular-weight 38312 #checksum 7408

Query Match 72.1%; Score 49; DB 2; Length 342;
Best Local Similarity 85.7%; Pred. NO. 1.05e+01;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 156 YTRAPYA 162
1:1:1:1:1:
QY 3 YNRPYA 9

RESULT 10
ENTRY JC5323 #type complete
TITLE anthranilate synthase (EC 4.1.3.27) alpha chain - Sulfolobus
solfataricus

ORGANISM #formal_name Sulfolobus solfataricus
DATE 15-May-1997 #sequence_revision 18-Jul-1997 #text_change
17-Mar-1999

ACCESSIONS JC5323; A40635
REFERENCE JC5323
#authors Tutilio, M.L.; Tosco, A.; Marino, G.; Sanna, G.;
Bischoff, B.; Res. Commun. (1997) 230:306-310
#journal Expression of Sulfolobus solfataricus tps and tps genes in
E. coli.

#cross-references MIMD:97168965
#accession JC5323
##status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-421 #label TUT
REFERENCE A40635
#authors Tutilio, M.L.; Scarrano, G.; Marino, G.; Sanna, G.; Cubellis,

#journal J. Bacteriol. (1993) 175:299-302

#title Tryptophan biosynthesis genes trpEGC in the thermocacidophilic
#cross-references archaebacterium Sulfolobus solfataricus.
#contents MT-4
#accession A40635
#status Preliminary
#molecule_type DNA
#residues 1-421 #label T02
#cross-references GB:M98048; NID:g152937
#note sequence extracted from NCBI backbone (NCBIN:121234,
NCBIR:121235)

COMMENT This enzyme catalyzes per se the conversion of chorismate into
anthranilate in the presence of high ammonia concentration and is
responsible for the chorismate binding and the allosteric
regulation.

GENETICS

#gene type
CLASSIFICATION #superfamily anthranilate synthase component I
KEYWORDS carbon-carbon lyase; oxo-acid-lyase
#length 421 #molecular-weight 47736 #checksum 7079

Query Match 72.1%; Score 49; DB 2; Length 421;
Best Local Similarity 55.6%; Pred. No. 1.05e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 350 EBYKRCPYA 358
:|:|:|
QY 1 QKYNRAPHYA 9

RESULT 11
ENTRY E71486 #type complete
TITLE probable s/t protein kinase - Chlamydia trachomatis (serotype
D, strain UW-3/CX)
ORGANISM #format_name Chlamydia trachomatis
DATE 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
21-Nov-1998

ACCESSIONS E71486
REFERENCE A71570

#authors Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe,
R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov,
R.L.; Zhao, Q.; Koonin, E.V.; Daviss, R.W.
#journal Science (1998) 282:754-759
#title Genome sequence of an obligate intracellular pathogen of
humans: Chlamydia trachomatis.
#cross-references MIMD:9900809
#accession E71486

#status Preliminary
#molecule_type DNA
#residues 1-490 #label ARN
#cross-references GB:AE001373; GB:AE001273; NID:g3329113; PID:g3329124
#experimental_source serotype D, strain UW-3/CX

GENETICS

#gene pkn5
SUMMARY #length 490 #molecular-weight 55926 #checksum 6253

Query Match 72.1%; Score 49; DB 2; Length 490;
Best Local Similarity 55.6%; Pred. No. 1.05e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 472 QKYDRSLYP 480
|||:|:|
QY 1 QKYNRAPHYA 9

RESULT 12
ENTRY ABCHS #type complete
TITLE serum albumin precursor - chicken
ORGANISM #format_name Gallus gallus #common_name chicken
DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
03-Sep-1997
ACCESSIONS S15571; A05078; A13451
REFERENCE S15571

#authors Cassady, A.I.; Salkild, C.K.; Baverstock, P.; Wallace, J.C.
#submission submitted to the EMBL Data Library, July 1991
#accession S15571
#molecule_type mRNA
#residues 1-615 #label CAS
#cross-references EMBL:X60688; NID:663747; PID:663748
REFERENCE A05078

#authors Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau,
P.C.K.; Dealey, R.G.
#journal J. Biol. Chem. (1983) 258:4556-4564
#title The 5' noncoding and flanking regions of the avian very low
density apolipoprotein II and serum albumin genes.
#cross-references MIMD:83161037
#accession A05078

#molecule_type DNA
#residues 1-28 #label HAC
#cross-references GB:V00381; NID:g63038; PID:g63039
REFERENCE A13451

#authors Rosen, A.M.; Geller, D.M.
#journal Biochem. Biophys. Res. Commun. (1977) 78:1060-1066
#title Chicken microsomal albumin: amino terminal sequence of
chicken proalbumin.
#cross-references MIMD:78019943
#accession A13451

#molecule_type protein
#residues 19-23, 'W', 25-30 #label ROS

COMMENT Serum albumin is synthesized in the liver as prealbumin. It
binds copper, nickel, calcium (weakly, at 2-3 sites), and
protoporphyrin, long-chain fatty acids, prostaglandins, steroid
hormones (weak bonds with these hormones promote their transfer
across the membranes), thyroxine, and triiodothyronine.
#superfamily serum albumin; serum albumin repeat homology
carrier protein; duplication; metal binding; plasma

CLASSIFICATION
KEYWORDS
FEATURES

1-18 #domain signal sequence #status predicted #label SIG\
19-26 #domain propeptide #status predicted #label PRO\
27-613 #domain serum albumin #status predicted #label MAT\
32-206 #domain serum albumin repeat homology #label SA1\
225-398 #domain serum albumin repeat homology #label SA2\
417-596 #domain serum albumin repeat homology #label SA3\
30 #binding_site copper (His) #status predicted\
80-99,102-118,
117-128,152-197,
196-205,228-274,
273-281,293-307,
306-317,344-389,
388-397,420-466,
465-476,489-505,
504-515,542-587,
586-595

SUMMARY #dsulfide_bonds #status predicted
#length 615 #molecular-weight 69918 #checksum 4822

Query Match 72.1%; Score 49; DB 1; Length 615;
Best Local Similarity 55.6%; Pred. No. 1.05e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 249 QKYPKAPPS 257
|||:|:|
QY 1 QKYNRAPHYA 9

RESULT 13
ENTRY G02630 #type complete
TITLE FcalphaRb - human
ORGANISM #format_name Homo sapiens #common_name man
DATE 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
17-Jul-1998

ACCESSIONS G02630
REFERENCE H01508

#authors van Dijk, T.B.; Morton, R.C.; Caldenhoven, E.; Bracke, M.;
Reaismakers, J.A.M.; Lamme, J.
#submission submitted to the EMBL Data Library, April 1996

#accession G02630
#status preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-239 ##label VAN
##cross-references EMBL:U56236; NID:g1326228; PID:g1326229
SUMMARY #length 239 #molecular-weight 26996 #checksum 5338

Query Match 70.6%; Score 48; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.64e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 197 YNRSFY 202
|||:|
QY 3 YNRSFY 8

RESULT 14
ENTRY JH0332 #type complete
TITLE Iga (Fc) receptor, myeloid cell (CD89) precursor - human
TERMINATE_NAMES myeloid glycoprotein CD89
ORGANISM #formal_name Homo sapiens #common_name man
12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
10-Sep-1997
JH0332; I37224; S14405
ACCESSIONS JH0332
REFERENCE JH0332
#authors Maliszewski, C.R.; March, C.J.; Schoenborn, M.A.; Gimpel, S.;
Shen, L.
#journal J. Exp. Med. (1990) 172:1665-1672
#title Expression cloning of a human Fc receptor for Iga.
#cross-references MIM:91079769
#accession JH0332
#molecule_type mRNA
#residues 1-287 ##label MAL
##cross-references GB:X54150; NID:g31329; PID:g31330
##experimental_source myeloid cell liver V937
REFERENCE I37224
#authors de Wit, T.P.; Morton, H.C.; Capel, P.J.; van de Winkel, J.G.
#journal J. Immunol. (1995) 155:1203-1209
#title Structure of the gene for the human myeloid Iga Fc receptor
(CD89).
#cross-references MIM:95363085
#accession I37224
#status preliminary: translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-287 ##label RES
##cross-references EMBL:X87767; NID:g963041; PID:g1054737

GENETICS
#gene GDB:FCAR; CD89
##cross-references GDB:127543; OMIM:147045
#map_position 19q13.2-19q13.4
#introns 12/1; 24/1; 121/1; 217/1
KEYWORDS glycoprotein; immunoglobulin receptor; transmembrane protein
FEATURE
1-21 #domain signal sequence #status predicted #label SIG
22-267 #product Iga receptor Fc alpha #status predicted #label
MFC
228-246 #domain transmembrane #status predicted #label TRA
65,79,141,177,186 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 287 #molecular-weight 32265 #checksum 5963

Query Match 70.6%; Score 48; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 1.64e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 197 YNRSFY 202
|||:|
QY 3 YNRSFY 8

RESULT 15
ENTRY S49009 #type complete
TITLE fork head protein 2 - African clawed frog

ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
17-Mar-1999
ACCESSIONS S49009
REFERENCE S49008
#authors Lee, J.; Clement, J.H.; Oschwald, R.; Koester, M.; Knoechel,
W.
#journal Mech. Dev. (1994) 45:117-126
#title Spatial and temporal transcription patterns of the forkhead
related XFD-2/XFD-2' genes in Xenopus laevis embryos.
#cross-references MIM:94257528
#accession S49009
#status preliminary
#molecule_type mRNA
#residues 1-367 ##label LEE
##cross-references EMBL:X74316; NID:g511161; PID:g511162
CLASSIFICATION #superfamily unassigned fork head proteins; fork head
DNA-binding domain homology

FEATURE
128-219 #domain fork head DNA-binding domain homology #label FHD
SUMMARY #length 367 #molecular-weight 40971 #checksum 6845

Query Match 70.6%; Score 48; DB 2; Length 367;
Best Local Similarity 83.3%; Pred. No. 1.64e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 337 YNRSFY 342
|||:|
QY 3 YNRSFY 8

Search completed: Thu Sep 2 11:27:56 1999
Job time : 14 secs.

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 CC -----
 DR EMBL: L20899; G388247; -.
 DR EMBL: X59868; G50356; -.
 DR PIR: S20730; S20730.
 DR PIR: S22693; S22693.
 DR MCD: MGI:99694; RASGRF1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR PROSITE: PS00741; GDS_CDC24; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PFAM: PF00169; PH; 2.
 DR PFAM: PF00612; IQ; 1.
 DR PFAM: PF00617; RASGEF; 1.
 DR PFAM: PF00618; RASGEF; 1.
 DR PFAM: PF00621; RHOGEF; 1.
 DR GUANINE-NUCLEOTIDE RELEASING FACTOR.
 KM DOMAIN 22 130 PH.
 FT CONFLICT 1033 1033 E -> D (IN REF. 3).
 SQ SEQUENCE 1262 AA; 144101 MW; 021C787F CRC32;
 Query Match 79.4%; Score 54; DB 1; Length 1262;
 Best Local Similarity 62.5%; Pred. No. 2.99e-01;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Db 1060 EKERPTYPY 1067
 QY 1 OKYNRPY 8
 RESULT 2
 ID PRG2_DROME STANDARD; PRT; 279 AA.
 AC P12881;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROTEASOME 29 KD SUBUNIT (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE
 DE COMPLEX 35 KD SUBUNIT).
 GN PROS35 OR PROS-35.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 CC EURARCTOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 CC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
 CC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-18 AND 194-206.
 RC STRAIN-OREGON-R;
 RC MEDLINE: 90005444.
 RA HAASS C., PESOLD-HURT B., MULTHAUP G., BEYREUTHER K.,
 RA KLOETZEL P.-M.;
 RT "The PROS-35 gene encodes the 35 kd protein subunit of Drosophila
 RT melangaster proteasome.";
 RL EMBO J. 8:2373-2379(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RC MEDLINE: 92249308.
 RA FRENTZEL S., TROXELL M., HAASS C., PESOLD-HURT B., GLAETZER K.H.,
 RA KLOETZEL P.-M.;
 RT "Molecular characterization of the genomic regions of the Drosophila
 RT alpha-type subunit proteasome genes PROS-Dm28.1 and PROS-Dm35.";
 RL EUR. J. BIOCHEM. 205:1043-1051(1992).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC AGC, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH. THE 35 KD SUBUNIT IS PROBABLY A
 CC REGULATOR SUBUNIT. THE PROTEASOME HAS AN ATP-DEPENDENT
 CC PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPE STRUCTURE.

CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X15497; G8382; -.
 DR EMBL: X62285; G8388; -.
 DR PIR: S05507; SNRPF5K.
 DR PIR: S23450; S23450.
 DR FLYBASE: FBgn0003151; PROS35.
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PFAM: PF00227; Proteasome; 1.
 DR HSSP: P25156; 1PMA.
 KM PROTEASOME; HYDROLASE; PROTEASE; PHOSPHORYLATION.
 FT MOD_RES 103 103 PHOSPHORYLATION (POTENTIAL).
 SQ SEQUENCE 279 AA; 31058 MW; AA18BBD F CRC32;
 Query Match 77.9%; Score 53; DB 1; Length 279;
 Best Local Similarity 55.6%; Pred. No. 5.08e-01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 121 QRYDRRPY 129
 QY 1 OKYNRPYA 9
 RESULT 3
 ID DCM_SOLTU STANDARD; PRT; 360 AA.
 AC Q04694;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYM (EC 4.1.1.50) (ADOMETDC)
 DE (SAMDC) (INDUCED STOLEN TIP PROTEIN TUB13).
 GN SAMDC OR TUB13.
 OS SOLANUM TUBEROSUM (POTATO).
 CC EURARCTOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYCOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 CC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; SOLANUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, RECORD; TISSUE-STOLON TIP;
 RC MEDLINE: 93081725.
 RA TAYLOR M.A., MAD ARIF S.A., KUMAR A., DAVIES H.V., SCOBIE L.A.,
 RA PEARCE S.R., FLAVELL A.J.;
 RT "Expression and sequence analysis of cDNAs induced during the early
 RT stages of tuberisation in different organs of the potato plant
 RT (Solanum tuberosum L.).";
 RL PLANT MOL. BIOL. 20:641-651(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, DESIREE;
 RC MEDLINE: 95036004.
 RA MAD ARIF S.A., TAYLOR M.A., GEORGE L.A., BUTLER A.R., BURCH L.R.,
 RA DAVIES H.V., STARK M.J., KUMAR A.;
 RT "Characterisation of the S-adenosylmethionine decarboxylase (SAMDC).
 RT gene of potato.";
 RL PLANT MOL. BIOL. 26:327-338(1994).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE = (5-DEOXY-5-ADENOSYL)
 CC (3-AMINOPROPYL)METHYLSULFONIUM SALT + CO(2).
 CC -1- COFACTOR: THIS ENZYME REQUIRES A PYRUVYL GROUP FOR ITS ACTIVITY.
 CC -1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
 CC AMINOPROPYL MOIETY REQUIRED FOR SPERMATINE AND SPERMINE
 CC BIOSYNTHESIS FROM PUTRESCINE.
 CC -1- TISSUE SPECIFICITY: STOLON, ALSO EXPRESSED IN LEAVES, STEMS

CC AND ROOTS.
 CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING THE
 CC EARLY STAGES OF TUBERIZATION. MAXIMUM EXPRESSION WAS IN NON-
 CC SWELLING STOLON TIPS FROM STAGE B, AND LEVEL DECLINED AS THE
 CC TUBER INCREASED IN SIZE.
 CC -----
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 CC -----
 CC EMBL: 211680; G21485; -
 CC DR EMBL: S74514; G807094; -
 CC DR PIR: S28047; S28047.
 CC KW SPERIDINE BIOSYNTHESIS; LYASE; DECARBOXYLASE; PYRUVATE; ZMOGEN.
 CC FT CHAIN 1
 CC FT CHAIN 72
 CC FT CHAIN 73 360
 CC FT SITE 72 73
 CC FT MOD_RES 73 73
 CC FT ACT_SITE 13 13
 CC FT ACT_SITE 16 16
 CC FT ACT_SITE 87 87
 CC FT ACT_SITE 174 174
 CC FT CONFLICT 257 257
 CC FT CONFLICT 291 291
 CC FT CONFLICT 305 305
 CC FT SEQUENCE 360 AA; 39726 MW; 4F29EFEE CRC32;
 CC SQ
 CC Query Match 76.5% Score 52; DB 1; Length 360;
 CC Best Local Similarity 62.5% Pred. No. 8.56e-01;
 CC Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 CC Db 332 OKTFRPY 339
 CC QY 1 OKYNRAVY 8
 CC RESULT 4
 CC PRC2_RAT STANDARD; PRT; 263 AA.
 CC P18430;
 CC 01-NOV-1990 (REL. 16, CREATED)
 CC 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 CC 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 CC DE PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
 CC DE (PROTEASOME NU CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT
 CC C2).
 CC DE PSM1.
 CC GN RATTUS NORVEGICUS (RAT).
 CC OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTUS.
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 CC RC TISSUE=LIVER;
 CC RX MEDLINE: 90057428.
 CC RA FUJIMURA T., TANAKA K., KUMATORI A., SHIN S., YOSHIMURA T.,
 CC ICHIHARA A., TOKUNAGA F., ARIGA R., IWANAGA S., KAKIZURA A.,
 CC NAKANISHI S.;
 CC RA "Molecular cloning of cDNA for proteasomes (multicatalytic proteinase
 CC RT complexes) from rat liver: primary structure of the largest component
 CC (C2)."
 CC RT BIOCHEMISTRY 28:7332-7340(1989).
 CC RL [2]
 CC RP SEQUENCE OF 1-30.

RC TISSUE=LIVER;
 RX MEDLINE: 90243011.
 RA TOKUNAGA F., ARIGA R., IWANAGA S., TANAKA K., ICHIHARA A., TAKAO T.,
 RA SHIMONISHI Y.;
 RA "The NH2-terminal residues of rat liver proteasome (multicatalytic
 RT proteinase complex) subunits, C2, C3 and C8, are N
 RT alpha-acetylated."
 CC FEBS LETT. 263:373-375(1990).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
 CC PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC -1- SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL RAT TISSUES.
 CC -1- PTM: ITS C-TERMINAL EXTENSION IS PARTIALLY CLEAVED OFF BY LIMITED
 CC PROTEOLYSIS LEADING TO A CONVERSION OF THE PROTEASOME FROM ITS
 CC LATENT INTO ITS ACTIVE FORM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M29859; G206382; -
 CC DR EMBL: D90265; G220877; -
 CC DR PIR: A32968; SNR02.
 CC DR PROSITE: P500388; PROTEASOME_A; 1.
 CC DR PRAM: P500227; proteasome; 1.
 CC DR HSSP: P25156; IPMA.
 CC KW PROTEASOME; HYDROLASE; PROTEASE; ACETYLATION.
 CC FT MOD_RES 1
 CC FT SEQUENCE 263 AA; 29517 MW; 01D55620 CRC32;
 CC SQ
 CC Query Match 73.5% Score 50; DB 1; Length 263;
 CC Best Local Similarity 55.6% Pred. No. 2.38e+00;
 CC Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 CC Db 121 ORYGBRPG 129
 CC QY 1 OKYNRAVY 9
 CC RESULT 5
 CC PRC2_HUMAN STANDARD; PRT; 263 AA.
 CC P25786;
 CC 01-MAY-1992 (REL. 22, CREATED)
 CC 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 CC 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 CC DE PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
 CC DE (PROTEASOME NU CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT
 CC C2) (30 KD PROSOMAL PROTEIN) (PROS-30).
 CC DE PSM1 OR PSC2 OR PROS30.
 CC GN HOMO SAPIENS (HUMAN).
 CC OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE: 93013039.
 CC RA SILVA-PEREIRA I., BEY F., COUX O., SCHERRER K.;
 CC "Two mRNAs exist for the Hs PROS-30 gene encoding a component of
 CC RT human proteasomes."
 CC RT GENE 120:235-242(1992).
 CC RL

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91223105.
RA TAMURA T., LEE D.H., OSAKA F., FUJIMURA T., SHIN S., CHUNG C.H.,
RT TANAKA K., ICHIHARA A.;
RT "Molecular cloning and sequence analysis of cDNAs for five major
RT subunits of human proteasomes (multi-catalytic proteinase
RT complexes).";
RL BIOCHIM. BIOPHYS. ACTA 1089:95-102(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91363412.
RA DEMARTINO G.N., ORTH K., MCCULLOUGH M.L., LEE L.W., MUNN T.Z.,
RA MOOMAM C.R., DAMSON P.A., SLAUGHTER C.A.;
RT "The primary structures of four subunits of the human,
RT high-molecular-weight proteinase, macropain (proteasome), are
RT distinct but homologous";
RL BIOCHIM. BIOPHYS. ACTA 1079:29-38(1991).
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC PROTEOLYTIC ACTIVITY.
CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
CC PROTEOLYTIC PATHWAY.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC ALSO IN THE NUCLEUS.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS (SHORT AND LONG) ARE PRODUCED BY
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
CC -----
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CC -----
DR EMBL: M69992; G190447; ALT_SEQ.
DR EMBL: D00759; G220022; -.
DR EMBL: X61969; G296738; -.
DR PIR: S15897; S15897.
DR PIR: JCI445; JCI445.
DR AARHUS/GHEHT-2DPAGE; 2223; IEF.
DR MIT: 602854; -.
DR PROSITE: PS00386; PROTEASOME.A; 1.
DR PFAM: PF00227; Proteasome; 1.
DR HSSP: P25156; 1PMA.
KM PROTEASOME: HYDROLASE; PROTEASE: ACETYLATION; ALTERNATIVE SPLICING.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT VARSPIC 1 1 M -> NQLSRYK (IN LONG FORM).
SQ SEQUENCE 263 AA; 29555 MW; 6CD09A93 CRC32;

Query Match 73.5%; Score 50; DB 1; Length 263;
Best Local Similarity 55.6%; Pred. No. 2.38e+00;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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GN YBR043C OR YBR0413.
OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCAROMYCETALES;
OC SACCAROMYCETACEAE; SACCAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-5289C;
RA ANDRE B., CIEPELOUCH C., HEIN C., JAUNIAUX J.C., URRESTARAZU A.,
RA VISSERS S.;
RT SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
CC AS THE DRUG RESISTANCE TRANSLUCASE FAMILY). BELONGS TO THE
CC CAR/CYHR SUBFAMILY.
CC -----
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CC -----
DR EMBL: Z5912; G536268; -.
DR PIR: S45901; S45901.
KM HYPOTHETICAL PROTEIN; TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 109 131 POTENTIAL.
FT TRANSMEM 140 163 POTENTIAL.
FT TRANSMEM 176 193 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 266 283 POTENTIAL.
FT TRANSMEM 476 493 POTENTIAL.
FT TRANSMEM 511 532 POTENTIAL.
FT TRANSMEM 559 577 POTENTIAL.
FT TRANSMEM 587 609 POTENTIAL.
FT TRANSMEM 625 642 POTENTIAL.
FT TRANSMEM 649 668 POTENTIAL.
SQ SEQUENCE 689 AA; 77300 MW; 3616EDAE CRC32;

Query Match 71.5%; Score 50; DB 1; Length 689;
Best Local Similarity 71.4%; Pred. No. 2.38e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 121 ORGRAPY 129
OY 1 OKYNRABYA 9

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DB 500 KYRNRY 506
OY 2 KYRNAPY 8

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RESULT 6
ID YBP3_YEAST STANDARD; PRT; 669 AA.
AC P38227;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 77.3 KD PROTEIN IN FTGL-GIPI INTERGENIC REGION.

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RESULT 7
ID TRPE_SULSO STANDARD; PRT; 421 AA.
AC O06128;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE.
OS SULFOLOBUS SOLFATARICUS.
OC ARCHAEA; CREMARCHAEOTA; SULFOLOBALES; SULFOLOBUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 49255 / MT4;
RX MEDLINE: 93106970.
RA TUTINO M.L., SCARANO G., MARINO G., SANNTA G., CUBELLIS M.V.;
RT "tryptophan biosynthesis genes trpGC in the thermocacidophilic
RT archaebacterium Sulfolobus solfataricus.";
RL J. BACTERIOL. 175:299-302(1993).
CC -1- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE -> ANTHRANILATE +
CC PYRUVATE + L-GLUTAMATE.
CC -1- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -1- SUBUNIT: Tetramer of two components I and two components II (BY
CC SIMILARITY).
CC -1- COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA
CC RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE

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CC MIDOTRANSFERASE ACTIVITY.
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 CC -----
 CC EMBL: M98048; G152937; -
 CC EMBL: Z50014; G1004323; -
 CC PIR: A40635; A40635.
 CC PIR: PF00425; Chorismate_bind; 1.
 CC TRYPTOPHAN BIOSYNTHESIS; LYASE.
 CC SEQUENCE 421 AA; 47736 MW; 658F857F CRC32;
 CC -----
 CC Query Match 72.1%; Score 49; DB 1; Length 421;
 CC Best Local Similarity 55.6%; Pred. No. 3.93e+00;
 CC Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC 350 EYKRGQPYA 358
 CC :||:||||
 CC 1 QKYNRPYA 9
 CC -----
 CC RESULT 8
 CC ID ALBU CHICK STANDARD; PRT; 615 AA.
 CC AC P19121;
 CC DT 01-NOV-1990 (REL. 16, CREATED)
 CC DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 CC DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 CC DE SERUM ALBUMIN PRECURSOR.
 CC GN ALB
 CC OS CALLUS GALLUS (CHICKEN).
 CC OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAUROTA; AVES;
 CC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; GALLUS.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RP TISSUE-LIVER;
 CC RA CASSADY A.I., SAKALUD C.K., BAYERSSTOCK P., WALLACE J.C.;
 CC SUBMITTED (JUL-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC [2]
 CC SEQUENCE OF 1-28 FROM N.A.
 CC RP MEDLINE: 83161037.
 CC RA HACHE R.J.G., MISKOCIL R., VASA M., ROY R.N., LAT P.C.K., DELEY R.G.;
 CC "The 5' noncoding and flanking regions of the avian very low density
 CC apolipoprotein II and serum albumin genes. Homologies with the egg
 CC white protein genes.";
 CC J. BIOL. CHEM. 258:4556-4564(1983).
 CC [3]
 CC SEQUENCE OF 19-30.
 CC RP MEDLINE: 78019943.
 CC RA ROSEN A.M., GELLER D.M.;
 CC "Chicken microsomal albumin: amino terminal sequence of chicken
 CC proalbumin.";
 CC RT BIOCHEM. BIOPHYS. RES. COMMUN. 78:1060-1066(1977).
 CC RL BIOCHEM. BIOPHYS. RES. COMMUN. 78:1060-1066(1977).
 CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
 CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
 CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
 CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -----
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CC -----
 CC EMBL: X60688; G63748; -
 CC EMBL: Y00381; G63039; -
 CC PIR: S15571; ARCHS.
 CC PROSITE: PS00212; ALBUMIN; 3.
 CC DR PFAM: PF00273; transport_prot; 1.
 CC DR HSSP: P02768; IUOR.
 CC KM PLASMA; METAL-BINDING; LIPID-BINDING; ALBUMIN; REPEAT; SIGNAL;
 CC COOPER.
 CC -----
 CC FT SIGNAL 1 18
 CC FT PROPEP 19 22
 CC FT CHAIN 24 615
 CC FT REPEAT 31 206
 CC FT REPEAT 225 398
 CC FT REPEAT 417 596
 CC FT METAL 30 30
 CC FT DISULFID 80 89
 CC FT DISULFID 102 118
 CC FT DISULFID 117 128
 CC FT DISULFID 152 197
 CC FT DISULFID 196 205
 CC FT DISULFID 228 224
 CC FT DISULFID 273 281
 CC FT DISULFID 293 307
 CC FT DISULFID 306 317
 CC FT DISULFID 344 389
 CC FT DISULFID 388 397
 CC FT DISULFID 420 466
 CC FT DISULFID 465 476
 CC FT DISULFID 489 505
 CC FT DISULFID 504 515
 CC FT DISULFID 542 587
 CC FT DISULFID 586 595
 CC FT CARBOHYD 500 500
 CC FT CONFLICT 24 24
 CC FT SEQUENCE 615 AA; 69918 MW; DC5E6E8A CRC32;
 CC -----
 CC Query Match 72.1%; Score 49; DB 1; Length 615;
 CC Best Local Similarity 55.6%; Pred. No. 3.93e+00;
 CC Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC DB 249 QKYPKAPFS 257
 CC :||:||||
 CC 1 QKYNRPYA 9
 CC -----
 CC RESULT 9
 CC ID FCAR_HUMAN STANDARD; PRT; 287 AA.
 CC AC P24071; Q15728; Q15727; Q13603; Q13604;
 CC DT 01-MAR-1992 (REL. 21, CREATED)
 CC DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 CC DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 CC DE IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR (IGA FC RECEPTOR) (CD89
 CC DE ANTIGEN).
 CC GN FCAR OR CD89.
 CC OS HOMO SAPIENS (HUMAN).
 CC OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RP TISSUE-BONE MARROW;
 CC RX MEDLINE: 95363085.
 CC RA DE WIT T.P.H., MORION H.C., CAPEL P.J.A., VAN DE WINKEL J.G.J.;
 CC "Structure of the gene for the human myeloid Iga Fc receptor (CD89).";
 CC J. IMMUNOL. 155:1203-1209(1995).
 CC [3]
 CC SEQUENCE FROM N.A. (FORMS A.2 AND A.3).
 CC -----

CC TISSUE=ALVEOLAR MACROPHAGE, AND MONOCYTES;
RX MEDLINE: 96247667.
RA PARRY C., STIBILLE Y., LEHDEN A., MONTEIRO R.C.;
RT "Identification of Fc alpha receptor (CD89) isoforms generated by
RT alternative splicing that are differentially expressed between blood
RT monocytes and alveolar macrophages";
RL J. IMMUNOL. 156:4442-4448(1996).
RN [4]
RP SEQUENCE FROM N.A. (FORMS B AND B-DELTA-S2).
RA VAN DIJK T.B., MORTON H.C., CALDENHOVEN E., BRACKE M.,
RA RAUWMAKERS J.A.M., LAMMERS J.M.J., KOENDEMAN L., GROOT R.P.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A. (FORM A.3/RLA2).
RX MEDLINE: 96433090.
RA PLEASS R.J., ANDREWS P.D., KERR M.A., WOOF J.M.;
RT "Alternative splicing of the human IGA Fc receptor CD89 in
RT neutrophils and eosinophils";
RL BIOCHEM. J. 318:771-777(1996).
RN [6]
RP SUBUNITS.
RX MEDLINE: 94375887.
RA PEEFERKORN L.C., YEAMAN G.R.;
RT "Association of IGA Fc receptors (Fc alpha R) with Fc epsilon RI
RT gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
RT phosphorylation of gamma 2";
RL J. IMMUNOL. 153:3228-3236(1994).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS ALPHA.
CC MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
CC -1- SUBUNIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
CC (FORM B).
CC -1- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN BLOOD AND
CC MUCOSAL MYELOID CELLS. MONOCYTES EXPRESS ISOFORMS A.1, A.2 AND A.3
CC WHILE ALVEOLAR MACROPHAGES EXPRESS A.1 AND A.2 TRANSCRIPTS;
CC HOWEVER THEY EXPRESS ONLY ONE ISOFORM AT THEIR SURFACES.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST FIVE FORMS; A.1 (SHOWN HERE), A.2,
CC A.3, B AND B-DELTA-S2 ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC C-2-LIKE DOMAINS.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD89 entry;
CC WWW:"http://www.ncbi.nlm.nih.gov/prov/cd/cd89.htm".
CC -----
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CC -----
DR EMBL: X54150; G31330; -;
DR EMBL: X87767; G1054737; -;
DR EMBL: X87768; G1054737; JOINED.
DR EMBL: X87769; G1054737; JOINED.
DR EMBL: X87765; G1054737; JOINED.
DR EMBL: X87765; G1054737; JOINED.
DR EMBL: U43774; G1439556; -;
DR EMBL: U43677; G1439558; -;
DR EMBL: U56236; G1326429; -;
DR EMBL: U56237; G1326231; -;
DR EMBL: S82919; E302400; -;
DR PIR: JH0332; JH0332.
DR MIM: 147045; -;
KW RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; IGA-BINDING PROTEIN;
KW IMMUNOGLOBULIN FOLD; SIGNAL; ALTERNATIVE SPLICING.
FT SIGNAL 1 21
FT CHAIN 22 287
FT DOMAIN 22 227
FT TRANSEM 228 246
FT DOMAIN 247 287
FT DOMAIN 42 107
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE DOMAIN.

FT	DOMAIN	139	200	IG-LIKE C2-TYPE DOMAIN.
FT	DISULFID	49	100	BY SIMILARITY.
FT	DISULFID	146	193	BY SIMILARITY.
FT	CARBOHYD	65	63	POTENTIAL.
FT	CARBOHYD	79	79	POTENTIAL.
FT	CARBOHYD	141	141	POTENTIAL.
FT	CARBOHYD	177	177	POTENTIAL.
FT	CARBOHYD	186	186	POTENTIAL.
FT	CARBOHYD	198	198	POTENTIAL.
FT	VARSPIC	12	23	MISSING (IN FORM B-DELTA-52).
FT	VARSPIC	121	216	MISSING (IN FORM A.3/RUA2).
FT	VARSPIC	195	216	MISSING (IN FORM A.2).
FT	VARSPIC	217	287	DSIHODYTONLIRMAVAGLVLLAALLIVENHSHITALNK EASADVAPSPMSOOCOPGLTFARTPSVCK -> GRYPVO PCVWVGCPGCHRAGI (IN FORM B AND IN FORM B-DELTA-52).
SO	SEQUENCE	287 AA;	32265 MW;	1B9B01DD CRC32:
Db	197 YNRSPY 202			
Oy	3 YNRPY 8			
RESULT	10			
ID	BHMT HUMAN	STANDARD;	PRT;	406 AA.
AC	O93088:			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)			
DE	BEAINE--HOMOCYSTEINE S-METHYLTRANSFERASE (EC 2.1.1.5).			
GN	BHMT			
OS	HOMO SAPIENS (HUMAN).			
OC	EUDARCYOTA; METAHOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	PRIMATES; CARNIVORINI; HOMINIDAE; HOMO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER;			
RX	MEDLINE; 96394355.			
RA	GARROW T.A.:			
RT	"Purification, kinetic properties, and cDNA cloning of mammalian			
RT	betaine-homocysteine methyltransferase.";			
RL	J. BIOL. CHEM. 271:22831-22838(1996).			
CC	-1- FUNCTION: INVOLVED IN THE REGULATION OF HOMOCYSTEINE METABOLISM.			
CC	CONVERTS BEAINE AND HOMOCYSTEINE TO DIMETHYLGLICINE AND			
CC	METHIONINE, RESPECTIVELY. THIS REACTION IS ALSO REQUIRED FOR THE			
CC	IRREVERSIBLE OXIDATION OF CHOLINE.			
CC	-1- CATALYTIC ACTIVITY: TRIMETHYLAMONIACETATE + L-HOMOCYSTEINE =			
CC	DIMETHYLGLICINE + L-METHIONINE.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- TISSUE SPECIFICITY: PRIMARILY FOUND IN LIVER AND KIDNEY.			
CC	-1- DISEASE: DEFECTS IN BHMT COULD LEAD TO HYPERHOMOCYST(E)INEMIA. BUT			
CC	SUCH A DEFECT HAS NOT YET BEEN OBSERVED. HYPERHOMOCYST(E)INEMIA IS			
CC	AN INDEPENDENT RISK FACTOR FOR THE DEVELOPMENT OF ARTERIOSCLEROTIC			
CC	VASCULAR DISEASE.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U50929; G1522683; -			
DR	MIM; 602888; -			
DR	HSPD; P06139; 1GRL			
DR	TRANSFERASE; METHYLTRANSFERASE.			
SO	SEQUENCE 406 AA; 44970 MW; 8DEC74F5 CRC32;			

RA VALENTIN K., ZETSCHKE K.;
 RT "Rubisco genes indicate a close phylogenetic relation between the
 RL plastids of Chromophyta and Rhodophyta.";
 CC PLANT MOL. BIOL. 15:575-584(1990).
 CC -1- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF
 CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 CC ACTIVE SITE.
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) -
 CC 2-3-PHOSPHO-D-GLYCERATE.
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) -
 CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
 CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
 CC
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 CC
 CC EMBL: X52503; G11544; -.
 CC DR PIR: S13123; RKFLE.
 CC DR PROSITE: P500157; RUBISCO_LARGE; 1.
 CC DR PRAM: PF00016; RUBISCO_LARGE; 1.
 CC DR MENDEL: 4884; ECTSL; ISCL; 1.
 CC DR HSSP: P00876; 3RUB.
 CC KM PHOTOSYNTHESIS: CARBON DIOXIDE FIXATION; PHOTORESPIRATION;
 CC LM LKASE; OXIDOREDUCTASE; MONOOXYGENASE; CHLOROPLAST.
 CC FT ACT_SITE 205 205 BINDING OF CO(2) ACTIVATES THE ENZYME.
 CC FT ACT_SITE 205 205 BINDING OF CO(2) ACTIVATES THE ENZYME.
 CC SQ SEQUENCE 488 AA; 53904 MW; A73CA424 CRC32;
 CC
 CC Query Match 70.6%; Score 48; DB 1; Length 488;
 CC Best Local Similarity 66.7%; Pred. No. 6.45e+00;
 CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Db 253 OMVERA261
 CC Oy 1 OKINRAPPA 9
 CC
 CC RESULT 14
 CC CG2A.DROME STANDARD; PRT; 491 AA.
 CC P14785;
 CC 01-APR-1990 (REL. 14, CREATED)
 CC 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 CC 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 CC DE G2/MITOTIC-SPECIFIC CYCLIN A.
 CC GN CYCA.
 CC OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 CC OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 CC OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
 CC OC DROSOPHILIDAE; DROSOPHILA.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE: 93077051.
 CC RA TAKAHISA M., TOGASHI S., UEDA R., MIKUNI M., TSUBUMURA S., KONDO K.,
 CC RA MIYAKE T.;
 CC RT "Structure of the Drosophila melanogaster gene encoding cyclin A.";
 CC RL GENE 121:343-346(1992).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE: 89168447.
 CC RA LEHNER C.F., O'FARRELL P.H.;
 CC RT "Expression and function of Drosophila cyclin A during embryonic cell
 CC cycle progression";
 CC RL CELL 56:957-968(1989).
 CC RN [3]

RP SEQUENCE OF 235-247 AND 288-300 FROM N.A.
 RX MEDLINE: 89159430.
 RA WHITFIELD W.G.F., GONZALEZ C., SANCHEZ-HERRERO E., GLOVER D.M.;
 RT "Transcripts of one of two Drosophila cyclin genes become localized
 CC in pole cells during embryogenesis";
 CC RL NATURE 338:337-340(1989).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
 CC KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
 CC AND ARE ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONGEST TO OTHER
 CC CYCLINS A.
 CC
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 CC
 CC EMBL: D10857; G407199; -.
 CC DR EMBL: D10856; G407199; JOINED.
 CC DR EMBL: D10858; G391659; -.
 CC DR EMBL: M24841; G157157; -.
 CC DR PIR: JC1390; JC1390.
 CC DR PIR: S03543; S03543.
 CC DR FLYBASE: FBgn000404; CYCA.
 CC DR PROSITE: P500292; CYCLINS; 1.
 CC DR PRAM: PF00134; CYCLIN; 1.
 CC DR HSSP: P20248; 1FIN.
 CC KM CYCLIN; CELL CYCLE; CELL DIVISION; MITOSIS.
 CC FT CONFLICT 147 147 M -> I (IN CDNA; G391659).
 CC FT CONFLICT 179 179 A -> V (IN REF. 2).
 CC FT CONFLICT 200 200 V -> M (IN CDNA; G391659).
 CC FT CONFLICT 223 223 L -> R (IN REF. 2).
 CC FT CONFLICT 474 474 H -> Q (IN CDNA; G391659).
 CC SQ SEQUENCE 491 AA; 56124 MW; 9F047FAD CRC32;
 CC
 CC Query Match 70.6%; Score 48; DB 1; Length 491;
 CC Best Local Similarity 62.5%; Pred. No. 6.45e+00;
 CC Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC Db 435 EKYNRDTY 442
 CC Oy 1 OKYNRAPY 8
 CC
 CC RESULT 15
 CC ID NPRE_BACAM STANDARD; PRT; 521 AA.
 CC AC P06832;
 CC DT 01-JAN-1988 (REL. 06, CREATED)
 CC DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 CC DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 CC DE BACILLIOLYSIN PRECURSOR (EC 3.4.24.28) (NEUTRAL PROTEASE).
 CC GN NPR.
 CC OS BACILLIUS AMILOQUEFIACIENS.
 CC OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC OC BACILLUS.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX STRAIN-ATCC 23844;
 CC RX MEDLINE: 85006739.
 CC RA VASANTHA N., THOMPSON L.D., RHODES C., BANNER C., NAGLE J.;
 CC RA FILIPPIA D.;
 CC RT "Genes for alkaline protease and neutral protease from Bacillus
 CC amyloliquefaciens contain a large open reading frame between the
 CC RT regions coding for signal sequence and mature protein";
 CC RL J. BACTERIOL. 159:811-819(1984).
 CC -1- FUNCTION: THERMOSTABLE EXTRACELLULAR ZINC METALLOPROTEASE.
 CC -1- CATALYTIC ACTIVITY: SIMILAR, BUT NOT IDENTICAL, TO THAT OF
 CC THERMOLYSIN.
 CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR

THIS PAGE BLANK (USPTO)

Best Local Similarity 87.5%; Pred. No. 4.92e-02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 81 OKYRAPY 88
|||:||||
QY 1 OKYNRAPY 8

RESULT 2
ID 044677 PRELIMINARY; PRT: 521 AA.
AC 044677;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE NEUTRAL PROTEASE.
OS BACILLUS AMYLOLOUEFACIENS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.

[1]
SEQUENCE FROM N.A.
SHIMADA H., HONTO M., MITA I., NAKAYAMA A., AKAKA A., MANBE K.,
FUJUTANI Y.;

RL J. BIOTECHNOLOGY 2:75-85(1985).
EMBL: M36723; G143353; -;
PFAM: PF00099; zn-protease; 1.
KW PROTEASE.
SQ SEQUENCE 521 AA; 56725 MW; 64AFFE5F CRC32;

Query Match 77.9%; Score 53; DB 2; Length 521;
Best Local Similarity 75.0%; Pred. No. 1.74e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 308 OKYNRSY 315
||||:|
QY 1 OKYNRAPY 8

RESULT 3
ID 036979 PRELIMINARY; PRT: 3082 AA.
AC 036979;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE POLYPROTEIN.

OS ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV).
OC VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
OC POTYVIRUS.

[1]
SEQUENCE FROM N.A.

LEE K.C., WONG S.M.;
STRAIN-SINGAPORE;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

EMBL: AF014811; G2462849; -;
PFAM: PF00271; helicase_C; 1.
PFAM: PF00680; RNA_dep_RNA_pol; 1.

PFAM: PF00767; Poty_coat; 1.
PFAM: PF00851; Peptidase_C6; 1.
PFAM: PF00863; Peptidase_C4; 1.
KW POLYPROTEIN.

FT CHAIN 1 313 P1.
FT CHAIN 314 769 HELPER COMPONENT-PROTEINASE.
FT CHAIN 770 1115 P3.

FT CHAIN 1116 1167 6K1.
FT CHAIN 1168 1801 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1802 1854 6K2.

FT CHAIN 1855 2044 SMALL NUCLEAR INCLUSION-GENOME LINKED
FT CHAIN 2045 2287 VPG.

FT CHAIN 2288 2803 SMALL NUCLEAR INCLUSION-PROTEINASE.
FT CHAIN 2804 3082 LARGE NUCLEAR INCLUSION.
COAT PROTEIN.

SO SEQUENCE 3082 AA; 350508 MW; 43030AF1 CRC32;

Query Match 77.9%; Score 53; DB 14; Length 3082;

Best Local Similarity 75.0%; Pred. No. 1.74e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 279 OKYSRLPY 286
|||:||||
QY 1 OKYNRAPY 8

RESULT 4
ID 074961 PRELIMINARY; PRT: 231 AA.
AC 074961;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 25.6 KD PROTEIN (FRAGMENT).
GN SPCC736.16.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

OC EUKARYOTA: FUNGI; ASCOMYCOTA; ARCHIASTOMYCETES;
OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.

[1]
SEQUENCE FROM N.A.

RC STRAIN-972H-;
RA WOOD V., RAJANDREAM M.A., BARRELL B.G., MORPHY L., HARRIS D.;
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AL023705; E1294543; -;
KW HYPOTHETICAL PROTEIN.
FT NON_TER 1 231
FT NON_TER 1 231
SQ SEQUENCE 231 AA; 25584 MW; FB84EB08 CRC32;

Query Match 75.0%; Score 51; DB 3; Length 231;
Best Local Similarity 62.5%; Pred. No. 4.58e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 120 DKYARSPY 127
|||:||||
QY 1 OKYNRAPY 8

RESULT 5
ID 034232 PRELIMINARY; PRT: 337 AA.
AC 034232;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ORF40X1 PROTEIN.

OS VIBRIO CHOLERAE.
OC BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.

[1]
SEQUENCE FROM N.A.

RA STROEHER U.H., PARASTYAM G., DREDGE B.K., MANNING P.A.;
RT "Novel vibrio cholerae O139 genes involved in lipopolysaccharide
biosynthesis";
RL J. BACTERIOLOGY 179:2740-2747(1997).

DR EMBL: Y07786; E274690; -;
SQ SEQUENCE 337 AA; 40132 MW; 2D4A7939 CRC32;

Query Match 75.0%; Score 51; DB 2; Length 337;
Best Local Similarity 75.0%; Pred. No. 4.58e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 147 OKYSAPY 154
|||:||||
QY 1 OKYNRAPY 8

RESULT 6
ID 087136 PRELIMINARY; PRT: 337 AA.
AC 087136;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 OS VIRBIO CHOLERAE.
 CC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: VIBRIONACEAE: VIBRIO.
 CC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NO45:
 RA YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,
 RA TAKEDA Y.;
 RT THE genes responsible for O-antigen synthesis of Vibrio cholerae
 RT 0139 are closely related to those of Vibrio cholerae 022.";
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567;
 SQ SEQUENCE 337 AA; 40147 MW; 176B46B CRC32;

Query Match 75.0%; Score 51; DB 2; Length 337;
 Best Local Similarity 75.0%; Pred. No. 4,58e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

147 OKYHAPY 154
 ||| |||
 1 OKYHAPY 8

RESULT 7 PRELIMINARY; PRT: 697 AA.
 ID 074504;
 AC 074504;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 OS HYPOTHEICAL 77.8 KD PROTEIN (FRAGMENT).
 DE SPCC594.01.
 GN SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 CC EUKARYOTA: FUNGI: ASCOMYCOTA: ARCHIASCOMYCETES:
 CC SCHIZOSACCHAROMYCETALES: SCHIZOSACCHAROMYCETACEAE:
 CC SCHIZOSACCHAROMYCES.
 CC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H;
 RA RIEGER M., LYNE M., RAJANDREAM M.A., BARRELL B.G.;
 RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AL031523; E1319371;
 KW HYPOTHEICAL PROTEIN.
 FT NON_TER 1
 SQ SEQUENCE 697 AA; 77841 MW; 9BC8CB3F CRC32;

Query Match 75.0%; Score 51; DB 3; Length 697;
 Best Local Similarity 62.5%; Pred. No. 4,58e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 26 DKYARSPY 33
 ||| |||
 1 OKYHAPY 8

RESULT 8 PRELIMINARY; PRT: 248 AA.
 ID 027562;
 AC 027562;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PRC.
 GN PRC.
 OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 CC EUKARYOTA: DICTYOSTELIIDA: DICTYOSTELIUM.
 CC [1]
 RP SEQUENCE FROM N.A.
 RA SHULSKY G., ESCALANTE R., LOOMIS W.F.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S25A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY.
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX

CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH.
 CC THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY.
 CC THE COMPONENT C3 MAY HAVE A POTENTIAL REGULATORY EFFECT ON
 CC ANOTHER COMPONENT(S) OF THE PROTEASOME COMPLEX THROUGH TYROSINE
 CC PHOSPHORYLATION.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 DR EMBL: U60168; G1405364;
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR FRAM: PF00227; proteasome; 1.
 KW PROTEASOME; HYDROLASE; PROTEASE.
 SQ SEQUENCE 248 AA; 27988 MW; BEE84ACC CRC32;

Query Match 73.5%; Score 50; DB 5; Length 248;
 Best Local Similarity 55.6%; Pred. No. 7,38e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 121 QRYGRPPY 129
 ||| |||
 1 OKYHAPY 9

RESULT 9 PRELIMINARY; PRT: 260 AA.
 ID 042265;
 AC 042265;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE 205 PROTEASOME SUBUNIT C2.
 GN CC2.
 OS GALLUS GALLUS (CHICKEN).
 CC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: ARCHOSAURIA: AVES:
 CC NEOGATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE: GALLUS.
 CC [1]
 RP SEQUENCE FROM N.A.
 RA SINGH I., WAGNER B.J.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF027978; G3136063;
 DR FRAM: PF00227; proteasome; 1.
 KW PROTEASOME.
 SQ SEQUENCE 260 AA; 28925 MW; EF38499F CRC32;

Query Match 73.5%; Score 50; DB 13; Length 260;
 Best Local Similarity 55.6%; Pred. No. 7,38e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 120 QRYGRPPY 128
 ||| |||
 1 OKYHAPY 9

RESULT 10 PRELIMINARY; PRT: 342 AA.
 ID 083923;
 AC 083923;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE TP33 PROTEIN.
 GN TP0957.
 OS TREPONEMA PALLIDUM.
 CC BACTERIA: SPIROCHAETALES: SPIROCHAETACEAE: TREPONEMA.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98332770.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM R.A.,
 RA SODERBERG E., HARDIAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,

RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
 RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RT "Complete Genome Sequence of *Treponema pallidum*, the Syphilis
 RT Spirochete.";
 RL SCIENCE 281:375-388(1998).

RP SEQUENCE FROM N.A.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
 RA SODERBERG E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
 RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL, AE001264; G3323279; -;
 SEQUENCE 342 AA; 38312 MW; 3C8FED88 CRC32;

Query Match 72.1%; Score 49; DB 2; Length 342;
 Best Local Similarity 85.7%; Pred. No. 1.18e+01;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 156 YTRAPYA 162
 QY 3 YNRAPYA 9

RESULT 11 PRELIMINARY; PRT; 448 AA.
 ID 002441;
 AC 002441;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GDP-DISSOCIATION INHIBITOR.
 GN GDI.
 OS GEODIA CYDONIUM (SPONGE).
 OC EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; TETRACINOMORPHA;
 CC ASTROPHORIDA; GEODIACE; GEODIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KRUSLER A., SCHEFFER U., KOZIOLO C., PANCER Z., BATEL R., BADRIA F.A.,
 RA MUELLER W.E.G.;
 RL AQUATIC TOXICOL. 37:157-168(1997).
 DR EMBL; X94983; E218570; -;
 DR PFAM; PF00996; GDI. 1;
 DR SEQUENCE 448 AA; 50215 MW; 848511EC CRC32;

Query Match 72.1%; Score 49; DB 5; Length 448;
 Best Local Similarity 50.0%; Pred. No. 1.18e+01;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 217 QRYGKSPY 224
 QY 1 QKNRAPY 8

RESULT 12 PRELIMINARY; PRT; 490 AA.
 ID 084680;
 AC 084680;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE S/T PROTEIN KINASE.
 GN PKNS.
 OS CHLAMYDIA TRACHOMATIS.
 OC BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D/WM-3/CX;
 RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
 RA MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,

RA DAVIS R.W.;
 RT "Genome Sequence of an Obligate Intracellular Pathogen of Humans:
 RT *Chlamydia trachomatis*.";
 RL SCIENCE 0:0-0(1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D/WM-3/CX;
 RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
 RA MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
 RA DAVIS R.W.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AE001337; G3329124; -;
 DR SEQUENCE 490 AA; 55926 MW; 11F98032 CRC32;

Query Match 72.1%; Score 49; DB 2; Length 490;
 Best Local Similarity 55.6%; Pred. No. 1.18e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 472 QKDRSLXP 480
 QY 1 QKNRAPYA 9

RESULT 13 PRELIMINARY; PRT; 509 AA.
 ID Q21017;
 AC Q21017;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE COSMID F58H12.
 GN F58H12.1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 CC RHABDITIA; RHABDITIOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU 2., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KINSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RICKEN L., ROOPRA A., SANDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., SPADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
 RT *elegans*.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MILLER N.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WATERSTON R.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U04016; G1065490; -;
 DR SEQUENCE 509 AA; 55953 MW; D0EC1387 CRC32;

Query Match 72.1%; Score 49; DB 5; Length 509;
 Best Local Similarity 50.0%; Pred. No. 1.18e+01;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 268 RYORTPYT 275
 QY 2 KYNRAPYA 9

RESULT 14 PRELIMINARY; PRT; 1277 AA.
 ID 017517;
 AC 017517;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ZC132.5 PROTEIN.
 GN ZC132.5.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA BRADSHAW H., DEVLIN K.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF014939; G2275629; -
 SQ SEQUENCE 1277 AA; 146496 MW; 8A6DB899 CRC32;

Query Match 72.1%; Score 49; DB 5; Length 1277;
 Best Local Similarity 85.7%; Pred. No. 1.18e+01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 877 QRYNRAP 883
 QY 1 QRYNRAP 7

RESULT 15 PRELIMINARY; PRT; 43 AA.
 049246; 049246;
 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE REVERSE TRANSCRIPTASE (FRAGMENT).
 GN RT.
 OS ALSTROEMERIA INODORA.
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; LILIALES;
 OC ALSTROEMERIACEAE; ALSTROEMERIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P002; TISSUE-YOUNG LEAVES;
 RC TRANSPOSON-TY1-COPIA-LIKE RETROTRANSPOSON;
 RA KUIPERS A.G.J., HESLOP-HARRISON J.S., JACOBSEN E.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ223610; E1252160; -
 KW RNA-DIRECTED DNA POLYMERASE.
 FT NON_TER 1
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 5333 MW; E61D18CF CRC32;

Query Match 70.6%; Score 48; DB 10; Length 43;
 Best Local Similarity 83.3%; Pred. No. 1.87e+01;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 14 YNRSPLY 19
 QY 3 YNRAPY 8

Search completed: Thu Sep 2 11:29:02 1999
 Job time : 23 secs.

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 WIREIMAGE (TM)

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MPSEARCH protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:32:18 1999; MasPar time 4.49 Seconds
 Molecular output not generated. 109.317 Million cell updates/sec

File: >US-08-599-226-13
 Description: (1-9) from US08599226.pep
 Perfect Score: 71
 Sequence: 1 QKXORAPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 179066 seqs, 5459741 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

sptemb19
 1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
 5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
 9:sp.phage 10:sp.plant 11:sp.potent 12:sp.unclassified
 13:sp.vertebrate 14:sp.virus

Statistics: Mean 22.965; Variance 27.995; scale 0.820

pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	59	83.1	509	5	Q21017	COSMID F58H12.	7.57e-02
2	59	83.1	560	5	Q44626	K1D12.1 PROTEIN.	7.57e-02
3	55	77.5	321	4	O99608	NECDIN RELATED PROTEIN	5.99e-01
4	53	74.6	337	2	O87136	ORF139-17 PROTEIN.	1.63e+00
5	53	74.6	337	2	O87136	ORF40X1 PROTEIN.	1.63e+00
6	52	73.2	4957	4	O14687	ALR.	2.67e+00
7	52	73.2	5262	4	O14686	ALR.	2.67e+00
8	51	71.8	641	5	O18586	COSMID C43H6.	4.34e+00
9	50	70.4	436	3	O74961	HYPOHETICAL 25.6 KD P	7.02e+00
10	50	70.4	496	2	O87348	LLAKR21 RESTRICTION EN	7.02e+00
11	50	70.4	697	3	O74504	HYPOHETICAL 77.8 KD P	7.02e+00
12	50	70.4	1496	4	O92626	MYELOBLAST KIAA0230 (F	7.02e+00
13	49	69.0	436	5	O10929	POLYPROTEIN.	7.02e+00
14	49	69.0	494	5	P92024	HYPOHETICAL 47.6 KD P	1.13e+01
15	49	69.0	523	5	O16822	MEX-1.	1.13e+01
16	49	69.0	523	5	O16822	F10D2.11 PROTEIN.	1.13e+01
17	49	69.0	563	2	P71864	HYPOHETICAL 60.6 KD P	1.13e+01
18	48	67.6	337	2	O48593	HLAI.2.	1.80e+01
19	48	67.6	400	3	O74958	HYPOHETICAL 44.6 KD P	1.80e+01
20	48	67.6	407	1	O26964	PEPTIDE CHAIN RELEASE	1.80e+01

RESULT	1	PRELIMINARY:	PRT:	509 AA.
ID	Q21017			
AC	Q21017			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	COSMID F58H12.			
GN	F58H12.1.			
OS	CAENORHABDITIS ELEGANS.			
OC	EUTRYPOTA; METAZOA; NEMATODA; SECCERNENTIA; RHABDITIA; RHABDITIDA;			
OC	RHABDITIA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 94150718.			
RA	WILSON R., AINSOUGHER R., ANDERSON K., BAYNES C., BERS M.,			
RA	BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,			
RA	CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,			
RA	GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,			
RA	JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,			
RA	LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,			
RA	PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,			
RA	SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STULSTON J.,			
RA	THERRER-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,			
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLIDMAN P.,			
RT	*2.2 Mb of contiguous nucleotide sequence from chromosome III of C.			
RT	elegans.*			
RL	NATURE 368:32-38(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MILLER N.,			
RA	SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	WATERSTON R.,			
RA	SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL: U40416; G1065490; -			
SO	SEQUENCE 509 AA; 55953 MW; DDEC1387 CRC32;			

Query Match 83.1%; Score 59; DB 5; Length 509;
 Best Local Similarity 75.0%; Pred. No. 7.57e-02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 DB 268 RXORAPYT 275 :|||:||||

OY 2 KYORAPY 9

RESULT 2 PRELIMINARY: PRT: 560 AA.

AC 044626;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE K11D12.1 PROTEIN.

GN K11D12.1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; SECERNITEA; RHABDITIDA;
 OC RHABDITIDA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 GARNER A., GREEN P., HARKINS T., HILLIER L., JETER M., JOHNSTON L.,
 JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 LIGHTNING J., LLOYD C., MCURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 SMITH R., SMITH A., SMITH K., THOMAS K., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLMAN P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans."
 RT elegans.
 RN NATURE 368:32-38(1994).

RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA HENKHAUS J., WOHLDMANN P., GILLAM B.;
 RN SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF039047; G2736445; -;
 DR PROSITE: P500028; ZINC_FINGER_C2H2; 1.
 KW ZINC-FINGER; METAL-BINDING; DNA-BINDING.
 SQ SEQUENCE 560 AA; 61136 MW; 5906E8YD CRC32;

Query Match 83.1%; Score 59; DB 5; Length 560;
 Best Local Similarity 87.5%; Pred. No. 7.57e-02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 81 OKYRAPY 88
 OY 1 OKYRAPY 8

RESULT 3 PRELIMINARY: PRT: 321 AA.
 AC 099608;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-MAY-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE NECDIN RELATED PROTEIN.
 GN NDN.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA JAY P., BERTA P.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA NAKADA Y., TANURA H., UETSUKI T., INAZAWA J., YOSHIKAWA K.;

RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U35139; G1754971; -;
 DR EMBL: AB007828; D1023528; -;
 SQ SEQUENCE 321 AA; 36085 MW; C6525F8C CRC32;

Query Match 77.5%; Score 55; DB 4; Length 321;
 Best Local Similarity 85.7%; Pred. No. 5.99e-01;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 246 KYORAPY 252
 OY 2 KYORAPY 8

RESULT 4 PRELIMINARY: PRT: 337 AA.
 AC 087136;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ORF139-17 PROTEIN.
 OS VIBRIO CHOLERAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-M045;
 RA YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,
 RA TAKEDA Y.;
 RT "The genes responsible for O-antigen synthesis of Vibrio cholerae
 RT O139 are closely related to those of Vibrio cholerae O22."
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567; -;
 SQ SEQUENCE 337 AA; 40147 MW; 176B46EB CRC32;

Query Match 74.6%; Score 53; DB 2; Length 337;
 Best Local Similarity 75.0%; Pred. No. 1.63e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 147 OKYRAPY 154
 OY 1 OKYRAPY 8

RESULT 5 PRELIMINARY: PRT: 337 AA.
 AC 034232;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ORF40X1 PROTEIN.
 OS VIBRIO CHOLERAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AI-1837;
 RX MEDLINE: 97252505.
 RA STROEHER U.H., PARASIVAM G., DREGE B.K., MANNING P.A.;
 RT "Novel Vibrio cholerae O139 genes involved in lipopolysaccharide
 RT biosynthesis."
 RT J. BACTERIOL. 179:2740-2747(1997).
 DR EMBL: Y07786; E274690; -;
 SQ SEQUENCE 337 AA; 40132 MW; 2D4A7939 CRC32;

Query Match 74.6%; Score 53; DB 2; Length 337;
 Best Local Similarity 75.0%; Pred. No. 1.63e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 147 OKYRAPY 154
 OY 1 OKYRAPY 8

RESULT 6

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ID 014687 PRELIMINARY: PRT: 4957 AA.
AC 014687:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ALR.
GN ALR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97388474.
RA PRASAD R., ZHADANOV A.B., SEDKOV Y., BULIRICH F., DRUCK T.,
RA BALAPALLI R., YANO T., ALDER H., CROCE C.M., HUEBNER K., MAZO A.,
RA CANANI E.;
RT "Structure and expression pattern of human ALR, a novel gene with
RT strong homology to ALR-1 involved in acute leukemia and to Drosophila
RT Lithorex."
ONCOGENE 15:549-560(1997).
EMBL: AF010404; G2358287; -.
PFAM: PF00628; PHD: 2.
DR PFAM: PF00856; SET: 1.
SQ SEQUENCE 4957 AA; 531848 MW; 49C95A53 CRC32;

Query Match 73.2%; Score 52; DB 4; Length 4957;
Best Local Similarity 100.0%; Pred. No. 2.67e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2219 YORAPY 2224
OY 3 YORAPY 8

RESULT 7
ID 014686 PRELIMINARY: PRT: 5262 AA.
AC 014686:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ALR.
GN ALR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97388474.
RA PRASAD R., ZHADANOV A.B., SEDKOV Y., BULIRICH F., DRUCK T.,
RA BALAPALLI R., YANO T., ALDER H., CROCE C.M., HUEBNER K., MAZO A.,
RA CANANI E.;
RT "Structure and expression pattern of human ALR, a novel gene with
RT strong homology to ALR-1 involved in acute leukemia and to Drosophila
RT Lithorex."
ONCOGENE 15:549-560(1997).
EMBL: AF010403; G2358285; -.
PFAM: PF00628; PHD: 4.
DR PFAM: PF00856; SET: 1.
SQ SEQUENCE 5262 AA; 564181 MW; A8C48CD2 CRC32;

Query Match 73.2%; Score 52; DB 4; Length 5262;
Best Local Similarity 100.0%; Pred. No. 2.67e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2524 YORAPY 2529
OY 3 YORAPY 8

RESULT 8
ID 018586 PRELIMINARY: PRT: 641 AA.
AC 018586:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

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DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE COSMID C43H6.
GN C43H6.4.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RC MEDLINE: 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MING J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA LE T.T.;
RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U51999; G1255325; -.
SQ SEQUENCE 641 AA; 75082 MW; 4B2E168D CRC32;

Query Match 71.8%; Score 51; DB 5; Length 641;
Best Local Similarity 62.5%; Pred. No. 4.34e+00;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 474 OXYOREQY 481
OY 1 OXYOREQY 8

RESULT 9
ID 074961 PRELIMINARY: PRT: 231 AA.
AC 074961:
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 25.6 KD PROTEIN (FRAGMENT).
GN SPCG736.16.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RX WOOD V., RAJANDREAN M.A., BARRELL B.G., MURPHY L., HARRIS D.;
RA SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AL023705; E1294543; -.
KW HYPOTHETICAL PROTEIN.
FT NON_TER 1
FT NON_TER 231
FT NON_TER 231
SQ SEQUENCE 231 AA; 25584 MW; FB84EB08 CRC32;

Query Match 70.4%; Score 50; DB 3; Length 231;
Best Local Similarity 62.5%; Pred. No. 7.02e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 120 DKYARSPY 127
QY 1 OKYORAPY 8

RESULT 10
ID 087348 PRELIMINARY; PRT; 496 AA.

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LIAKRI RESTRICTION ENZYME.

GN LIAKRI2R.
OS LACTOCOCCUS LACTIS (STREPTOCOCCUS LACTIS).

OG PLASMID PKR223.

OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC LACTOCOCCUS.

RN [1]
RP SEQUENCE FROM N.A.

RT TWOMEY D.P., MCKAY L.L., O'SULLIVAN D.J.;

"Molecular characterization of the Lactococcus lactis LIAKRI2
restriction-modification system and effect of an IS982 element
positioned between the restriction and modification genes.";

RL J. BACTERIOLOGICAL 180:0-01(1998).

DR EMBL; AF051563; G3702799; -.

KM PLASMID.

SO SEQUENCE 496 AA; 58081 MM; A04BA2A9 CRC32;

Query Match 70.4%; Score 50; DB 2; Length 496;

Best Local Similarity 62.5%; Pred. No. 7.02e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 33 EKYOSTPY 40
QY 1 OKYORAPY 8

RESULT 11
ID 074504 PRELIMINARY; PRT; 697 AA.

AC 074504;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 77.8 KD PROTEIN (FRAGMENT).

GN SPCC594.01.

OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

OC EUKARYOTA: FUNGI: ASCOMYCOTA: ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;

RN [1]
RP SEQUENCE FROM N.A.

RT STRAIN-972H-;

RA RIEGER M., LYNE M., RAJANDREAM M.A., BARRELL B.G.;

RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; AL031523; E1319371; -.

KW HYPOTHETICAL PROTEIN.

FT NON_TER

SO SEQUENCE 697 AA; 77841 MM; 9BC8CB3F CRC32;

Query Match 70.4%; Score 50; DB 3; Length 697;

Best Local Similarity 62.5%; Pred. No. 7.02e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 26 DKYARSPY 33
QY 1 OKYORAPY 8

RESULT 12
ID 092626 PRELIMINARY; PRT; 1496 AA.

AC 092626;

DT 01-FEB-1997 (TREMBLREL. 02, CREATED)

DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MYELOBLAST KIAA0230 (FRAGMENT).

GN KIAA0230.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.

RN [1]
RP SEQUENCE FROM N.A.

RT TISSUE-BONE MARROW;

RX MEDLINE; 97191544.

RA NAGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAMARABAYASI Y., OHARA O.,

TANAKA A., KOTANI H., MIYAJIMA N., NOKURA N.;

"Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";

RL DNA RES. 3:321-329(1996).

DR EMBL; D86983; D1013908; -.

DR PFAM; PF00047; 1g; 4.

DR PFAM; PF00093; vwc; 1.

DR PFAM; PF00141; peroxidase; 1.

DR PFAM; PF00560; LRR; 3.

FT NON_TER

SO SEQUENCE 1496 AA; 167209 MM; 5731E51 CRC32;

Query Match 70.4%; Score 50; DB 4; Length 1496;

Best Local Similarity 62.5%; Pred. No. 7.02e+00;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 679 RYRDPPT 686
QY 2 KYORAPY 9

RESULT 13
ID 036979 PRELIMINARY; PRT; 3082 AA.

AC 036979;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE POLYPEPTIDE.

OS ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV).

OC VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
OC POTYVIRUS.

RN [1]
RP SEQUENCE FROM N.A.

RT STRAIN-SINGAPORE.

RA LEE K.C., WONG S.M.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; AF014811; G2462849; -.

DR PFAM; PF00271; helicase_C; 1.

DR PFAM; PF00680; RNA_dep_RNA_pol; 1.

DR PFAM; PF00767; poly_coat; 1.

DR PFAM; PF00851; peptidase_C6; 1.

DR PFAM; PF00863; peptidase_C4; 1.

KW POLYPEPTIDE.

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OY 1 OKYORAPY 8

RESULT 14
ID 010929 PRELIMINARY; PRT; 436 AA.
AC 010929;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 47.6 KD PROTEIN B0336.6 IN CHROMOSOME III.
GN B0336.6.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA TAICH A.;
RA SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U32305; G912758;
DR WORMPEP: B0336.6; CE00774.
DR PFAM: PF00018; SH3; 1.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 436 AA; 47603 MW; F64538F0 CRC32;

Query Match 69.0%; Score 49; DB 5; Length 436;
Best Local Similarity 71.4%; Pred. No. 1.13e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 103 ORYORP 109
OY 1 OKYORAP 7

RESULT 15
ID P92024 PRELIMINARY; PRT; 494 AA.
AC P92024;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MEX-1.
GN MEX-1.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RA STRAIN-N2;
RA MEDLINE: 97195715.
RA GUEDES S.; PRIESS J.R.;
RT "The C. elegans MEX-1 protein is present in germline blastomeres and
is a p granule component."
RL DEVELOPMENT 124:731-739(1997).
DR EMBL: U81043; G1899062;
DR PFAM: PF00642; zf-CCCH; 2.
SQ SEQUENCE 494 AA; 56608 MW; 716506D2 CRC32;

Query Match 69.0%; Score 49; DB 5; Length 494;
Best Local Similarity 50.0%; Pred. No. 1.13e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 263 ORYORPPF 270
OY 1 OKYORAPY 8

Search completed: Thu Sep 2 11:32:44 1999
Job time : 26 secs.

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 W I D E R E I F (TM)

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MPSEARCH protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:31:53 1999; Maspar time 2.11 Seconds
 120.583 Million cell updates/sec
 Modular output not generated.

Title: >US-08-599-226-13
 Description: (1-9) from US08599226.pep
 Perfect Score: 71
 Sequence: 1 OKYORAPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 23.724; Variance 26.945; scale 0.880

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	56	78.9	1262	1	GNRP_MOUSE	1.33e+01
2	51	71.8	615	1	ALBU_CHICK	1.79e+00
3	50	70.4	279	1	PRC2_DROME	2.96e+00
4	50	70.4	299	1	YE05_YEAST	2.96e+00
5	50	70.4	360	1	DCAM_SOLTU	2.96e+00
6	49	69.0	340	1	VL51_YEAST	4.85e+00
7	48	67.6	288	1	DJLA_HAETN	7.88e+00
8	48	67.6	337	1	MTF1_SACKT	7.88e+00
9	48	67.6	360	1	FARX_LYVST	7.88e+00
10	48	67.6	488	1	RBL_ECTSI	7.88e+00
11	48	67.6	488	1	RBL_PYLIC	7.88e+00
12	48	67.6	544	1	H15_DROME	7.88e+00
13	48	67.6	626	1	BGAL_LETUA	7.88e+00
14	47	66.2	108	1	KVIO_HUMAN	1.27e+01
15	47	66.2	406	1	BHMT_HUMAN	1.27e+01
16	47	66.2	407	1	YBP3_YEAST	1.27e+01
17	47	66.2	689	1	Y143_HUMAN	1.27e+01
18	47	66.2	885	1	HYPOHETICAL PROTEIN K	1.27e+01
19	46	64.8	108	1	KVIL_HUMAN	2.04e+01
20	46	64.8	263	1	PRC2_HUMAN	2.04e+01
21	46	64.8	263	1	PRC2_RAT	2.04e+01
22	46	64.8	329	1	E2B1_METJA	2.04e+01
23	46	64.8	421	1	TRPE_SUJOS	2.04e+01

24	46	64.8	423	1	ARGD_KIOLA	ACETYLORNITHINE AMINOT	2.04e+01
25	46	64.8	478	1	VPEA_ARATH	VACUOLAR PROCESSING EN	2.04e+01
26	46	64.8	513	1	MANB_BACSM	MANNAN ENDO-1,4-BETA-M	2.04e+01
27	46	64.8	530	1	YHGL_CLOPA	HYPOTHETICAL PROTEIN 1	2.04e+01
28	46	64.8	664	1	ER72_CHEEL	PROBABLE ERP72 PROTEIN	2.04e+01
29	46	64.8	767	1	AMDM_SCHPO	AMP DEAMINASE (EC 3.5.)	2.04e+01
30	46	64.8	1085	1	DNA_REPAIR	DNA REPAIR AND RECOMBI	2.04e+01
31	46	64.8	1347	1	YCB9_YEAST	TRANSPOSON TY1-17 PROT	2.04e+01
32	45	63.4	210	1	REPB_STRPN	REPLICATION PROTEIN RE	3.23e+01
33	45	63.4	348	1	GMAD_VIBCH	PROBABLE GDP-MANNOSE 4	3.23e+01
34	45	63.4	351	1	NOEL_RHISN	GDP-MANNOSE 4,6-DEHYDR	3.23e+01
35	45	63.4	362	1	DCAM_DATST	S-ADENOSYLMETHIONINE D	3.23e+01
36	45	63.4	372	1	GMAD_YEREN	PROBABLE GDP-MANNOSE 4	3.23e+01
37	45	63.4	455	1	HMC2_BLAG	HYDROXYMETHYLGLUTARYL-	3.23e+01
38	45	63.4	464	1	TKR4_YEAST	PROBABLE MANNOSYLTRANS	3.23e+01
39	45	63.4	503	1	TCPT_VIBCH	TOXIN CORREGULATED PIL	3.23e+01
40	45	63.4	1328	1	YMOU_YEAST	TRANSPOSON TY1 PROTEIN	3.23e+01
41	45	63.4	1328	1	YMT9_YEAST	TRANSPOSON TY1 PROTEIN	3.23e+01
42	45	63.4	1328	1	YMD9_YEAST	TRANSPOSON TY1 PROTEIN	3.23e+01
43	45	63.4	1328	1	YME4_YEAST	TRANSPOSON TY1 PROTEIN	3.23e+01
44	45	63.4	1755	1	YJ29_YEAST	TRANSPOSON TY1 PROTEIN	3.23e+01
45	45	63.4	1755	1	YJ27_YEAST	TRANSPOSON TY1 PROTEIN	3.23e+01

ALIGNMENTS

RESULT	ID	GNRP_MOUSE	STANDARD:	PRG:	1262 AA.
AC	P27671				
DT	01-AUG-1992 (REL. 23, CREATED)				
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).				
GN	RASGRF1 OR CDC25M OR GRF1.				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BAB/C.				
RA	MEDLINE: 93010996.				
RT	CEN H., LOWY D.D.;				
RT	*Isolation of multiple mouse cDNAs with coding homology to				
RT	Saccharomyces cerevisiae CDC25. Identification of a region related to				
RT	Bcr, Vav, Dbl and CDC24.;				
RT	EMBO J. 11:4007-4015(1992).				
RN	[2]				
RP	SEQUENCE OF 791-1262 FROM N.A.				
RC	STRAIN-SWISS; TISSUE-BRAIN;				
RA	MEDLINE: 92289680.				
RT	MAREGANI E., VANONT M., ZIPPEL R., COCCETTI P., BRAMBILLA R.,				
RT	FERRARI C., STURANI E.P., ALBERGHINA L.;				
RT	*Cloning by functional complementation of a mouse cDNA encoding a				
RT	homologue of CDC25, a Saccharomyces cerevisiae RAS activator.;				
RT	EMBO J. 11:2151-2157(1992).				
RN	[3]				
RP	SEQUENCE OF 1031-1226 FROM N.A.				
RC	MEDLINE: 92357779.				
RA	WEI W., MOSTELLER R.D., SANAYL P., GONZALES E., MCKINNEY D.,				
RA	DASGUPTA C., LI P., LIU B.X., BROEK D.;				
RT	*Identification of a mammalian gene structurally and functionally				
RT	related to the CDC25 gene of Saccharomyces cerevisiae.;				
RT	PROC. NATL. ACAD. SCI. U.S.A. 89:7100-7104(1992).				
CC	-1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.				
CC	-1- TISSUE SPECIFICITY: BRAIN.				
CC	-1- SIMILARITY: TO OTHER GUANINE-NUCLEOTIDE RELEASING FACTORS OF THE				
CC	CDC25 FAMILY.				
CC	-1- SIMILARITY: CONTAINS 2 PH DOMAINS.				
CC	-----				
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EMBL: L20899; G388247; -
 DR EMBL: X59868; G50358; -
 DR PIR: S20730; S20730.
 DR PIR: S22693; S22693.
 DR MGI: 99694; RASGR1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR PROSITE: PS00741; GDS_CDC24; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PFAM: PF00169; PH; 2.
 DR PFAM: PF00612; IQ; 1.
 DR PFAM: PF00617; RASGEF; 1.
 DR PFAM: PF00618; RASGEF; 1.
 DR PFAM: PF00621; RHOGEF; 1.
 KM GUANINE-NUCLEOTIDE RELEASING FACTOR.
 FT DOMAIN 22 130
 FT PH.
 FT 460 588
 FT 1033 1033
 E -> D (IN REF. 3).
 CONFLICT 1262 AA; 144101 MW; 021C787F CRC32;
 SEQUENCE

Query Match 78.98; Score 56; DB 1; Length 1262;
 Best Local Similarity 62.38; Pred. No. 1,33e-01;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1060 EKEREPT 1067
 :||:|:|
 QY 1 QKXORAPY 8

RESULT 2
 ID ALBU-CHICK STANDARD; PRT; 615 AA.
 AC P19121;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE SERUM ALBUMIN PRECURSOR.
 OS ALB.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSUURIA; AVES;
 OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA CASSADY A.I., SALKILD C.R., BAYERSROCK P., WALLACE J.C.;
 RN SUBMITTED (JUL-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
 [2]
 SEQUENCE OF 1-28 FROM N.A.
 MEDLINE: 83161037.
 RA HACHE R.J.G., WISKOCIL R., VASA M., ROY R.N., LAV P.C.R., DEELEY R.G.;
 RT "The 5' noncoding and flanking regions of the avian very low density
 RT apolipoprotein II and serum albumin genes. Homologies with the egg
 RT white protein genes.";
 RL J. BIOL. CHEM. 258:4556-4564(1983).
 [3]
 RP SEQUENCE OF 19-30.
 RX MEDLINE: 78019943.
 RA ROSEN A.M., GELLER D.M.;
 RT "Chicken microsomal albumin: amino terminal sequence of chicken
 RT proalbumin.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 78:1060-1066(1977).
 CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
 CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
 CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
 CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
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EMBL: X60688; G63748; -
 DR EMBL: V00381; G63039; -
 DR PIR: S15571; ARCHS.
 DR PROSITE: PS00212; ALBUMIN; 3.
 DR PFAM: PF00273; transport_prot; 1.
 DR HSSP: P02768; 100R.
 KM PLASMA; METAL-BINDING; LIPID-BINDING; ALBUMIN; REPEAT; SIGNAL;
 KM COOPER.
 FT SIGNAL 1 18
 FT PROPEP 19 23
 FT CHAIN 24 615
 FT REPEAT 31 206
 FT REPEAT 225 398
 FT REPEAT 417 596
 FT METAL 30 30
 FT 80 89
 FT DISULFID 102 118
 FT DISULFID 117 128
 FT DISULFID 152 197
 FT DISULFID 196 205
 FT DISULFID 228 274
 FT DISULFID 273 281
 FT DISULFID 293 307
 FT DISULFID 306 317
 FT DISULFID 344 389
 FT DISULFID 388 397
 FT DISULFID 420 466
 FT DISULFID 465 476
 FT DISULFID 489 505
 FT DISULFID 504 515
 FT DISULFID 542 587
 FT DISULFID 586 595
 FT CARBOHYD 500 500
 FT CONFLICT 24 24
 SQ SEQUENCE 615 AA; 69918 MW; DC5B6EBA CRC32;
 F -> M (IN REF. 3).
 Query Match 71.88; Score 51; DB 1; Length 615;
 Best Local Similarity 55.68; Pred. No. 1,79e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 249 QKTPKAPFS 257
 :||:|:|
 QY 1 QKXORAPY 9

RESULT 3
 ID PRO2-DROME STANDARD; PRT; 279 AA.
 AC P12881;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROPEASOME 29 KD SUBUNIT (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE
 DE COMPLEX 35 KD SUBUNIT).
 GN PRO35 OR PROS-35.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OS EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PTERYGOTA; DIPTERA; BRACHYCERA; MOSCOMORPHA; EPHYDROIDEA;
 CC DROSOPHILIDAE; DROSOPHILA.
 RN 11
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-18 AND 194-206.
 RC STRAIN=OREGON-R;
 RX MEDLINE: 90005444.
 RA HAAS C., PESOLD-HURT B., MUTHAUP G., BEYREUTHER K.,
 RA KLOTZEL P.-M.;
 RT "The PROS-35 gene encodes the 35 kd protein subunit of Drosophila
 RT melanogaster proteasome.";

EMBO J. 8:2373-2379(1989).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RX MEDLINE: 92249308.
 RA FRETWELT S., TROKELL M., HAASS C., PESOLD-HURT B., GLAETZER K.H.,
 RT KLOETZEL P.-M.;
 RT "Molecular characterization of the genomic regions of the Drosophila
 alpha-type subunit proteasome genes PROS-Dm8.1 and PROS-Dm3.5";
 RL EUR. J. BIOCHEM. 205:1043-1051(1992).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 NEUTRAL OR SLIGHTLY BASIC PH. THE 35 KD SUBUNIT IS PROBABLY A
 REGULATORY SUBUNIT. THE PROTEASOME HAS AN ATP-DEPENDENT
 PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 ALSO IN THE NUCLEUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A, ALSO KNOWN AS THE
 PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X15497; G8382; -;
 DR EMBL: X62285; G8388; -;
 DR PIR: S05507; SNEFSK.
 DR PIR: S23450; S23450.
 DR FLYBASE: FBgn0003151; Procs35.
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PFAM: PF00227; Proteasome; 1.
 DR HSRP: P23156; 1PMA.
 KW PROTEASOME: HYDROLASE; PROTEASE: PHOSPHORYLATION.
 FT MOD.RES 103 103 PHOSPHORYLATION (POTENTIAL).
 SQ SEQUENCE 279 AA; 31058 MW; AA18BDF CRC32;
 Query Match 70.4%; Score 50; DB 1; Length 279;
 Best Local Similarity 62.5%; Pred. No. 2,96e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 121 ORYDAPY 128
 1:1:1:1:1
 1 OKYORAPY 8
 RESULT 4
 ID YE05 YEAST STANDARD: PRT: 299 AA.
 AC P32643;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOHETICAL 34.8 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION.
 GN YER175C OR STYCP-ORF63.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMETES; SACCAROMYCETALES;
 CC SACCAROMYCETACEAE; SACCAROMYCES.
 CC [1]
 RP SEQUENCE FROM N.A.
 RA MULIGAN J.T., DIETRICH F.S., HENNESSEY K.M., SEHL P., KOMP C.,
 RA WEI Y., TAYLOR P., NAKAHARA K., ROBERTS D., DAVIS R.W.;
 RL SUBMITTED (FEB-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC [2]
 CC SEQUENCE FROM N.A.
 RP STRAIN-S288C / AB972;

RA DIETRICH F.S., MULIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
 RA AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,
 RA CHING E., DUNCAN M., GUZMAN E., HARTZEL G., HUNNICKE-SMITH S.,
 RA HYMAN R., KAISER A., KOMP C., LASHKARI D., LEW H., LIN D.,
 RA MOSSEDALE D., NAKAHARA K., NAMATH A., NOKGREN R., OEFNER P., OH C.,
 RA PETEL F.X., ROBERTS D., SEHL P., SCHRAM S., SHOGREN T., SMITH V.,
 RA TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: TO YEAST YHR209W.
 CC -----
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 CC -----
 DR EMBL: U18922; G603416; -;
 DR PIR: S30861; S30861.
 KW HYPOHETICAL PROTEIN
 SQ SEQUENCE 299 AA; 34768 MW; 2A733702 CRC32;
 Query Match 70.4%; Score 50; DB 1; Length 299;
 Best Local Similarity 44.4%; Pred. No. 2,96e+00;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 129 ERFOSNAYA 137
 1:1:1:1:1
 1 OKYORAPY 9
 DB 129 ERFOSNAYA 137
 1:1:1:1:1
 1 OKYORAPY 9

RESULT 5
 ID DCAN SOLTU STANDARD: PRT: 360 AA.
 AC 004694;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE S-ADENOSYLMETHIONINE DECARBOXYLASE PHOENZYME (EC 4.1.1.50) (ADOMETDC)
 DE (SAMDC) (INDUCED STOLEN TIP PROTEIN TUB13).
 GN SAMDC OR TUB13.
 OS SOLANUM TUBEROSUM (POTATO).
 OC EUKARYOTA: VIRIDIPHYTES: EMBRYOPHYTES: TRACHEOPHYTES;
 CC EUPHYLOPHITES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS;
 CC ASTRIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; SOLANUM.
 CC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. RECORD; TISSUE-STOLON TIP;
 RX MEDLINE: 93081725.
 RA TAYLOR M.A., MAD ARIE S.A., KOMAR A., DAVIES H.V., SCOBIE L.A.,
 RA PEARCE S.R., FLAVELL A.J.;
 RT "Expression and sequence analysis of cDNAs induced during the early
 stages of tuberisation in different organs of the potato plant
 (Solanum tuberosum L.).";
 RL PLANT MOL. BIOL. 20:641-651(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. DESIREE;
 RX MEDLINE: 95036004.
 RA MAD ARIE S.A., TAYLOR M.A., GEORGE L.A., BUTLER A.R., BURCH L.R.,
 RA TAYLOR H.V., STARK M.J., KOMAR A.;
 RT "Characterisation of the S-adenosylmethionine decarboxylase (SAMDC)
 gene of potato.";
 RL PLANT MOL. BIOL. 26:327-338(1994).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE - (5'-DEOXY-5'-ADENOSYL)
 (3'-AMINOPROPYL)METHYL SULFONIUM SALT + CO(2).
 CC -1- COFACTOR: THIS ENZYME REQUIRES A PYRUVYL GROUP FOR ITS ACTIVITY.
 CC -1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
 AMINOPROPYL MOIETY REQUIRED FOR SPERMATIDINE AND SPERMINE
 BIOSYNTHESIS FROM PUTRESCINE.
 CC -1- TISSUE SPECIFICITY: STOLON, ALSO EXPRESSED IN LEAVES, STEMS
 AND ROOTS.
 CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING THE

```
CC EARLY STAGES OF TUBERIZATION-MAXIMUM EXPRESSION WAS IN NON-
CC SWELLING STOLON TIPS FROM STAGE B, AND LEVEL DECLINED AS THE
CC TUBER INCREASED IN SIZE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; Z11680; G21485; -.
CC DR EMBL; S74514; G807094; -.
CC DR PIR; S28047; S28047.
CC KM SPERMIDINE BIOSYNTHESIS; LYASE: DECARBOXYLASE: PYRUVATE; ZYMOCEN.
CC FT CHAIN 1 72 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
CC FT CHAIN 73 360 CHAIN (BY SIMILARITY).
CC FT SITE 72 73 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
CC FT MOD_RES 73 73 CHAIN (BY SIMILARITY).
CC FT ACT_SITE 13 13 CLEAVAGE (NONHYDROLYTICAL)
CC FT ACT_SITE 16 16 (BY SIMILARITY).
CC FT ACT_SITE 16 16 CONVERTED TO A PYRVOYL GROUP
CC FT ACT_SITE 87 87 (BY SIMILARITY).
CC FT CONFLICT 174 174 S->P (IN REF. 2).
CC FT CONFLICT 257 257 T->S (IN REF. 2).
CC FT CONFLICT 291 291 V->I (IN REF. 2).
CC FT CONFLICT 305 305 I->T (IN REF. 2).
CC SQ SEQUENCE 360 AA; 39726 MW; 4F29EBE4 CRC32;
CC
CC Query Match 70.4%; Score 50; DB 1; Length 360;
CC Best Local Similarity 62.5%; Pred. No. 2,96e+00;
CC Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC Db 332 OKFTPTPY 339
CC QY 1 OKYORAPY 8
CC
CC RESULT 6
CC ID Y151_YEAST STANDARD; PRY; 340 AA.
CC AC 012524;
CC 01-NOV-1997 (REL. 35, CREATED)
CC 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
CC 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CC DE HYPOTHEETICAL 39,8 KD PROTEIN IN MP14-ACG2 INTERGENIC REGION.
CC GN YKRIJ1C OR L9634.8.
CC OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
CC OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMETES; SACCHAROMYCETALES;
CC OC SACCHAROMYCETACEAE; SACCHAROMYCES.
CC [1]
CC RP SEQUENCE FROM N.A.
CC RA RIEGER M., MOELLER-AUER S., BRUECKNER M.;
CC RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC [2]
CC RP STRAIN-S288C / AB972;
CC RA JOHNSON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
CC RA FAVELLO A., FULTON L., GATTUNG S., GRECO T., KRISTEN J., KUCABA T.,
CC RA HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
CC RA JOHLSTON L., LANGSTON Y., LATHEILLE P., LE T., MARDIS E., MENEZES S.,
CC RA MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
CC RA TAICH A., TREVAISKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
CC RA WILSON R., WATERSTON R.;
CC RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC CC -1- SIMILARITY: BELONGS TO THE OEP0035 FAMILY.
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DR EMBL; Z73323; E245586; -
DR EMBL; U53879; G126231; -
DR PROSITE; PS01293; UPE0035; 1.
DR PFM; PFM0293; multi; 1.
DR KW
DR HYPOTHETICAL PROTEIN.
SO SEQUENCE 340 AA; 39755 MW; F8F4D4B7 CRC32;

Query Match 69.0%; Score 49; DB 1; Length 340;
Best Local Similarity 50.0%; Pred.No. 4,85e+00;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 22 KFKKTPY 29
1:::111
2 KYGRAPY 9

RESULT 7
ID DJLA_HAEIN STANDARD; PRT; 288 AA.
AC P44607;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE DNAJ-LIKE PROTEIN DJLA.
GN DJLA OR HI0271.
OS HAEMOPHILUS INFLUENZAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURRELLACEAE;
OC HAEMOPHILUS.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-RD / KW20;
RX MEDLINE; 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERNLAUGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCCENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYAN J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GUODK A., KELLEY J.M.,
RA WEDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,
RA UETTERACK T.R., HANNA M.C., NGUYEN D.T., SAUDER D.M., BRANDON R.C.,
RA FINE L.D., FITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA GENSEM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Influenzae Rd.
RC Science 269:496-512(1995).
CC -1- FUNCTION: CHAPERONE THAT MAY PLAY A ROLE IN THE CORRECT ASSEMBLY,
CC ACTIVITY AND/OR MAINTENANCE OF A NUMBER OF MEMBRANE PROTEINS,
CC INCLUDING TWO-COMPONENT SIGNAL-TRANSDUCTION SYSTEMS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
CC -----
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DR EMBL; U32713; G1573237; -
DR TIGR; HI0271; -
DR PROSITE; PS00636; DNAJ_1; FALSE_NEG.
DR PROSITE; PS50076; DNAJ_2; 1.
DR PFM; PFM0226; DnaJ; 1.
DR HSSP; P25685; 1HDJ.
DR CHAPERONE; TRANSMEMBRANE; INNER MEMBRANE.
```

FT DOMAIN 1 6 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 7 27 POTENTIAL.
 FT DOMAIN 28 288 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 222 288 DNA-LIKE.
 SO SEQUENCE 288 AA: 32523 MW: BEDE4D6A CRC32:
 Query Match 67.6%; Score 48; DB 1; Length 288;
 Best Local Similarity 62.5%; Pred. No. 7.88e+00;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 191 OKYOGAY 198
 |||||:1
 1 OKYORAPY 8

RESULT 8
 ID MTE1_SACKL STANDARD; PRT: 337 AA.
 AC P87292;
 DT 15-JUL-1998 (REL. 36, CREATED)
 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE MITOCHONDRIAL REPLICATION PROTEIN MTE1 (MITOCHONDRIAL TRANSCRIPTION FACTOR MTE1FB).
 GN MTE1.
 OS SACCHAROMYCES KILUYERI (YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCHAROMYCETALES;
 CC SACCHAROMYCETACEAE; SACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:ATCC 22512;
 RA CARROGGIUS J.A., YUN S., SHADEL G.S., CLAYTON D.A., BOGENHAGEN D.F.;
 SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: ESSENTIAL FOR MITOCHONDRIAL REPLICATION AND TRANSCRIPTION. CONFERES SELECTIVE PROMOTER RECOGNITION ON THE CORE SUBUNIT OF THE YEAST MITOCHONDRIAL RNA POLYMERASE. INTERACTS WITH DNA IN A NON-SPECIFIC MANNER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: FAINT SIMILARITY WITH THE T4 GENE 32 PRODUCT AND WITH BACTERIAL SIGMA FACTORS.
 CC
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 CC
 CC EMBL: U81619; G2209024; -
 CC MITOCHONDRION; DNA REPLICATION; TRANSCRIPTION REGULATION; DNA-BINDING.
 CC INIT MET 0 BY SIMILARITY.
 CC SEQUENCE 337 AA: 39072 MW: DBAEB78A CRC32:
 SO SEQUENCE 337 AA: 39072 MW: DBAEB78A CRC32:
 Query Match 67.6%; Score 48; DB 1; Length 337;
 Best Local Similarity 83.3%; Pred. No. 7.88e+00;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 96 YOROPY 101
 |||||1
 3 YORAPY 8

RESULT 9
 ID FARK_LYMTST STANDARD; PRT: 360 AA.
 AC P42565;
 DT 01-NOV-1995 (REL. 32, CREATED)
 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.
 OS LYMANEA STAGNALIS (GREAT POND SNAIL).
 OC EUKARYOTA; METAZOA; MOLUSCA; GASTROPODA; PULMONATA; BASOMMATOPHORA;
 CC LYMANEIDAE; LYMANEA.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-CNS;
 RX MEDLINE: 95054375.
 RA KELLET E., SAUNDERS S.E., LI K.W., STADON J.W., BENJAMIN P.R., BURKE J.F.;
 RT "Genomic organization of the FMRFamide gene in Lymanea: multiple exons encoding novel neuropeptides";
 RL J. NEUROSCI. 14:6564-6570(1994).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE: 91162302.
 RA SAUNDERS S.E., BRIGHT K., KELLET E., BENJAMIN P.R., BURKE J.F.;
 RT "Neuropeptides Gly-Asp-Pro-Phe-Leu-Arg-Phe-amide (GDPFLRFamide) and Ser-Asp-Pro-Phe-Leu-Arg-Phe-amide (SDPFLRFamide) are encoded by an exon 3' to Phe-Met-Arg-Phe-NH2 (FMRFamide) in the snail Lymanea stagnalis";
 RL J. NEUROSCI. 11:740-745(1991).
 RN [3]
 RP PARTIAL SEQUENCE FROM N.A.
 RX TISSUE-CNS;
 RX MEDLINE: 92165507.
 RA SAUNDERS S.E., KELLET E., BRIGHT K., BENJAMIN P.R., BURKE J.F.;
 RT "Cell-specific alternative RNA splicing of an FMRFamide gene transcript in the brain";
 RL J. NEUROSCI. 12:1033-1039(1992).
 RN [4]
 RP SEQUENCE OF 276-282 (SKPYRF-AMIDE).
 RX MEDLINE: 93042993.
 RA DE WITH N.D., VAN DER SCHORS R.C.;
 RT "SKPYRFamide, a novel FMRFamide-related peptide in the snail Lymanea stagnalis";
 RL NEUROREPORT 3:612-614(1992).
 CC -1- FUNCTION: SDPFLRF-AMIDE INHIBITS NEURONS.
 CC -1- FUNCTION: SKPYRF-AMIDE EXCITES NEURONS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN 57 CELLS INCLUDING A CARDIORESPIRATORY CELL AND AND THE VISCERAL WHITE INTERNEURON (W1).
 CC
 CC -1- ALTERNATIVE PRODUCTS: BY ALTERNATIVE SPLICING TWO FORMS ARE PRODUCED. ONE WHICH ENCODES ONLY FMRFAMIDE AND RELATED TETRAPEPTIDES AND A SECOND FORM (SHOWN HERE) WHICH ENCODES FMRFAMIDE-RELATED HEPTAPEPTIDES. BOTH FORMS ONLY SHARE THE N-TERMINAL SIGNAL SEQUENCE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 CC
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 CC
 CC EMBL: U03137; G416208; -
 CC DR EMBL: S38684; G247117; -
 CC AMIDATION: CLEAVAGE ON PAIR OF BASIC RESIDUES; REPEAT: SIGNAL;
 CC NEUROPEPTIDE; ALTERNATIVE SPLICING.
 CC
 CC SIGNAL 1 35 POTENTIAL.
 FT CHAIN 1 48 EFPL-AMIDE.
 FT CHAIN 71 77 GDPFLRF-AMIDE 1.
 FT CHAIN 80 86 GDPFLRF-AMIDE 2.
 FT CHAIN 89 95 GDPFLRF-AMIDE 3.
 FT CHAIN 98 104 GDPFLRF-AMIDE 4.
 FT CHAIN 107 113 SDPFLRF-AMIDE 1.
 FT CHAIN 116 122 GDPFLRF-AMIDE 5.
 FT CHAIN 125 131 GDPFLRF-AMIDE 6.
 FT CHAIN 134 140 SDPFLRF-AMIDE 2.
 FT CHAIN 143 149 SDPFLRF-AMIDE 3.
 FT CHAIN 152 158 SDPFLRF-AMIDE 4.
 FT CHAIN 161 167 SDPFLRF-AMIDE 5.
 FT CHAIN 170 176 SDPFLRF-AMIDE 6.
 FT CHAIN 179 185 SDPFLRF-AMIDE 7.
 FT CHAIN 188 194 GDPFLRF-AMIDE 7.

FT CHAIN 197 203 SDPFRR-AMIDE.
 FT CHAIN 276 282 SKPMRF-AMIDE.
 FT CHAIN 318 323 SEPPRY-AMIDE.
 FT CHAIN 331 336 HDYMR-AMIDE.
 FT MOD_RES 77 77 AMIDATION (G-78 PROVIDE AMIDE GROUP).
 FT MOD_RES 86 86 AMIDATION (G-87 PROVIDE AMIDE GROUP).
 FT MOD_RES 95 95 AMIDATION (G-96 PROVIDE AMIDE GROUP).
 FT MOD_RES 104 104 AMIDATION (G-105 PROVIDE AMIDE GROUP).
 FT MOD_RES 113 113 AMIDATION (G-114 PROVIDE AMIDE GROUP).
 FT MOD_RES 122 122 AMIDATION (G-123 PROVIDE AMIDE GROUP).
 FT MOD_RES 131 131 AMIDATION (G-132 PROVIDE AMIDE GROUP).
 FT MOD_RES 140 140 AMIDATION (G-141 PROVIDE AMIDE GROUP).
 FT MOD_RES 149 149 AMIDATION (G-150 PROVIDE AMIDE GROUP).
 FT MOD_RES 158 158 AMIDATION (G-159 PROVIDE AMIDE GROUP).
 FT MOD_RES 167 167 AMIDATION (G-168 PROVIDE AMIDE GROUP).
 FT MOD_RES 176 176 AMIDATION (G-177 PROVIDE AMIDE GROUP).
 FT MOD_RES 185 185 AMIDATION (G-186 PROVIDE AMIDE GROUP).
 FT MOD_RES 194 194 AMIDATION (G-195 PROVIDE AMIDE GROUP).
 FT MOD_RES 203 203 AMIDATION (G-204 PROVIDE AMIDE GROUP).
 FT MOD_RES 282 282 AMIDATION (G-283 PROVIDE AMIDE GROUP).
 FT MOD_RES 332 332 AMIDATION (G-334 PROVIDE AMIDE GROUP).
 FT MOD_RES 336 336 AMIDATION (G-337 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 360 AA; 41785 MW; A727612C CRC32;

Query Match 67.6%; Score 48; DB 1; Length 360;
 Best Local Similarity 71.4%; Pred. No. 7.88e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 309 ORYORP 315
 1:1:1:1:
 QY 1 OKYORAP 7

RESULT 10
 ID RBL_ECTSI STANDARD; PRT; 488 AA.
 AC P2413;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE RUBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
 DE LARGE SUBUNIT).
 GN RBCL.
 OS ECTOCARPUS SILICULOSUS.
 OG CHLOROPLAST.
 OC EUKARYOTA; STRAMENOPILLES; PHAEOPHYCEAE/XANTHOPHYCEAE GROUP;
 OC PHAEOPHYCEAE; ECTOCARPALES; ECTOCARPACEAE; ECTOCARPUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RT STRAIN-DILIMYN (LYNGBYE);
 RT MEDLINE; 9138696.
 RT VALENTIN K., ZETSCHE K.;
 RT "Rubisco genes indicate a close phylogenetic relation between the
 RT plastids of Chromophyta and Rhodophyta."
 RT PLANT MOL. BIOL. 15:575-584(1990)
 CC -1- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF
 CC D-RUBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 CC ACTIVE SITE.
 CC -1- CATALYTIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + CO(2) =
 CC 2 3-PHOSPHO-D-GLYCERATE.
 CC -1- CATALYTIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + O(2) =
 CC 3-PHOSHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
 CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
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 CC -----

DR EMBL; X52503; G11544; -
 CC PIR; S13123; RKPELE
 DR PROSITE; P500157; RUBISCO_LARGE; 1.
 DR PFAM; PF00016; RUBISCO_large; 1.
 DR MENDEL; 4884; ECTSI;rbcl;1.
 DR HSSP; P00876; 3RUB.
 KW PHOTOSYNTHESIS; CARBON DIOXIDE FIXATION; PHOTORESPIRATION;
 FT LYSASE; OXIDOREDUCTASE; MONOOXYGENASE; CHLOROPLAST
 FT ACT_SITE 205 205 BINDING OF CO(2) ACTIVATES THE ENZYME.
 SQ SEQUENCE 488 AA; 53904 MW; A73CA424 CRC32;

Query Match 67.6%; Score 48; DB 1; Length 488;
 Best Local Similarity 55.6%; Pred. No. 7.88e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 253 ONYERAERA 261
 1:1:1:1:
 QY 1 OKYORAPY 9

RESULT 11
 ID RBL_PYLTI STANDARD; PRT; 488 AA.
 AC P23651;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE RUBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
 DE LARGE SUBUNIT).
 GN RBCL.
 OS PYLAELLA LITTORALIS.
 OG CHLOROPLAST.
 OC EUKARYOTA; STRAMENOPILLES; PHAEOPHYCEAE/XANTHOPHYCEAE GROUP;
 OC PHAEOPHYCEAE; ECTOCARPALES; ECTOCARPACEAE; PYLAELLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RT MEDLINE; 91355877.
 RA ASSALI N.E., MACHE R., LOISEUX-DE GOER S.;
 RT "Evidence for a composite phylogenetic origin of the plastid genome
 RT of the brown alga *Pylaeella littoralis* (L.) Kjellm."
 RT PLANT MOL. BIOL. 15:307-315(1990).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE; 92003695.
 CC ASSALI N.E., MARTIN W.F., SOMMERVILLE C.C., LOISEUX-DE GOER S.;
 RT "Evolution of the Rubisco operon from prokaryotes to algae: structure
 RT and analysis of the *rbcs* gene of the brown alga *Pylaeella*
 RT *littoralis*."
 RT PLANT MOL. BIOL. 17:853-863(1991).
 CC -1- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF
 CC D-RUBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 CC ACTIVE SITE.
 CC -1- CATALYTIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + CO(2) =
 CC 2 3-PHOSPHO-D-GLYCERATE.
 CC -1- CATALYTIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + O(2) =
 CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
 CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
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 CC -----

DR EMBL: X55372; G14187; -
 DR PIR: S11964; RKPEFL.
 DR PROSITE: PS00157; RUBISCO_LARGE; 1.
 DR PFAM: PF00016; RUBISCO_large; 1.
 DR MENDEL: 2981; PFL1; fdbcl; 1.
 DR HSSP: P00876; 3R0B.
 KW PHOTOSYNTHESIS; CARBON DIOXIDE FIXATION; PHOTORESPIRATION;
 LYSASE; OXIDOREDUCTASE; MONOOXYGENASE; CHLOROPLAST
 ACT SITE 205 BINDING OF CO(2) ACTIVATES THE ENZYME.
 FT SEQUENCE 488 AA; 54124 MW; 315PBEF CRC32;
 SQ

Query Match 67.6%; Score 48; DB 1; Length 488;
 Best Local Similarity 55.6%; Pred. No. 7.88e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 253 OMYERREYA 261
 1:1:1111
 QY 1 OKTORAPYT 9

HLT 12
 H15 DROME STANDARD; PRT; 544 AA.

AC 094690;
 DT 01-NOV-1997 (REL. 35; CREATED)
 DT 01-NOV-1997 (REL. 35; LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35; LAST ANNOTATION UPDATE)
 DE T-BOX PROTEIN H15.
 GN H15.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PTERYGOTA; DIPTERA; BRACHYCERA; MOSCOMORPHA; EPHYROIDEA;
 CC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EYE;
 RA BROOK W.J.; COHEN S.M.;
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS A T-BOX DOMAIN.

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EMBL: X98766; E255227; -
 FLYBASE: FBgn0016660; H15.
 DR PROSITE: PS01264; TBOX_2; FALSE_NEG.
 DR PROSITE: PS01283; TBOX_1; 1.
 DR PFAM: PF00907; T-box; 1.
 DR HSSP: P24781; 1XR.
 KW DNA-BINDING; NUCLEAR PROTEIN.
 FT DOMAIN 56 59 POLY-ALA.
 FT DOMAIN 83 91 POLY-GLN.
 FT DOMAIN 118 125 POLY-PRO.
 FT DNA_BIND 170 356 T-BOX.
 DT DOMAIN 242 245 POLY-PRO.
 FT DOMAIN 436 443 POLY-PRO.
 SQ SEQUENCE 544 AA; 60010 MW; 701FD98D CRC32;

Query Match 67.6%; Score 48; DB 1; Length 544;
 Best Local Similarity 55.6%; Pred. No. 7.88e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 414 OMYERREYA 422
 1:1:1111
 QY 1 OKTORAPYT 9

RESULT 13

ID BGAL_LEULA STANDARD; PRT; 626 AA.
 AC 002603;
 DT 01-JUL-1993 (REL. 26; CREATED)
 DT 01-JUL-1993 (REL. 26; LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37; LAST ANNOTATION UPDATE)
 DE BETA-GALACTOSIDASE LARGE SUBUNIT (EC 3.2.1.23) (LACTASE).
 GN LACT.
 OS LECANOSTOC LACTIS.
 OC PLASMID PHE63.
 CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; LACTOBACILLACEAE;
 CC LECANOSTOC.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-6.
 RC STRAIN-NZ6009.
 RX MEDLINE: 92325034.
 RA DAVID S., STEVENS H., VAN RIEL M., SIMONS G., DE VOS W.M.;
 RT "Leucostoc lactis beta-galactosidase is encoded by two overlapping
 RT genes".
 RL J. BACTERIOL. 174:4475-4481(1992).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
 CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
 CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
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EMBL: M92281; G149635; -
 DR PIR: A42891; A42891.
 DR PROSITE: PS00719; GLYCOSYL_HYDROL_F2_1; 1.
 DR PROSITE: PS00608; GLYCOSYL_HYDROL_F2_2; 1.
 DR PFAM: PF00703; glycosyl_hydrol; 1.
 DR HSSP: P00722; 1BGL.
 KW HYDROLASE; GLYCOSIDASE; PLASMID.
 FT ACT_SITE 318 318 HAS AN EFFECT ON THERMOSTABILITY
 FT ACT_SITE 466 466 PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 534 534 NUCLEOPHILE (BY SIMILARITY).
 SQ SEQUENCE 626 AA; 72113 MW; 802C903C CRC32;

Query Match 67.6%; Score 48; DB 1; Length 626;
 Best Local Similarity 71.4%; Pred. No. 7.88e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 104 YRRPPT 110
 1:1:1111
 QY 3 YORAPYT 9

RESULT 14
 ID K10A_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (REL. 01; CREATED)
 DT 21-JUL-1986 (REL. 01; LAST SEQUENCE UPDATE)
 DT 01-MAR-1992 (REL. 21; LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (REL).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 76023758.
 RA PALM W., HILSCHMANN N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); isolation
 RT and characterization of the tryptic peptides; the complete amino acid
 RT sequence of the protein; a contribution to the elucidation of the
 RT three-dimensional structure of antibodies, in particular their

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RT combining site."
RL HOPE-SEYLER'S Z. PHYSIOL. CHEM. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RA MEDLINE: 76039968.
RA EPP O., LATTMAN E.E., SCHIFFER M., HUBER R., PALM W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution."
RL BIOCHEMISTRY 14:4943-4952(1975).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -1- THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01873; KIHORE.
DR PDB: 1REI; 17-FEB-84.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN; 3D-STRUCTURE.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 FRAMEWORK 2.
FT DOMAIN 35 49 FRAMEWORK 3.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 45 49
FT STRAND 50 52
FT STRAND 53 54
FT STRAND 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11902 MW; D08P51A4 CRC32;

Query Match 56.2%; Score 47; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.27e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

89 QOYOSLEPYT 97
QY 1 OYORAPYT 9

RESULT 15
ID BHMT_HUMAN STANDARD; PRT; 406 AA.
AC Q93088;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE BETAINE--HOMOCYSTEINE S-METHYLTRANSFERASE (EC 2.1.1.5).
GN BHMT.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE: 96394355.
RA GARROW T.A.;
RT "Purification, kinetic properties, and cDNA cloning of mammalian
RT betaine-homocysteine methyltransferase."
RL J. BIOL. CHEM. 271:22831-22838(1996).

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CC -1- FUNCTION: INVOLVED IN THE REGULATION OF HOMOCYSTEINE METABOLISM.
CC CONVERTS BETAINE AND HOMOCYSTEINE TO DIMETHYLGLYCINE AND
CC METHIONINE. RESPECTIVELY, THIS REACTION IS ALSO REQUIRED FOR THE
CC IRREVERSIBLE OXIDATION OF CHOLINE.
CC -1- CATALYTIC ACTIVITY: TRIMETHYLAMMONIACETATE + L-HOMOCYSTEINE =
CC DIMETHYLGLYCINE + L-METHIONINE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: PRIMARILY FOUND IN LIVER AND KIDNEY.
CC -1- DISEASE: DEFECTS IN BHMT COULD LEAD TO HYPERHOMOCYSTE(INE)NEMIA, BUT
CC SUCH A DEFECT HAS NOT YET BEEN OBSERVED. HYPERHOMOCYSTE(INE)NEMIA IS
CC AN INDEPENDENT RISK FACTOR FOR THE DEVELOPMENT OF ARTERIOSCLEROTIC
CC VASCULAR DISEASE.
CC -----
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CC -----
DR EMBL: U50929; G1522683; -.
DR MIM: 602888; -.
DR HSSP: P06139; IGRU.
KW TRANSFERASE; METHYLTRANSFERASE.
SQ SEQUENCE 406 AA; 44970 MW; 8DEC74F5 CRC32;

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Query Match 66.2%; Score 47; DB 1; Length 406;
Best Local Similarity 62.5%; Pred. No. 1.27e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 282 OKYAREAY 289
QY 1 OKYORAPYT 8

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Search completed: Thu Sep 2 11:32:01 1999
Job time : 8 secs.

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:31:22 1999; Maspar time 3.03 Seconds
 118.953 Million cell updates/sec
 Popular output not generated.

Title: >US-08-599-226-13
 Description: (1-9) from US08599226.pep
 Perfect Score: 71
 Sequence: 1 OKYGRAPYT 9

Scoring table:
 PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r60
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 23.067; Variance 29.847; scale 0.773

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	56	78.9	1260	2	S28407	guanine nucleotide-ex	4.96e+01
2	52	73.2	4957	2	T03455	ALR protein - human	3.28e+00
3	52	73.2	5262	2	T03454	ALR protein - human	3.28e+00
4	51	71.8	615	1	ABCHS	serum albumin precurs	5.19e+00
5	50	70.4	279	1	SNF5K	multicatalytic endope	8.16e+00
6	50	70.4	299	2	S30861	hypothetical protein	8.16e+00
7	50	70.4	360	2	S28047	TUBB3 protein - potat	8.16e+00
8	50	70.4	360	2	S52662	S-adenosylmethionine	8.16e+00
9	49	69.0	321	2	B71854	type II DNA modificat	1.27e+01
10	49	69.0	340	2	S65000	probable membrane pro	1.27e+01
11	49	69.0	563	2	B70676	hypothetical protein	1.27e+01
12	48	67.6	288	2	G64146	yabH protein homolo	1.98e+01
13	48	67.6	407	2	G69217	peptide chain release	1.98e+01
14	48	67.6	488	1	RKPFLL	ribulose-bisphosphate	1.98e+01
15	48	67.6	488	1	RKPFLL	ribulose-bisphosphate	1.98e+01
16	48	67.6	521	1	R39956	neutral proteinase (E	1.98e+01
17	48	67.6	626	2	A42891	beta-galactosidase (E	1.98e+01
18	48	67.6	707	2	T01803	hypothetical protein	1.98e+01
19	47	66.2	114	1	K15901	Ig kappa chain V-I re	3.06e+01
20	47	66.2	689	2	S45901	probable membrane pro	3.06e+01
21	46	64.8	104	2	G69482	hypothetical protein	4.68e+01
22	46	64.8	263	1	SNR2C	multicatalytic endope	4.68e+01
23	46	64.8	269	2	JC1445	multicatalytic endope	4.68e+01

24	46	64.8	329	2	F64356	translational initiat	4.68e+01
25	46	64.8	342	2	S76447	hypothetical protein	4.68e+01
26	46	64.8	421	2	JC5323	anthranilate synthase	4.68e+01
27	46	64.8	478	2	S60049	vacuolar processing e	4.68e+01
28	46	64.8	490	2	E71486	probable s/tc protein	4.68e+01
29	46	64.8	513	2	A37219	mannan endo-1,4-beta	4.68e+01
30	46	64.8	530	2	S38903	hypothetical protein	4.68e+01
31	46	64.8	578	2	C70350	penicillin binding pr	4.68e+01
32	46	64.8	664	2	S44756	probable protein disu	4.68e+01
33	46	64.8	1009	2	C64483	hypothetical protein	4.68e+01
34	46	64.8	1085	2	JC2227	probable helicase RAD	4.68e+01
35	46	64.8	1348	2	B23496	TyB protein - yeast	4.68e+01
36	46	64.8	1598	2	S69967	TyB protein - yeast	4.68e+01
37	46	64.8	1749	2	S69972	TyB protein - yeast	4.68e+01
38	46	64.8	1755	2	S69949	TyB protein - yeast	4.68e+01
39	46	64.8	1770	2	S70230	TyB protein - yeast	4.68e+01
40	46	64.8	1770	2	S70233	TyB protein - yeast	4.68e+01
41	46	64.8	1770	2	S69953	TyB protein - yeast	4.68e+01
42	46	64.8	1770	2	S69966	TyB protein - yeast	4.68e+01
43	46	64.8	1770	2	S69948	TyB protein - yeast	4.68e+01
44	46	64.8	1770	2	S45842	TyB protein - yeast	4.68e+01
45	46	64.8	1771	2	S53592	TyB protein - yeast	4.68e+01

ALIGNMENTS

RESULT	ENTRY	1
ENTRY	S28407	#type complete
TITLE	guanine nucleotide-exchange activator CDC25 homolog - mouse	
ORGANISM	formal_name Mus musculus #common_name mouse	
DATE	17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 10-Sep-1997	
ACCESSIONS	S28407; S22693; B46199; S20730	
REFERENCES	S28407 Cen, H.; Papageorge, A.G.; Zippel, R.; Lowy, D.R.; Zhang, K. EMBO J. (1992) 11:4007-4015	
#authors	Isolation of multiple mouse cDNAs with coding homology to Saccharomyces cerevisiae CDC25: identification of a region related to Bcr, Vav, Dbl and CDC24.	
#title	related to Bcr, Vav, Dbl and CDC24.	
#cross-references	WU:93010596	
#accession	S28407	
#status	not compared with conceptual translation	
#molecule_type	RNA	
#residues	1-1260 #label CEN	
REFERENCE	S22693 Martegani, E.; Vanoni, M.; Zippel, R.; Cocchetti, P.; Brambilla, R.; Ferrari, C.; Sturani, E.; Albergina, L. EMBO J. (1992) 11:2151-2157	
#authors	Cloning by functional complementation of a mouse cDNA encoding a homologue of CDC25, a Saccharomyces cerevisiae RAS activator.	
#title	RAS activator.	
#cross-references	WU:92289680	
#accession	S22693	
#molecule_type	RNA	
#residues	789-1260 #label MAR	
REFERENCE	A46199 #cross-references EMBL:X59868; NID:950357; PIR:505058	
#authors	Wei, W.; Mosteller, R.D.; Sanayal, P.; Gonzales, E.; McKinney, D.; Dasgupta, C.; Li, P.; Liu, B.X.; Broek, D. Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104	
#journal	Identification of a mammalian gene structurally and functionally related to the CDC25 gene of Saccharomyces cerevisiae.	
#title	Cerevisiae.	
#cross-references	WU:92537779	
#accession	B46199	
#status	preliminary	
#molecule_type	nucleic acid	
#residues	1029-1030, 'D', 1032-1224 #label WEI	
#experimental_source	sequence extracted from NCBI backbone (NCBI:111101, NCBI:111102)	
#note	#superfamily CDC25-type guanine nucleotide exchange activator homology; CDC24 homology; pleckstrin repeat homology	

FEATURE
242-428 #domain CDC24 homology #label CD24\
1021-1257 homology #label SOS

SUMMARY #length 1260 #molecular-weight 143900 #checksum 9725

Query Match 78.9%; Score 56; DB 2; Length 1260;
Best Local Similarity 62.5%; Pred. No. 4,96e-01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1058 EXERTPY 1065
QY 1 QYORAPY 8

RESULT 2
ENTRY T03455 #type complete
TITLE ALR protein - human
ORGANISM #formal_name Homo sapiens #common_name man
#date 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

ACCESSIONS T03455
REFERENCES T03455
#authors Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, T.; Alder, H.; Croce, C.M.; Huebner, K.; Mazo, A.; Canaan, E.
#journal Oncogene (1997) 15:549-560
#title Structure and expression pattern of human ALR, a novel gene with strong homology to ALR-1 involved in acute leukemia, and to Drosophila trithorax.

#accession T03455
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-4957 #label PRA
#cross-references EMBL:AF010404; NID:g2358286; PID:g2358287

GENETICS
#gene ALR
#map_position 12
KEYWORDS alternative splicing
SUMMARY #length 4957 #molecular-weight 531848 #checksum 6143

Query Match 73.2%; Score 52; DB 2; Length 4957;
Best Local Similarity 100.0%; Pred. No. 3,28e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2219 YORAPY 2224
QY 3 YORAPY 8

RESULT 3
ENTRY T03454
TITLE ALR protein - human
ORGANISM #formal_name Homo sapiens #common_name man
#date 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

ACCESSIONS T03454
REFERENCES T03454
#authors Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, T.; Alder, H.; Croce, C.M.; Huebner, K.; Mazo, A.; Canaan, E.
#journal Oncogene (1997) 15:549-560
#title Structure and expression pattern of human ALR, a novel gene with strong homology to ALR-1 involved in acute leukemia, and to Drosophila trithorax.

#accession T03454
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-5262 #label PRA
#cross-references EMBL:AF010403; NID:g2358284; PID:g2358285

GENETICS
#gene ALR
#map_position 12

KEYWORDS alternative splicing
SUMMARY #length 5262 #molecular-weight 564181 #checksum 92

Query Match 73.2%; Score 52; DB 2; Length 5262;
Best Local Similarity 100.0%; Pred. No. 3,28e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2524 YORAPY 2529
QY 3 YORAPY 8

RESULT 4
ENTRY ABCBS #type complete
TITLE serum albumin precursor - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
#date 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Sep-1993

ACCESSIONS S15571; A05078; A13451
REFERENCES S15571
#authors Cassidy, A.I.; Salkild, C.K.; Baverstock, P.; Wallace, J.C.
#accession submitted to the EMBL Data Library, July 1991
#molecule_type mRNA
#residues 1-615 #label CAS
#cross-references EMBL:X60688; NID:g63747; PID:g63748

REFERENCE A05078
#authors Hache, R.J.G.; Miskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Dealey, R.G.
#journal J. Biol. Chem. (1983) 258:4556-4564
#title The 5' noncoding and flanking regions of the avian very low density apolipoprotein II and serum albumin genes. Homologies with the egg white protein genes.

#cross-references M01D:83161037
#accession A05078
#molecule_type DNA
#residues 1-28 #label HAC
#cross-references GB:V00381; NID:g63038; PID:g63039

REFERENCE A13451
#authors Rosen, A.M.; Geller, D.M.
#journal Biochem. Biophys. Res. Commun. (1977) 78:1060-1066
#title Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.

#cross-references M01D:78019943
#accession A13451
#molecule_type protein
#residues 19-23,'M',25-30 #label ROS
COMMENT Serum albumin is synthesized in the liver as preproalbumin. It binds copper, nickel, calcium (weakly, at 2-3 sites), and protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (weak bonds with these hormones promote their transfer across the membranes), thyroxine, and triiodothyronine. #superfamily serum albumin; serum albumin repeat homology carrier protein; duplication; metal binding; plasma

CLASSIFICATION
KEYWORDS
FEATUERE 1-28
19-26 #domain signal sequence #status predicted #label SIG\
27-613 #domain propeptide #status predicted #label PRO\
32-206 #product serum albumin #status predicted #label MAT\
225-398 #domain serum albumin repeat homology #label SA1\
411-596 #domain serum albumin repeat homology #label SA2\
30 #domain serum albumin repeat homology #label SA3\
80-89,102-118, #binding_site copper (His) #status predicted\
117-128,152-197, 196-205,228-274, 273-281,293-307, 306-317,344-389, 388-397,420-466, 465-476,489-505, 504-515,542-587, 586-595

SUMMARY #disulfide_bonds #status predicted
#length 615 #molecular-weight 69918 #checksum 4822

Query Match 71.8%; Score 51; DB 1; Length 615;
Best Local Similarity 55.6%; Pred. No. 5.19e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 249 OKYKAPPS 257
111:111:
1 OKYORAPYT 9

RESULT 5
ENTRY SNFEK #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) 35k chain
- fruit fly (Drosophila melanogaster)
ALTERNATE_NAMES 19S cylinder particle 35k chain; multicatalytic proteinase
35k chain; prosome 35k chain; proteasome 35k chain
ORGANISM #formal_name Drosophila melanogaster
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Sep-1997

ACCESSIONS S23450; S05507; A38761
REFERENCE S23450
#map_position 5R
#molecule_type DNA
#residues 1-279 #label FREN
#cross-references EMBL:X62285; NID:g8387; PID:g8388
#experimental_source strain Canton S

REFERENCE S05507
#authors Haass, C.; Pesold-Hurt, B.; Mulhaupt, G.; Beyreuther, K.; Kloeckel, P.M.
#journal EMBO J. (1989) 8:2373-2379
#title The PROS-35 gene encodes the 35 kd protein subunit of Drosophila melanogaster proteasome.
#cross-references MVID:9005444
#accession S05507
#molecule_type mRNA
#residues 1-279 #label HAA
#cross-references EMBL:X15497; NID:g8381; PID:g8382
#accession A38761
#molecule_type protein
#residues 4-18;194-206 #label HAA2

GENETICS PROS-35
#gene #cross-references FlyBase:FBgn0003151
#map_position 89F-90A
#introns 1/3; 211/3
CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9.
KEYWORDS hydrolase; phosphoprotein; proteinase
SUMMARY #length 279 #molecular_weight 31058 #checksum 365

Query Match 70.4%; Score 50; DB 1; Length 279;
Best Local Similarity 62.5%; Pred. No. 8.16e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 121 OKYRRPY 128
111:111:
1 OKYORAPY 8

RESULT 6
ENTRY S30861 #type complete
TITLE hypothetical protein YER175c - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 26-May-1993 #sequence_revision 28-May-1993 #text_change 05-Dec-1997
ACCESSIONS S30861; S50678
REFERENCE S30812

#authors Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wel, Y.; Taylor, P.; Nakahara, K.; Roberts, D.; Davis, R.W.
#submission submitted to the EMBL Data Library, February 1993
#accession S30861
#molecule_type DNA
#residues 1-299 #label MCL
#cross-references GB:U18922; EMBL:L11229; NID:g603405; PID:g603416
REFERENCE S50678
#authors Dietrich, F.S.
#submission submitted to the EMBL Data Library, December 1994
#description The sequence of S. cerevisiae cosmid 9163 and 9132.
#accession S50678
#molecule_type DNA
#residues 1-299 #label DIE
#cross-references EMBL:U18922; NID:g603405; PID:g603416; MIPS:YER175c

GENETICS
#map_position 5R
#length 299 #molecular_weight 34768 #checksum 6480

SUMMARY

Query Match 70.4%; Score 50; DB 2; Length 299;
Best Local Similarity 44.4%; Pred. No. 8.16e+00;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 129 EKFORSAYA 137
111:111:
1 OKYORAPYT 9

RESULT 7
ENTRY S28047 #type complete
TITLE TUB13 protein - potato
ORGANISM #formal_name Solanum tuberosum #common_name potato
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997

ACCESSIONS S28047
REFERENCE S28046
#authors Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flavell, A.J.
#journal Plant Mol. Biol. (1992) 20:641-651
#title Expression and sequence analysis of cDNAs induced during the early stages of tuberisation in different organs of the potato plant (Solanum tuberosum L.).
#accession S28047
#molecule_type mRNA
#residues 1-360 #label TAY
#cross-references EMBL:211680; NID:g21484; PID:g21485

GENETICS TUB13
#gene #cross-references EMBL:211680; NID:g21484; PID:g21485
SUMMARY #length 360 #molecular_weight 39726 #checksum 7941

Query Match 70.4%; Score 50; DB 2; Length 360;
Best Local Similarity 62.5%; Pred. No. 8.16e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 332 OKFRTPY 339
111:111:
1 OKYORAPY 8

RESULT 8
ENTRY S52662 #type complete
TITLE S-adenosylmethionine decarboxylase (SAMDC) - potato
ORGANISM #formal_name Solanum tuberosum #common_name potato
DATE 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
ACCESSIONS S52662
REFERENCE S52662
#authors Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.; Burch, L.R.; Davies, H.V.; Stark, M.J.R.; Kumar, A.
#journal Plant Mol. Biol. (1994) 26:327-338
#title Characterisation of the S-adenosylmethionine decarboxylase (SAMDC) gene of potato.

#accession S52662
#status preliminary
#molecule_type DNA
#residues 1-360 #label ARI
SUMMARY #length 360 #molecular-weight 39724 #checksum 8045

Query Match 70.4%; Score 50; DB 2; Length 360;
Best Local Similarity 62.5%; Pred. No. 8.16e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 332 OKYRPPY 339
1:1:111
QY 1 OKYRAPPY 8

RESULT 9
ENTRY B71854 #type complete
TITLE Helicobacter pylori (strain J99)
#formal_name Helicobacter pylori
#strain J99
#variety
12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
12-Feb-1999

ACCESSIONS B71854
REFERENCE A71800
#authors Alm, R.A.; Ling, I.S.L.; Moll, D.T.; King, B.L.; Brown, E.D.;
Dolg, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deLonge,
B.L.; Carmel, G.; Tummlino, P.J.; Caruso, A.;
Ulla-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
G.F.; Trust, T.J.
Nature (1999) 397:176-180
Genomic sequence comparison of two unrelated isolates of the
human gastric pathogen Helicobacter pylori.

#journal #title
#cross-references MUID:99120557
#accession B71854 preliminary
#status preliminary
#molecule_type DNA
#residues 1-321 #label ARN
#cross-references GB:AE001533; GB:AE001439; NID:94155636; PID:94155654
#experimental_source strain J99

GENETICS
#gene jhp1050
SUMMARY #length 321 #molecular-weight 36919 #checksum 5430

Query Match 69.0%; Score 49; DB 2; Length 321;
Best Local Similarity 62.5%; Pred. No. 1.27e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

204 OKYLRNPY 211
1:1:111
QY 1 OKYRAPPY 8

RESULT 10
ENTRY S65000 #type complete
TITLE Probable membrane protein YLR151c - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein L3325
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 01-Aug-1995 #sequence_revision 24-May-1996 #text_change
14-Nov-1997

ACCESSIONS S65000
REFERENCE S64987
#authors Rieger, M.; Mueller-Auer, S.; Brueckner, M.
#submission submitted to the Protein Sequence Database, May 1996
#accession S65000
#molecule_type DNA
#residues 1-340 #label RIE
#cross-references EMBL:Z73323; NID:91360581; PID:e245586; PID:91360582;
MIPS:YLR151C
#experimental_source strain S288C

GENETICS

#map_position 12R
KEYWORDS transmembrane protein
FEATURE
42-58
SUMMARY #length 340 #molecular-weight 39754 #checksum 3107

Query Match 69.0%; Score 49; DB 2; Length 340;
Best Local Similarity 50.0%; Pred. No. 1.27e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 22 KFKTRPYT 29
1:1:111
QY 2 KYORAPPY 9

RESULT 11
ENTRY B70676 #type complete
TITLE hypothetical protein RV3537 - Mycobacterium tuberculosis (strain H37Rv)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
15-Jan-1999

ACCESSIONS B70676
REFERENCE A70500
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
Skellon, S.; Squares, S.; Squires, R.; Sultoni, J.E.;
Taylor, K.; Whitehead, S.; Barrett, B.G.
Nature (1998) 393:537-544
Deciphering the biology of Mycobacterium tuberculosis from
the complete genome sequence.

#journal #title
#cross-references MUID:98295987
#accession B70676
#status preliminary; nucleic acid sequence not shown;
translation not shown

GENETICS
#gene RV3537
CLASSIFICATION #superfamily 3-oxosteroid 1-dehydrogenase homology
FEATURE
432-548
SUMMARY #domain 3-oxosteroid 1-dehydrogenase homology #label OXD
#length 563 #molecular-weight 60636 #checksum 7740

Query Match 69.0%; Score 49; DB 2; Length 563;
Best Local Similarity 87.5%; Pred. No. 1.27e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 280 KYORAPPY 287
1:1:111
QY 2 KYORAPPY 9

RESULT 12
ENTRY G64146 #type complete
TITLE yabH protein homolog H1071 - Haemophilus influenzae (strain Rd KW20)
ORGANISM #formal_name Haemophilus influenzae
DATE 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
15-May-1998

ACCESSIONS G64146
REFERENCE A64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;

Dougherty, B.A.; Merrick, J.M.; Mckenney, K.; Sutton, G.; Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Uterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C. Science (1995) 269:496-512

Genome random sequencing and assembly of Haemophilus influenzae Rd.

#journal #title

#cross-references M01D:9350630

#accession G64146

#status #molecule_type DNA

#residues 1-288 #label TIGR

#cross-references GB:U02713; GB:I42023; NID:g1573231; PID:g1573237; TIGR:H10271

CLASSIFICATION #superfamily_dnaa amino-terminal homology

TURE

222-288 #domain_dnaa amino-terminal homology #label DNJ

length 288 #molecular_weight 32523 #checksum 4197

Query Match 67.6%; Score 48; DB 2; Length 288; Best Local Similarity 62.5%; Pred. No. 1.98e+01; Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 191 OKYOGAY 198

11111111

1 OKYORAPY 8

RESULT 13

ENTRY C69217

TITLE #type complete

peptide chain release factor erf, subunit 1 -

ORGANISM Methanobacterium thermoautotrophicum (strain Delta H)

#formal_name Methanobacterium thermoautotrophicum

DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Aug-1998

ACCESSIONS C69217

REFERENCE A69000

#authors Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.; Huang, L.; Keagle, P.; Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Viscare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivani, N.; Caruso, A.; Bush, D.; Sater, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Shimer, G.; Goyal, A.; Pietrowski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. (1997) 179:7135-7155

Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis and comparative genomics.

#cross-references M01D:98037514

#accession C69217

#status preliminary: nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-407 #label MTH

#cross-references GB:AE000664; GB:AE000666; NID:g2621970; PID:g2621972

#experimental_source strain Delta H

GENETICS

#gene MTH878

#start_codon GTG

CLASSIFICATION #superfamily translation releasing factor erf-1

SUMMARY #length 407 #molecular_weight 46418 #checksum 8748

Query Match 67.6%; Score 48; DB 2; Length 407; Best Local Similarity 71.4%; Pred. No. 1.98e+01; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 321 KYORGTY 327

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2 KYORAPY 8

RESULT 14

ENTRY RRFLL

TITLE #type complete

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain precursor - brown alga (Pylaeella littoralis) chloroplast

ORGANISM #formal_name chloroplast Pylaeella littoralis

DATE 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 05-Dec-1997

ACCESSIONS S11964

REFERENCE S11964

#authors Assali, N.E.; Mache, R.; Loiseaux-de Goer, S.

#journal Plant Mol. Biol. (1990) 15:307-315

#title Evidence for a composite phylogenetic origin of the plastid genome of the brown alga Pylaeella littoralis (L.) Kjellm.

#cross-references M01D:91355877

#accession S11964

#molecule_type DNA

#residues 1-488 #label ASS

#cross-references EMBL:X55372; NID:g14186; PID:g14187

GENETICS

#gene rbcL

#genome chloroplast

CLASSIFICATION #superfamily ribulose-bisphosphate carboxylase large chain

KEYWORDS Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; chloroplast; magnesium; monooxygenase; photorespiration; photosynthesis

FEATURE

16-488

179,337

205

207

SUMMARY #length 488 #molecular_weight 54124 #checksum 1178

Query Match 67.6%; Score 48; DB 1; Length 488; Best Local Similarity 55.6%; Pred. No. 1.98e+01; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 253 OMYERAPYA 261

11111111

1 OKYORAPYT 9

RESULT 15

ENTRY RRFLL

TITLE #type complete

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain precursor - brown alga (Ectocarpus siliculosus) chloroplast

ORGANISM #formal_name chloroplast Ectocarpus siliculosus

DATE 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Dec-1997

ACCESSIONS S13123

REFERENCE S13123

#authors Valentini, K.; Zetsche, K.

#journal Plant Mol. Biol. (1990) 15:575-584

#title Rubisco genes indicate a close phylogenetic relation between the plastids of Chromophyta and Rhodophyta.

#cross-references M01D:91338696

#accession S13123

#molecule_type DNA

#residues 1-488 #label VAL

#cross-references EMBL:X52503; NID:g11543; PID:g11544

COMMENT In addition to lys-205, another lysine, it is not certain which, may be the site of autocatalytic carboxylation.

GENETICS

#genome chloroplast

CLASSIFICATION #superfamily ribulose-bisphosphate carboxylase large chain

KEYWORDS Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; chloroplast; magnesium; monooxygenase;

FEATURE photorespiration; photosynthesis

16-488

179,337

205

SUMMARY

#product ribulose-bisphosphate carboxylase large chain
#status predicted #label MAR
#active-site Lys (ribulose-bisphosphate-binding) #status
predicted
#binding-site carbon dioxide (Lys) (covalent) (by
Rubisco activase) #status predicted
#binding-site magnesium (Asp) #status predicted
#length 488 #molecular-weight 53904 #checksum 2273

Query Match

Best Local Similarity 67.6%; Score 48; DB 1; Length 488;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 253 OMVEBAEYA 261

OY 1 OKYORAPYT 9

Search completed: Thu Sep 2 11:31:35 1999
Job time : 13 secs.

MORSE
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:33:01 1999; Maspar time 1.34 Seconds
68.332 Million cell updates/sec
Modular output not generated.

Title: >US-08-599-226-13
Description: (1-9) from US08599226.pep
Perfect Score: 71
Sequence: 1 OKYORAPYT 9

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: a-issued
1:5A-COMB 2:5B-COMB 3:PCT9-COMB 4:backfiles1

Statistics: Mean 15.728; Variance 47.259; scale 0.333

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	49	69.0	107	3	PCT-US95-0	Sequence 87, Applicat	4.53e+01
2	49	69.0	107	1	US-08-276-	Sequence 87, Applicat	4.53e+01
3	49	69.0	107	2	US-08-899-	Sequence 87, Applicat	4.53e+01
4	49	69.0	107	2	US-08-899-	Sequence 87, Applicat	4.53e+01
5	47	66.2	23	3	PCT-US95-0	Sequence 9, Applicatio	7.48e+01
6	47	66.2	107	3	PCT-US95-0	Sequence 8, Applicatio	7.48e+01
7	47	66.2	107	2	US-08-561-	Sequence 8, Applicatio	7.48e+01
8	47	66.2	107	2	US-08-561-	Sequence 8, Applicatio	7.48e+01
9	47	66.2	107	3	PCT-US95-0	Sequence 6, Applicatio	7.48e+01
10	47	66.2	107	2	US-08-652-	Sequence 34, Applicati	7.48e+01
11	47	66.2	107	2	US-08-651-	Sequence 6, Applicatio	7.48e+01
12	47	66.2	108	2	US-08-070-	Sequence 7, Applicatio	7.48e+01
13	47	66.2	480	1	US-07-882-	Sequence 2, Applicatio	7.48e+01
14	47	66.2	480	3	PCT-US95-0	Sequence 2, Applicatio	7.48e+01
15	46	64.8	269	1	US-08-202-	Sequence 4, Applicatio	9.58e+01
16	45	63.4	419	1	US-08-440-	Sequence 2, Applicatio	1.23e+02
17	45	63.4	942	1	US-08-439-	Sequence 3, Applicatio	1.23e+02
18	45	63.4	942	1	US-08-141-	Sequence 14, Applicati	1.23e+02
19	45	63.4	942	1	US-08-541-	Sequence 14, Applicati	1.23e+02
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21	44	62.0	52	2	US-08-162-	Sequence 43, Applicati	1.57e+02
22	44	62.0	109	2	US-08-162-	Sequence 23, Applicati	1.57e+02
23	44	62.0	109	3	PCT-US93-0	Sequence 23, Applicati	1.57e+02

24	44	62.0	364	1	US-08-318-	Sequence 6, Applicatio	1.57e+02
25	44	62.0	423	2	US-08-290-	Sequence 11, Applicati	1.57e+02
26	44	62.0	423	2	US-08-290-	Sequence 10, Applicati	1.57e+02
27	44	62.0	430	2	US-08-290-	Sequence 9, Applicatio	1.57e+02
28	44	62.0	458	2	US-08-336-	Sequence 24, Applicati	1.57e+02
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35	44	62.0	1572	2	US-08-290-	Sequence 5, Applicatio	1.57e+02
36	44	62.0	1708	2	US-08-508-	Sequence 2, Applicatio	1.57e+02
37	44	62.0	1708	2	US-08-493-	Sequence 2, Applicatio	1.57e+02
38	44	62.0	3056	2	US-08-629-	Sequence 3, Applicatio	1.57e+02
39	44	62.0	3056	2	US-08-508-	Sequence 8, Applicatio	1.57e+02
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41	43	60.6	354	1	US-08-753-	Sequence 2, Applicatio	2.00e+02
42	43	60.6	354	2	US-08-984-	Sequence 2, Applicatio	2.00e+02
43	43	60.6	372	1	US-08-753-	Sequence 3, Applicatio	2.00e+02
44	43	60.6	372	2	US-08-984-	Sequence 3, Applicatio	2.00e+02
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ALIGNMENTS

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CC	Sequence 87, Application PC/TUS9508743				
CC	GENERAL INFORMATION:				
CC	APPLICANT:				
CC	TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES				
CC	NUMBER OF SEQUENCES: 170				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	OPERATING SYSTEM: IBM PC compatible				
CC	SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: PCT/US95/08743				
CC	FILING DATE: 11-JUL-1995				
CC	PRIOR APPLICATION DATA:				
CC	APPLICATION NUMBER: US 08/276,852				
CC	FILING DATE: 18-JUL-1994				
CC	INFORMATION FOR SEQ ID NO: 87:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 107 amino acids				
CC	TYPE: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
CC	SEQUENCE 107 AA: 11654 MW, 62438 CN,				
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Query Match 69.0%; Score 49; DB 3; Length 107;
Best local Similarity 55.6%; Pred. No. 4.53e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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XX XX Sequence 87, Application US/08276852
DE CC
CC CC Sequence 87, Application US/08276852
CC CC Patent No. 5652138
CC CC GENERAL INFORMATION:
CC CC APPLICANT: Burton, Dennis R
CC CC APPLICANT: Barbas, Carlos F
CC CC APPLICANT: Lerner, Richard A
CC CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC CC NUMBER OF SEQUENCES: 170
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: The Scripps Research Institute, Office of
CC CC ADDRESSEE: Patent Counsel
CC CC STREET: 10666 NO. 5652138th Torrey Pines Road, Suite 220,
CC CC STREET: Mail Drop TPC8
CC CC CITY: La Jolla
CC CC STATE: CA
CC CC COUNTRY: USA
CC CC ZIP: 92037
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/08/276,852
CC CC FILING DATE: 18-JUL-1994
CC CC CLASSIFICATION: 514
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CC CC APPLICATION NUMBER: US 08/178,302
CC CC FILING DATE: 30-SEP-1993
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: US 07/954,148
CC CC FILING DATE: 30-SEP-1992
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Fitting, Thomas
CC CC REGISTRATION NUMBER: 34,163
CC CC REFERENCE/DOCKET NUMBER: SCRI452P
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: 619-554-2937
CC CC TELEFAX: 619-554-6312
CC CC INFORMATION FOR SEQ ID NO: 87:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 107 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
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SQ
Db      88 QOYHSSPYT 96
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    1 OKYQRAYPT 9
Oy
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XX AC xxxxxx
XX DT
XX DE Sequence 87, Application US/08899575
XX CC
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XX CC Patent No. 5804440
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CC      CC      GENERAL INFORMATION:  
CC      CC      APPLICANT: Burton, Dennis R  
CC      CC      APPLICANT: Barbas, Carlos F  
CC      CC      APPLICANT: Lerner, Richard A  
CC      CC      TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
CC      CC      TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
CC      CC      NUMBER OF SEQUENCES: 170  
CC      CC      CORRESPONDENCE ADDRESS:  
CC      CC      ADDRESSEE: The Scripps Research Institute, Office of  
CC      CC      ADDRESSEE: Patent Counsel  
CC      CC      STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
CC      CC      STREET: Mail Drop TPC8  
CC      CC      City: La Jolla  
CC      CC      STATE: CA  
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CC      CC      COMPUTER READABLE FORM:  
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CC      CC      APPLICATION NUMBER: US 07/954,148  
CC      CC      FILING DATE: 30-SEP-1992  
CC      CC      ATTORNEY/AGENT INFORMATION:  
CC      CC      NAME: Fitting, Thomas  
CC      CC      REGISTRATION NUMBER: 34,163  
CC      CC      REFERENCE/DOCKET NUMBER: SCRI452P  
CC      CC      TELECOMMUNICATION INFORMATION:  
CC      CC      TELEPHONE: 619-554-2937  
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CC      CC      SEQUENCE CHARACTERISTICS:  
CC      CC          LENGTH: 107 amino acids  
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CC      CC      SEQUENCE 107 AA; 11654 MM; 62438 CN;  
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Best Local Similarity 55.6%; Pred.No. 4.53e+01;  
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Db      88 QOYHSPPT 96  
QY      1 OKTORAPPT 9  
  
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DT  
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DE      Sequence 87, Application US/08899575  
CX  
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CC      Patent No. 5770440  
CC      GENERAL INFORMATION:  
CC      APPLICANT: Burton, Dennis R  
CC      APPLICANT: Barbas, Carlos F  
CC      APPLICANT: Lerner, Richard A  
CC      TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
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CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC CC
CC SEQUENCE 107 AA; 11843 MW; 64131 CN;
SQ

Query Match 66.2%; Score 47; DB 3; Length 107;
Best Local Similarity 66.7%; Pred. No. 7.48e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

89 OQYOSLPYT 97
| | | | |
1 OYGRAPYT 9

RESULT 7 STANDARD; PRT; 107 AA.
ID US-08-561-521-8
XX AC xxxxxx
XX DT
XX DE
XX Sequence 8, Application US/08561521
XX
CC Sequence 8, Application US/08561521
CC Patent No. 5840299
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourle and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/561,521
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/186,269A
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC
CC

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[illegible]

RESULT 9
ID PCT-US95-01219-6 STANDARD; PRT: 107 AA.
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AC xxxxxx
XX
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XX
DE Sequence 6, Application PC/TUS9501219
XX
CC Sequence 6, Application PC/TUS9501219
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/186,269
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11746 MW: 66196 CN;
SQ
Query Match 66.2%; Score 47; DB 3; Length 107;
Best Local Similarity 66.7%; Pred. No. 7.48e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 89 QOYOSLPT 97
QY 1 QKYORAPYT 9
ID US-08-652-558-34 STANDARD; PRT: 107 AA.
XX
AC xxxxxx
XX
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XX
DE Sequence 34, Application US/08652558
XX
CC Sequence 34, Application US/08652558

CC Patent No. 5861155
CC GENERAL INFORMATION:
CC APPLICANT: LIN, AUGUSTINE YEE-THARN
CC TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 52
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BANNER & WITCOFF
CC STREET: 75 STATE STREET, 23RD FLOOR
CC CITY: BOSTON
CC STATE: MASSACHUSETTS
CC COUNTRY: USA
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Wordperfect 6.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/652,558
CC FILING DATE: JUNE 6, 1996
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/IB94/00387
CC FILING DATE: NOVEMBER 21, 1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: YANKWICH, LEON R.
CC REGISTRATION NUMBER: 30,237
CC REFERENCE/DOCKET NUMBER: 95,497-L
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617-345-9100
CC TELEFAX: 617-345-9111
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11746 MW: 66196 CN;
SQ
Query Match 66.2%; Score 47; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 7.48e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 89 QOYOSLPT 97
QY 1 QKYORAPYT 9
ID US-08-561-521-6 STANDARD; PRT: 107 AA.
XX
AC xxxxxx
XX
XX
XX
DE Sequence 6, Application US/08561521
XX
CC Sequence 6, Application US/08561521
CC Patent No. 5840299
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California

CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/561,521
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US/08/186,269A
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11746 MW; 66196 CN;
SQ

Query Match 66.2%; Score 47; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 7.48e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 89 OQYOSLPYT 97
1 111111
1 OKTORAPYT 9
QY

RESULT 12
ID US-08-070-116A-7 STANDARD; PRT: 108 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 7, Application US/08070116A
Sequence 7, Application US/08070116A
Patent No. 5885573
GENERAL INFORMATION:
CC APPLICANT: Zivlin, Robert A.
CC APPLICANT: Jolliffe, Linda K.
CC APPLICANT: Bluestone, Jeffrey A.
CC TITLE OF INVENTION: Methods and Materials for Modulation
CC TITLE OF INVENTION: Of the Immuno-suppressive Activity and
CC TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
CC NUMBER OF SEQUENCES: 18
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P.O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: United States of America
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WordPerfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/070,116A
CC FILING DATE: 01-JUN-1993

CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wilson, Mark B.
CC REGISTRATION NUMBER: 37,259
CC REFERENCE/DOCKET NUMBER: ARCD:082
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-3000
CC TELEFAX: (512) 474-7577
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11902 MW; 66412 CN;
SQ

Query Match 66.2%; Score 47; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 7.48e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 89 OQYOSLPYT 97
1 111111
1 OKTORAPYT 9
QY

RESULT 13
ID US-07-882-292-2 STANDARD; PRT: 480 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 2, Application US/07882292
Sequence 2, Application US/07882292
Patent No. 5324638
GENERAL INFORMATION:
CC APPLICANT: Tao, Wufan
CC APPLICANT: Lai, Eseng
CC TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC ACIDS
CC TITLE OF INVENTION: ENCODING SAME AND USES THEREOF
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: John P. White
CC STREET: c/o Cooper and Dunham, 30 Rockefeller
CC STREET: Plaza
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10112
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.24
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/882,292
CC FILING DATE: 19920513
CC CLASSIFICATION: 514
CC ATTORNEY/AGENT INFORMATION:
CC NAME: White, John P.
CC REGISTRATION NUMBER: 28,678
CC REFERENCE/DOCKET NUMBER: 41472
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212-977-9550
CC TELEFAX: 212-664-0525
CC TELEEX: 422523 COOP UI
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 480 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear

CC MOLECULE TYPE: protein
SQ SEQUENCE 480 AA; 51591 MW; 1261073 CN;

Query Match
Best Local Similarity 50.0%; Score 47; DB 1; Length 480;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 169 KYKPPFT 176

OY 2 KYORAPYT 9

RESULT 14
ID PCT-US93-04102-2 STANDARD; PRT; 480 AA.

AC xxxxxx

Sequence 2, Application PC/TUS9304102

GENERAL INFORMATION:
APPLICANT: Tao, Wufan

APPLICANT: Lai, Eseng

TITLE OF INVENTION: BRAIN TRANSCRIPTION FACTOR, NUCLEIC
ACID TITLE OF INVENTION: ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:
ADDRESSEE: John P. White

STREET: C/O Cooper and Dunham, 30 Rockefeller Plaza
CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/TUS93/04102

FILING DATE: 19930430

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/882,292

FILING DATE: 13-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41472A-PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550

TELEFAX: 212-664-0525

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 480 amino acids
TYPE: AMINO ACID

MOLECULE TYPE: linear
SEQUENCE 480 AA; 51591 MW; 1261073 CN;

Query Match
Best Local Similarity 50.0%; Score 47; DB 3; Length 480;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

ID US-08-202-857-4 STANDARD; PRT; 269 AA.

AC xxxxxx

Sequence 4, Application US/08202857

Sequence 4, Application US/08202857

Patent No. 5635345

GENERAL INFORMATION:
APPLICANT: Scherier, Klaus

APPLICANT: Bureau, Jean-Paul

APPLICANT: Bey, Fay al

TITLE OF INVENTION: Diagnostic Method

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:
ADDRESSEE: PRO-SOMA SARL C/O AKZO PHARMA

STREET: 1330-A PICCARD DRIVE

CITY: ROCKVILLE

STATE: MARYLAND

COUNTRY: USA

ZIP: 20850-4377

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,857

FILING DATE: 11-JUNE-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/860,492

FILING DATE: 10-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: BOBROWICZ, DONNA

REGISTRATION NUMBER: 32,196

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-258-5200

TELEFAX: 301-977-1403

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids
TYPE: amino acid

MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: human

SEQUENCE 269 AA; 30227 MW; 341084 CN;

Query Match
Best Local Similarity 62.5%; Score 46; DB 1; Length 269;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

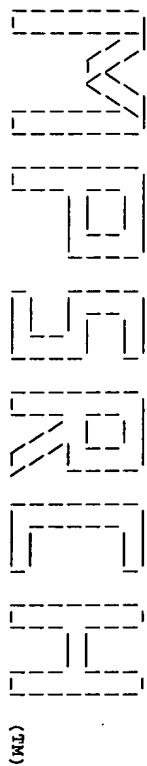
Db 127 OYGRPPY 134

OY 1 OYORAPY 8

Search completed: Thu Sep 2 11:33:08 1999

Job time : 7 secs.

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MSearch.PP protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:30:44 1999; Maspar time 3.35 Seconds

57.200 Million cell updates/sec

Similar output not generated.

Title: >US-08-599-226-13
Description: (1-9) from US08599226.pep
Perfect Score: 71
Sequence: 1 OKYORAPYR 9

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 16.742; Variance 48.748; scale 0.343

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	71	100.0	9 27	W27572	Anti-TNF-alpha antio	2.65e-01
2	64	80.1	9 27	W27575	Anti-TNF-alpha antio	1.84e+00
3	61	85.9	9 27	W27584	Anti-TNF-alpha antio	4.15e+00
4	61	85.9	9 27	W27571	Anti-TNF-alpha antio	4.15e+00
5	61	85.9	107 27	W27568	Anti-TNF-alpha antio	4.15e+00
6	59	83.1	9 27	W27579	Anti-TNF-alpha antio	7.09e+00
7	58	81.7	9 27	W27585	Anti-TNF-alpha antio	9.26e+00
8	56	78.9	9 27	W27582	Anti-TNF-alpha antio	1.57e+01
9	54	76.1	9 27	W27574	Anti-TNF-alpha antio	2.66e+01
10	52	73.2	9 27	W27578	Anti-TNF-alpha antio	4.47e+01
11	52	73.2	9 27	W27573	Anti-TNF-alpha antio	4.47e+01
12	51	71.8	9 27	W27570	Anti-TNF-alpha antio	5.78e+01
13	50	70.4	9 27	W27583	Anti-TNF-alpha antio	7.46e+01
14	50	70.4	9 27	W27582	Anti-TNF-alpha antio	7.46e+01
15	50	70.4	360 13	R75006	Tomato S-adenosyl-met	7.46e+01
16	49	69.0	9 27	W27577	Anti-TNF-alpha antio	9.62e+01

17	49	69.0	9 27	W27576	Anti-TNF-alpha antio	9.62e+01
18	49	69.0	107 19	W01266	VL region of HIV neut	9.62e+01
19	49	69.0	107 10	R54308	Anti-HIV gp120 immu	9.62e+01
20	48	67.6	67 31	W28077	Amino acid sequence	1.24e+02
21	47	66.2	107 39	W87455	Humanised anti-alpha	1.59e+02
22	47	66.2	107 15	R81329	Human REI antibody 11	1.59e+02
23	47	66.2	107 24	W22422	Humanised alpha-4 int	1.59e+02
24	47	66.2	107 15	R81322	Humanized VLA-4 antib	1.59e+02
25	47	66.2	108 14	R65163	Human REI monoclonal	1.59e+02
26	47	66.2	108 5	R28745	Light chain variable	1.59e+02
27	47	66.2	364 27	W27224	Human growth factor H	1.59e+02
28	47	66.2	364 35	W71683	Human growth and dif	1.59e+02
29	46	64.8	10 25	W24159	Peanut allergen Ara h	2.04e+02
30	46	64.8	10 25	W24190	Peanut allergen Ara h	2.04e+02
31	46	64.8	157 25	W24164	Peanut allergen Ara h	2.04e+02
32	46	64.8	157 25	W24153	Peanut allergen Ara h	2.04e+02
33	46	64.8	263 4	R22957	Human proteasome comp	2.04e+02
34	46	64.8	263 1	R22666	Protein used to raise	2.04e+02
35	46	64.8	487 2	P91007	Beta-mannase of alk	2.04e+02
36	45	63.4	170 8	R42371	Prod. of ORFs of plas	2.61e+02
37	45	63.4	469 3	R15510	Tomato ACC synthase	2.61e+02
38	45	63.4	509 29	W34847	Lys-glycylalanyl high mo	2.61e+02
39	45	63.4	970 14	R72458	Porphyromonas gingiva	2.61e+02
40	45	63.4	1358 17	R96032	P. gingivalis hagd ha	2.61e+02
41	45	63.4	1358 36	W69494	Haemagglutinin protei	3.34e+02
42	44	62.0	249 39	W84049	Rice OSMAD57 protein	3.34e+02
43	44	62.0	316 39	W89783	Staphylococcus aureus	3.34e+02
44	44	62.0	3026 22	W19676	ATM mutant 2377del190	3.34e+02
45	44	62.0	3056 23	W19733	Cell cycle checkpoint	3.34e+02

ALIGNMENTS

RESULT	ID	Standard: peptide: 9 AA.
1	W27572	
AC	W27572	
DE	19-MAR-1998 (first entry)	
KW	Anti-TNF-alpha antibody light chain CDR3.	
KW	Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;	
KW	light chain; complementarity determining region 3; inhibition;	
KW	treatment; sepsis; disease; autoimmune disease; infectious disease;	
KW	malnutrition; pulmonary disorder; intestinal disorder; hepatitis;	
KW	cardiac disorder; inflammatory bone disorder; reperfusion injury;	
KW	bone resorption disease; coagulation disturbance; burn; ELAM-1;	
KW	keloid formation; scar tissue formation; pyrexia; HIVEC;	
KW	periodontal disease; obesity; radiation toxicity;	
KW	endothelial cell leukocyte adhesion molecule-1;	
OS	human umbilical vein endothelial cell.	
PN	MO9729131-AI.	
PD	14-AUG-1997.	
PF	10-FEB-1997; U02219.	
PR	25-NOV-1996; US-031476.	
PR	09-FEB-1996; US-599226.	
PA	(BADI) BASE AG.	
PI	Allen DJ, Hoogenboom HRJM, Kaymakcan Z, Labkovsky B,	
PI	Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,	
PI	Sallied JG, Schoemhaut D, Vaughan TV, White M, Willton AJ;	
DR	WPI; 97-415302/38.	
PT	High affinity antibodies against human TNF alpha - useful to inhibit	
PT	TNF alpha activity, e.g. to treat autoimmune diseases and cancer	
PS	Claim 20: Page 68: 102pp; English.	
CC	The present sequence is a novel anti-human tumour necrosis	
CC	factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity	
CC	determining region 3 (CDR3).	
CC	The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or	
CC	less and has a Koff rate constant of 1x10 power -3 s power -1 or	
CC	less (both determined by surface plasmon resonance), and	
CC	neutralises human TNF-alpha cytotoxicity in a standard in vitro	
CC	L229 assay with an IC50 of 1x10 power -7 M or less. The Ab, which	
CC	inhibits TNF-alpha activity, can be used to treat sepsis,	
CC	autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid	
CC	spondylitis, osteoarthritis, gouty arthritis, allergy, multiple	

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 100.0%; Score 71; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2,65e-01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qKyrarpyt 9
 ||| |||||
 QY 1 OKYQRAPT 9

RESULT 2
 W27575 standard; peptide; 9 AA.

AC W27575:
 DE 19-MAR-1998 (first entry)
 KW Anti-TNF-alpha antibody; light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-AL.

PD 14-AUG-1997: U02219.
 PF 10-FEB-1997: US-031476.
 PR 25-NOV-1996: US-599226.
 PA 09-FEB-1996: US-599226.

PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 68; 102pp: English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 90.1%; Score 64; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.84e+00;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 qKyrarpyt 9
 ||| |||||
 QY 1 OKYQRAPT 9

RESULT 3
 W27584 standard; peptide; 9 AA.

AC W27584:
 DE 19-MAR-1998 (first entry)
 KW Anti-TNF-alpha antibody; light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997: U02219.
 PF 10-FEB-1997: US-031476.
 PR 25-NOV-1996: US-599226.
 PA 09-FEB-1996: US-599226.

PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 72; 102pp: English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 85.9%; Score 61; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 4.15e+00;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qKyrarpyt 9
 ||| |||||
 QY 1 OKYQRAPT 9

RESULT 4
 W27571 standard; peptide; 9 AA.

AC W27571:
 DE 19-MAR-1998 (first entry)
 KW Anti-TNF-alpha antibody; light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PS High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 85.98; Score 61; DB 27; Length 9;
 Best Local Similarity 77.88; Pred. No. 4.15e+00;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 qkynrpya 9
 1 111111:
 1 OKTORAPYT 9

RESULT 5
 ID W2568 standard; Protein: 107 AA.
 AC W2568:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
 KW light chain; variable region; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.

PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 DR N-PSDB; T88403.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 15; Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 107 AA:
 SQ

Query Match 85.98; Score 61; DB 27; Length 107;
 Best Local Similarity 77.88; Pred. No. 4.15e+00;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DB 89 qkynrpyt 97
 1 111111:
 1 OKTORAPYT 9

RESULT 6
 ID W2579 standard; peptide: 9 AA.
 AC W2579:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC Sequence 107 AA:
 SQ

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption diseases,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 83.1%; Score 59; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 7.09e+00;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gqynrpy 8
 ||| ||||
 QY 1 OKYGRAPY 8

RESULT 7
 ID W27585 standard; peptide: 9 AA.
 AC W27585;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PT (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 72; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 81.7%; Score 58; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 9.26e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 gqynrpy 9
 ||| ||||
 QY 1 OKYGRAPYT 9

RESULT 8
 ID W27562 standard; peptide: 9 AA.
 AC W27562;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PT (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9: Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 78.9%; Score 56; DB 27; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.57e+01;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkyrsapyt 8
| | | | |
QY 1 QXQYRAPYT 8

RESULT 9
ID W27574 standard; peptide: 9 AA.

AC W27574;
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVBC;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
Homo sapiens.

MO9729131-1.

PD 14-AUG-1997.
PF 10-FEB-1997; 002219.
PR 25-NOV-1996; US-031476.
PW 09-FEB-1996; US-599226.

W27

PA (BAD1) BASP AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
PI Manakovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 69; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVBC).
CC Sequence 9 AA;

QY 1 QXQYRAPYT 9

Query Match 76.1% Score 54; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 2.66e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkyrsapyt 9
| | | | |
QY 1 QXQYRAPYT 9

RESULT 10
ID W27578 standard; peptide: 9 AA.

AC W27578;

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVBC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
Homo sapiens.

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVBC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
Homo sapiens.

MO9729131-1.

PD 14-AUG-1997.
PF 10-FEB-1997; 002219.
PR 25-NOV-1996; US-031476.
PW 09-FEB-1996; US-599226.

W27

PA (BAD1) BASP AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
PI Manakovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 70; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVBC).
CC Sequence 9 AA;

QY 1 QXQYRAPYT 9

Query Match 73.2% Score 52; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.47e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkyrsapyt 9
| | | | |
QY 1 QXQYRAPYT 9

RESULT 11
ID W27573 standard; peptide: 9 AA.

AC W27573;

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVBC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
Homo sapiens.

MO9729131-1.

PD 14-AUG-1997.

PF 10-FEB-1997; 002219.

PW 09-FEB-1996; US-031476.

PA (BAD1) BASP AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
PI Manakovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 70; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVBC).
CC Sequence 9 AA;

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA.

Query Match 73.2%; Score 52; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 4.47e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkysappt 9
 ||| |||
 OY 1 OKYORAPYT 9

RESULT 12
 ID W27570 standard; peptide: 9 AA.
 AC W27570;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain: complementarity determining region 3; inhibition;
 KM treatment: sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 KM Homo sapiens.
 OS WO9729131-A1.
 PN 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 67; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 71.8%; Score 51; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 5.78e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkysappt 9
 ||| |||
 OY 1 OKYORAPYT 9

RESULT 13
 ID W27583 standard; peptide: 9 AA.
 AC W27583;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain: complementarity determining region 3; inhibition;
 KM treatment: sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 KM Homo sapiens.
 OS WO9729131-A1.
 PN 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 72; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 70.4%; Score 50; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 7.46e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 gkylsapyt 9
 ||| |||
 QY 1 OKYORAPYT 9

RESULT 14
 ID W27582; standard; peptide: 9 AA.
 AC W27582;

DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 CC light chain; complementarity determining region 3; inhibition;
 CC treatment; sepsis; disease; autoimmune disease; infectious disease;
 CC malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 CC cardiac disorder; inflammatory bone disorder; reperfusion injury;
 CC keloid formation; scar tissue formation; pyrexia; ELAM-1;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PA 09-FEB-1996: US-599226.
 PI (BADI) BASF AG.

MS

PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kolff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 70.4%; Score 50; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.46e+01;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 gkynsapyt 9
 ||| |||
 QY 1 OKYORAPYT 9

RESULT 15
 ID R75006; standard; Protein: 360 AA.
 AC R75006;

DE 01-NOV-1995 (first entry)
 DT Tomato S-adenosyl-methionine-decarboxylase.
 KW SAM-decarboxylase; transgenic plant; senescence;
 KW fruit ripening.
 CC Lycopersicon esculentum.
 OS WO9514092-A.
 PN 26-MAR-1995.
 PD 17-NOV-1994: G02532.
 PR 18-NOV-1993: GB-023771.
 PA (ZENEC) ZENEC LTD.
 PI Fray RG, Grierson D, Wallace AD;
 DR WPI: 95-200382/26.
 DR N-PSDB: Q90508.

PT New S-adenosyl methionine-decarboxylase DNA - used to transform
 PT plants to modify senescence and fruit-ripening characteristics.
 PS Disclosure: Page 25-26; 34pp; English.
 CC DNA encoding SAM-decarboxylase is used to transform plants.
 CC Modifying SAM-decarboxylase (SAM) gene expression in transgenic
 CC plants modifies senescence or fruit-ripening characteristics.
 CC Increased SAMD levels reduce ethene production by the plant, and
 CC decreased SAMD levels increase ethene production by the plant.
 SQ Sequence 360 AA;

Query Match 70.4%; Score 50; DB 13; Length 360;
 Best Local Similarity 62.5%; Pred. No. 7.46e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 332 gkytrpy 339
 ||| |||
 QY 1 OKYORAPYT 8

Search completed: Thu Sep 2 11:31:05 1999
 Job time : 21 secs.

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 WIRENET (TM)

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MSPrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:34:27 1999; MasPar time 3.36 Seconds
 Molecular output not generated. 56.961 Million cell updates/sec

Title: >US-08-599-226-14
 Description: (1-9) from US08599226.pep
 Perfect Score: 63
 Sequence: 1 OKXSSAPRT 9

Scoring table: PAM 150
 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 15.851; Variance 49.026; scale 0.323

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	63	100.0	9	27	W27573	Anti-TNF-alpha antibo
2	61	96.8	9	27	W27578	Anti-TNF-alpha antibo
3	60	95.2	9	27	W27574	Anti-TNF-alpha antibo
4	57	90.5	9	27	W27570	Anti-TNF-alpha antibo
5	56	88.9	9	27	W27583	Anti-TNF-alpha antibo
6	56	88.9	9	27	W27582	Anti-TNF-alpha antibo
7	55	87.3	9	27	W27577	Anti-TNF-alpha antibo
8	55	87.3	9	27	W27576	Anti-TNF-alpha antibo
9	55	87.3	9	27	W27575	Anti-TNF-alpha antibo
10	52	82.5	9	27	W27571	Anti-TNF-alpha antibo
11	52	82.5	9	27	W27584	Anti-TNF-alpha antibo
12	52	82.5	9	27	W27572	Anti-TNF-alpha antibo
13	52	82.5	9	27	W27568	Anti-TNF-alpha antibo
14	51	81.0	9	27	R38672	Anti-TNF-alpha antibo
15	50	79.4	9	27	W27579	Anti-TNF-alpha antibo
16	50	79.4	9	27	W27580	Anti-TNF-alpha antibo

17	50	79.4	107	28	W31726	Alpha light chain ami
18	50	79.4	533	9	R44617	Human retinol binding
19	49	77.8	9	27	W27585	Anti-TNF-alpha antibo
20	49	77.8	9	23	W24551	CDR #3 of r101-2 ligh
21	49	77.8	108	10	R54316	Anti-HIV gp120 immuno
22	49	77.8	108	19	W01278	VL region of HIV neut
23	49	77.8	124	23	W24539	Immunoglobulin r101-2
24	48	76.2	107	19	W01266	VL region of HIV neut
25	48	76.2	107	10	R54308	Anti-HIV gp120 immuno
26	48	76.2	109	10	R50218	HSV glycoprotein F bl
27	48	76.2	357	9	R44618	Human retinol binding
28	48	76.2	653	33	W69845	Amino acid sequence o
29	47	74.6	9	27	W27562	Anti-TNF-alpha antibo
30	46	73.0	108	15	R75624	VL Feb H4L3-4 binds t
31	46	73.0	109	9	R47041	Sequence of the conse
32	46	73.0	109	6	R30764	Consensus humanised a
33	46	73.0	780	14	R72798	Phospholipase D.
34	46	73.0	808	21	W32911	Castor bean phospholip
35	46	73.0	812	21	W06134	Phospholipase D prote
36	46	73.0	812	14	R72797	Phospholipase D.
37	46	73.0	812	26	W25675	Phospholipase D.
38	45	71.4	90	16	R80079	Mouse derived light c
39	45	71.4	90	16	R80078	Mouse derived light c
40	45	71.4	92	39	W95480	Mouse derived RT3 pha
41	45	71.4	92	39	W95476	Mouse derived RT3 pha
42	45	71.4	107	25	W27121	Murine antibody light
43	45	71.4	121	19	R98942	Humanised anti-CD38 m
44	45	71.4	145	39	W87593	Antibody 11D10 light
45	45	71.4	245	19	R98943	Humanised anti-CD38 m

ALIGNMENTS

RESULT 1
 ID W27573 standard; peptide: 9 AA.
 AC W27573:
 DE 19-MAR-1998 (first entry)
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226. *nm21*
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakcalan Z, Labkovsky B,
 PI Manoyevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Sallfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 100.0%; Score 63; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.60e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|||||
 QY 1 QKSSAPPT 9

RESULT 2
 W27578 standard; peptide: 9 AA.

AC W27578;
 DE 19-MAR-1998 (first entry)
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997;
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BA01) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manokovich JA, McGuinness BT, Roberts AJ, Sakoraitis P,
 PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: page 70; 102pp; English.

The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 96.8%; Score 61; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.37e+00;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 qkysappt 9
 |||:|||||
 QY 1 QKSSAPPT 9

RESULT 3
 W27574 standard; peptide: 9 AA.

AC W27574;
 DE 19-MAR-1998 (first entry)
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997;
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BA01) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manokovich JA, McGuinness BT, Roberts AJ, Sakoraitis P,
 PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20: page 69; 102pp; English.

The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 95.2%; Score 60; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 5.67e+00;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|||||
 QY 1 QKSSAPPT 9

RESULT 4
 W27570 standard; peptide: 9 AA.

AC W27570;
 DE 19-MAR-1998 (first entry)
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain: complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476. *ms*
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 CC Claim 20; page 67; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 CC Sequence 9 AA;
 SQ

Query Match 90.5% Score 57; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.22e+01; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 0;
 QY 1 qkysapya 9
 1 QKYSAPYT 9
 RESULT 5
 ID W27582 standard; peptide: 9 AA.
 AC W27583;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.

PR 25-NOV-1996; US-031476. *ms*
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 CC Claim 20; page 72; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 CC Sequence 9 AA;
 SQ

Query Match 88.9% Score 56; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.58e+01; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1;
 DB 1 qkysapya 9
 1 QKYSAPYT 9
 RESULT 6
 ID W27582 standard; peptide: 9 AA.
 AC W27582;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476. *ms*
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 CC Claim 20; page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 88.98; Score 56; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.58e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsdyt 9
 ||:|||||
 1 QKYSAPYT 9

RESULT 7
 ID W2577 standard; peptide: 9 AA.
 AC W2577;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PF 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankevlch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR MPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 87.38; Score 55; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.04e+01;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsdyt 8
 ||:|||||
 1 QKYSAPY 8

RESULT 8
 ID W2576 standard; peptide: 9 AA.
 AC W2576;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PF 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankevlch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR MPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 87.38; Score 55; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.04e+01;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsdyt 8
 ||:|||||
 1 QKYSAPY 8

RESULT 9
 ID W2575 standard; peptide: 9 AA.
 AC W2575;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 14-AUG-1997.
 10-FEB-1997: U02219.
 25-NOV-1996: US-031476.
 09-FEB-1996: US-599226.
 (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR MPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcohollic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 87.3%; Score 55; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.04e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynrpyt 9
 |||: |||
 QY 1 QKYSAPYT 9

RESULT 10
 ID W2571 standard; peptide: 9 AA.
 AC W2571;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 14-AUG-1997.
 10-FEB-1997: U02219.
 25-NOV-1996: US-031476.
 09-FEB-1996: US-599226.
 (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR MPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcohollic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 82.5%; Score 52; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 4.33e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynrpyt 9
 |||: |||
 QY 1 QKYSAPYT 9

RESULT 11
 ID W2584 standard; peptide: 9 AA.
 AC W2584;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 14-AUG-1997.
 10-FEB-1997: U02219.
 25-NOV-1996: US-031476.
 09-FEB-1996: US-599226.
 (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PT Claim 20: Page 72; 102pp; English.
 PS The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leucocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 82.5%; Score 52; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 4.33e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkyrppyt 9
 |||: |||
 QY 1 QKXSAPYT 9

RESULT 12
 ID W27572 standard; peptide: 9 AA.
 AC W27572;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leucocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997;
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leucocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 82.5%; Score 52; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 4.33e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 qkyrppyt 9
 |||: |||
 QY 1 QKXSAPYT 9

RESULT 13
 ID W27568 standard; Protein: 107 AA.
 AC W27568;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody;
 KW light chain; variable region; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leucocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-A1.
 PD 14-AUG-1997;
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 DR N-PSDB; T88403.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 15: Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leucocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 107 AA;

Query Match 82.5%; Score 52; DB 27; Length 107;
Best Local Similarity 66.7%; Pred. No. 4.33e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 89 qkynrasyt 97
1 OKYSSAPYR 9

RESULT 14
ID R38672 standard; Protein: 129 AA.
AC R38672;
DT 01-NOV-1993 (first entry)
DE VK325-JK2.
KW Monoclonal antibody; MA5; envelope; glycoprotein; gp120; HIV; AIDS;
KW CD4; receptor; hydroloma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
Key Location/Qualifiers
peptide 1..20
/label= sig-peptide
protein 21..129
/label= mat-protein
region 1..116
/label= VK325
region 117..129
/label= JK2
region 44..55
/label= CDR1
region 71..77
/label= CDR2
region 110..117
/label= CDR3
FT m1sc-difference 1 /note= "Met encoded by ATC (sic)"
FT m1sc-difference 35 /note= "Pro encoded by GCA (sic)"
FT m1sc-difference 99 /note= "Leu encoded by GTG (sic)"
FT m1sc-difference 113 /note= "Gly encoded by GAT (sic)"
FT m1sc-difference 114 /note= "Ser encoded by AAC (sic)"
FT m1sc-difference 116 /note= "Pro encoded by GTT (sic)"
PN WO9312232-A.
24-JUN-1993.
10-DEC-1993. U10928.
10-DEC-1991; US-804652.
PA (DAND) DANA FARBER CANCER INST INC.
PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
PI WPI: 93-214174/26.
DR N-PSB: Q42706.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection.
PS Disclosure: Page 74-75; 109pp; English.
CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
CC other F105 VK sequences given elsewhere in the specification) was
CC compared with germline gene HumyK325 (Q42706), showing 97.7%
CC similarity. By nucleotide sequence analysis, F105 appears to
CC be derived from a member of the VK III subgroup gene family.
SQ Sequence 129 AA;

Query Match 81.0%; Score 51; DB 7; Length 129;
Best Local Similarity 66.7%; Pred. No. 5.55e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 110 qkygsspyt 118
1 OKYSSAPYR 9

RESULT 15
ID W27579 standard; peptide: 9 AA.

AC W27579;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumor necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HIVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PD 14-AUG-1997.
PF 14-FEB-1997.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
PI Manovich JA, McGinness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
PI WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumor necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUEC).
SQ Sequence 9 AA;

Query Match 79.4%; Score 50; DB 27; Length 9;
Best Local Similarity 75.0%; Pred. No. 7.10e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkynrasyt 8
1 OKYSSAPYR 8

Search completed: Thu Sep 2 11:34:48 1999
Job time : 21 secs.

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Query Match 79.4%; Score 50; DB 1; Length 533;
Best Local Similarity 66.7%; Pred. No. 3.06e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 424 QKYGKPYT 432
| | | : | | |
QY 1 QKYSAPYT 9

RESULT 2
ID PCT-US95-08743-99 STANDARD; PRT; 108 AA.
AC xxxxxx
XX
XX
XX
XX
XX
XX
XX

Sequence 99, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 108 AA; 11738 MW; 63142 CN;

Query Match 77.8%; Score 49; DB 3; Length 108;
Best Local Similarity 55.6%; Pred. No. 3.93e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 88 QOYGTSPYT 96
| | | : | | |
QY 1 QKYSAPYT 9

RESULT 3
ID US-08-276-852-99 STANDARD; PRT; 108 AA.
AC xxxxxx
XX
XX
XX
XX
XX
XX
XX

Sequence 99, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Filling, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 108 AA; 11738 MW; 63142 CN;

Query Match 77.8%; Score 49; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 3.93e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 88 QOYGTSPYT 96
| | | : | | |
QY 1 QKYSAPYT 9

RESULT 4
ID US-08-899-575-99 STANDARD; PRT; 108 AA.
AC xxxxxx
XX
XX
XX
XX
XX
XX
XX

Sequence 99, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN;

Query Match 77.8%; Score 49; DB 2; Length 108;
Best Local Similarity 55.6%; Pred. No. 3.93e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 88 QOYGTSPYT 96
| : : : : |
1 OKYSSAPYT 9
XX
AC xxxxxx
XX
DT
RESULT 5
ID US-08-899-575-99 STANDARD; PRT; 108 AA.
XX
AC xxxxxx
XX
DT
Sequence 99, Application US/08899575
CC Sequence 99, Application US/08899575
CC Patent No. 3804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: lemer, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN;

Query Match 77.8%; Score 49; DB 2; Length 108;
Best Local Similarity 55.6%; Pred. No. 3.93e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 88 QOYGTSPYT 96
| : : : : |
1 OKYSSAPYT 9
XX
AC xxxxxx
XX
DT
DT
DT
DE
XX
XX
XX
XX
Sequence 44, Application US/08162102C
CC Sequence 44, Application US/08162102C
CC Patent No. 5762905
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Barbas, Titi, Carlos F.
CC APPLICANT: Chanock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr., James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/162,102C
CC FILING DATE: 10-DEC-1993
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Haile, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07300/007001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 678-5070
CC TELEFAX: (619) 678-5099
CC INFORMATION FOR SEQ ID NO: 44:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 53 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 53 AA: 5857 MW: 16217 CN;

Query Match 76.2%; Score 48; DB 2; Length 53;
Best Local Similarity 55.6%; Pred. No. 5.03e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

33 QOYGSAPT 41
1 : : : :
1 QKYSAPT 9

RESULT 7
ID PCT-US95-08743-87 STANDARD: PRT: 107 AA.
XX xxxxxx
DT
DE Sequence 87, Application PC/TUS9508743
CC Sequence 87, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11654 MW: 62438 CN;

Query Match 76.2%; Score 48; DB 3; Length 107;
Best Local Similarity 66.7%; Pred. No. 5.03e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 88 QOYHSAPT 96
1 : : : :
1 QKYSAPT 9

RESULT 8
ID US-08-899-575-87 STANDARD: PRT: 107 AA.
XX xxxxxx
AC
XX
XX
DT
DE Sequence 87, Application PC/TUS9508743
CC Sequence 87, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Bardas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mall Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11654 MW: 62438 CN;

Query Match 76.2%; Score 48; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 5.03e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 88 QOYHSAPT 96
1 : : : :
1 QKYSAPT 9

RESULT 9
ID US-08-899-575-87 STANDARD: PRT: 107 AA.
XX xxxxxx
AC
XX
XX
DT
DE Sequence 87, Application US/08899575
CC Sequence 87, Application US/08899575
CC Patent No. 5804440

XX Sequence 87, Application US/08899575
DE Sequence 87, Application US/08899575
XX Sequence 87, Application US/08899575
CC Patent No. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Bardas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mall Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11654 MW: 62438 CN;

Query Match 76.2%; Score 48; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 5.03e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 88 QOYHSAPT 96
1 : : : :
1 QKYSAPT 9

RESULT 9
ID US-08-899-575-87 STANDARD: PRT: 107 AA.
XX xxxxxx
AC
XX
XX
DT
DE Sequence 87, Application US/08899575
CC Sequence 87, Application US/08899575
CC Patent No. 5804440

CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: The Scripps Research Institute, Office of
CC ADDRESS: Patent Counsel
CC STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11654 MW: 62438 CN;
SQ
Query Match 76.2%; Score 48; DB 2; Length 107;
Best local similarity 66.7%; Pred. No. 5.03e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 88 QOYHSSPYT 96
QY 1 OKYSSAPYT 9
RESULT 10
ID US-08-276-852-87 STANDARD: PRT: 107 AA.
XX xxxxxx
DE Sequence 87, Application US/08276852
XX Sequence 87, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: The Scripps Research Institute, Office of
CC ADDRESS: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11654 MW: 62438 CN;
SQ
Query Match 76.2%; Score 48; DB 1; Length 107;
Best local similarity 66.7%; Pred. No. 5.03e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 88 QOYHSSPYT 96
QY 1 OKYSSAPYT 9
RESULT 11
ID US-08-162-102C-24 STANDARD: PRT: 109 AA.
XX xxxxxx
DE Sequence 24, Application US/08162102C
XX Sequence 24, Application US/08162102C
CC Patent No. 5762905
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Barbas, Ili, Carlos F.
CC APPLICANT: Chanock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr., James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400

```
CC CITY: La Jolla
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATOR: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/86/162,102C
CC FILING DATE: 10-DEC-1993
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hallé, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07300/007001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 678-5070
CC TELEFAX: (619) 678-5099
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 23L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
CC SEQUENCE 109 AA; 11858 MW; 64524 CN;

Query Match 76.2%; Score 48; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 5.03e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 89 OQYGSPTY 97
QY 1 QKYSAPYT 9

RESULT 12
ID PCT-US93-08786-24 STANDARD; PRT; 109 AA.
AC xxxxxx
XX

Sequence 24, Application PC/TUS9308786
DE
XX Sequence 24, Application PC/TUS9308786
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Barbas, III, Carlos F.
CC APPLICANT: Charnock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr., James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TOW RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATOR: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
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CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08786
CC FILING DATE: 16-SEP-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wetherell, Jr., Ph.D., John R.
CC REGISTRATION NUMBER: 31,678
CC REFERENCE/DOCKET NUMBER: FD-2791
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 23L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
CC SEQUENCE 109 AA; 11858 MW; 64524 CN;
SQ
Query Match 76.2%; Score 48; DB 3; Length 109;
Best Local Similarity 55.6%; Pred. No. 5.03e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 89 QOYGSPPY 97
| : : : : |
OY 1 QKYSAPYT 9
RESULT 13
ID US-07-934-373C-3 STANDARD; PRT; 109 AA.
XX xxxxxx
XX
XX
XX
DE Sequence 3, Application US/07934373C
DE
CC Sequence 3, Application US/07934373C
CC Patent No. 5821337
CC GENERAL INFORMATION:
CC APPLICANT: Paul J. Carter
CC APPLICANT: Leonard G. Presta
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 1 DNA Way
CC City: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: winpatin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/934,373C
CC FILING DATE: 21-Aug-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05126
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/715272
CC FILING DATE: 14-JUN-1991
CC

```

CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Lee, Wendy M.
CC	REGISTRATION NUMBER: 40,378
CC	REFERENCE/DOCKET NUMBER: P0709P2
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: 650/225-1994
CC	TELEFAX: 650/952-9881
CC	INFORMATION FOR SEQ ID NO: 3:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 109 amino acids
CC	TYPE: Amino Acid
CC	TOPOLOGY: Linear
SQ	SEQUENCE 109 AA; 11850 MW; 69772 CN;
Dh	Query Match 73.0%; Score 46; DB 2; Length 109;
	Best Local Similarity 66.7%; Pred. No. 8.21e+01;
Matches	6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Dh	89 QOYNSLPYT 97
	I I : I I I I
	1 OKYSAPYT 9
RESULT 14	
ID	PCT-US93-07832-3 STANDARD; PRT; 109 AA.
XX	XXXXXX
DT	
DX	
DE	Sequence 3, Application PC/TUS9307832
CC	Sequence 3, Application PC/TUS9307832
CC	GENERAL INFORMATION:
CC	APPLICANT: Genentech, Inc.
CC	TITLE OF INVENTION: Immunoglobulin Variants
CC	NUMBER OF SEQUENCES: 40
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Genentech, Inc.
CC	STREET: 460 Point San Bruno Blvd
CC	CITY: South San Francisco
CC	STATE: California
CC	COUNTRY: USA
CC	ZIP: 94080
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: patln (Genentech)
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: PCT/US93/07832
CC	FILING DATE: 19930820
CC	CLASSIFICATION:
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: 07/715272
CC	FILING DATE: 14-JUN-1991
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: PCT/US92/05126
CC	FILING DATE: 15-JUN-1992
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: 07/934373
CC	FILING DATE: 21-AUG-1992
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME:
CC	REGISTRATION NUMBER:
CC	REFERENCE/DOCKET NUMBER: 709P2PCT
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE:
CC	TELEFAX: 415/952-9881
CC	TELEX: 910/371-7168
CC	INFORMATION FOR SEQ ID NO: 3:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 109 amino acids

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CC      TYPE: amino acid
CC      TOPOLOGY: linear
SQ      SEQUENCE 109 AA; 11850 MW; 69772 CN;

Query Match          73.0%; Score 46; DB 3; Length 109;
Best Local Similarity 66.7%; Pred. No. 8.21e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db      89 OOVNSLPYT 97
      ||:|||
OY      1 KRTSAPYT 9

RESULT 15
ID      US-08-471-251A-2    STANDARD; PRT; 808 AA.
XX      xxxxxx
DT
XX
DE      Sequence 2, Application US/08471251A
XX
CC      Sequence 2, Application US/08471251A
CC      Patent No. 5670366
CC      GENERAL INFORMATION:
CC      APPLICANT: Mang, Xuemin
CC      TITLE OF INVENTION: RECOMBINANT DNA SEQUENCES ENCODING
CC      TITLE OF INVENTION: PHOSPHOLIPASE
CC      NUMBER OF SEQUENCES: 4
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
CC      ADDRESSEE: Collins
CC      STREET: 2405 Grand Boulevard, Suite 400
CC      CITY: Kansas City
CC      STATE: Missouri
CC      COUNTRY: U.S.A.
CC      ZIP: 64108
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/471, 251A
CC      FILING DATE: June 6, 1995
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Collins, John M.
CC      REGISTRATION NUMBER: 26262
CC      REFERENCE/DOCKET NUMBER: 23703
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (816) 474-9050
CC      TELEFAX: (816) 474-9057
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 808 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      HYPOTHEICAL: NO
SQ      SEQUENCE 808 AA; 92336 MW; 3340041 CN;

Query Match          73.0%; Score 46; DB 1; Length 808;
Best Local Similarity 62.5%; Pred. No. 8.21e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      164 KYPGVPT 171
OY      2 KYSSAPYT 9
```

Job time : 7 secs.

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 109 QOYSSPYT 117
| | | | |
1 QKYSAPYT 9

RESULT 2
ENTRY S67940 #type fragment
TITLE Ig kappa chain V region, subgroup III (clone MH52) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998

ACCESSIONS S67940
REFERENCE S67940
#authors Hexham, J.M.; Furmanak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.

#journal Autoimmunity (1992) 12:135-141
#title Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial approach.

#cross-references MWID:92314301
#accession S67940
#status preliminary
#molecule_type mRNA
#residues 1-91 #label HEX
#cross-references EMBL:X73852

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 91 #checksum 3259

Query Match 81.0%; Score 51; DB 2; Length 91;
Best Local Similarity 66.7%; Pred. No. 1.77e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 71 QOYSSPYT 79
| | | | |
1 QKYSAPYT 9

RESULT 3
ENTRY S37513 #type fragment
TITLE Ig kappa chain V region (V-kappa 3) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

ACCESSIONS S37513
REFERENCE S37501
#authors Klein, U.; Kuipers, R.; Rajewsky, K.
#submission submitted to the EMBL Data Library, September 1993
#description Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood, expresses V(kappa) genes with no or little somatic mutation throughout life.

#accession S37513
#status preliminary
#molecule_type mRNA
#residues 1-92 #label KLE
#cross-references EMBL:Z26598; NID:q405668; PID:q405669

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 92 #checksum 6096

Query Match 81.0%; Score 51; DB 2; Length 92;
Best Local Similarity 66.7%; Pred. No. 1.77e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 73 QOYSSPYT 81
| | | | |
1 QKYSAPYT 9

RESULT 4
ENTRY A30608 #type fragment

TITLE Ig kappa chain V-III region (Son) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS A30608
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.

#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.

#cross-references MWID:89215279
#accession A30608
#status preliminary
#molecule_type protein
#residues 1-109 #label GON
#cross-references EMBL:U00000

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6031

Query Match 81.0%; Score 51; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.77e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 90 QOYSSPYT 98
| | | | |
1 QKYSAPYT 9

RESULT 5
ENTRY H30601 #type fragment
TITLE Ig kappa chain V-III region (Gar and Flo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS H30601; E30601
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.

#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.

#cross-references MWID:89215279
#accession H30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON1
#cross-references EMBL:U00000

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5951

Query Match 81.0%; Score 51; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.77e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 90 QOYSSPYT 98
| | | | |
1 QKYSAPYT 9

RESULT 6
ENTRY A47143 #type complete
TITLE retinal pigment microsomal protein RPE65, epithelium-specific
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change

10-Sep-1997
#accessions A47143; A48017; S28503
#reference A47143
#authors Hamel, C.P.; Tsilou, E.; Pfeiffer, B.A.; Hooks, J.J.; Detrick, B.; Redmond, T.M.
#journal J. Biol. Chem. (1993) 268:15751-15757
#title Molecular cloning and expression of RPE65, a novel retinal pigment epithelium-specific microsomal protein that is post-transcriptionally regulated in vitro.
#cross-references MUID:93340181
#accession A47143
#status preliminary
#molecule-type mRNA
#residues 1-533 #label HAM
#cross-references GB:L1356; NID:g163656; PID:g163657
#reference A48017
#authors Bavik, C.O.; Levy, F.; Hellman, U.; Wernstedt, C.; Eriksson, U.
#journal J. Biol. Chem. (1993) 268:20540-20546
#title The retinal pigment epithelial membrane receptor for plasma retinol-binding protein. Isolation and cDNA cloning of the 63-kDa protein.
#cross-references MUID:93388633
#accession A48017
#status preliminary
#molecule-type mRNA
#residues 1-340/L', 342-533 #label BA2
#cross-references EMBL:X66277; NID:g563; PID:g564
#keywords membrane protein
#summary #length 533 #molecular-weight 60944 #checksum 3885

Query Match 79.4%; Score 50; DB 2; Length 533;
Best Local Similarity 66.7%; Pred. No. 2,89e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 424 OKYGSAPY 432
| | | | |
| | | | |
QY 1 OKYGSAPY 9

RESULT 7
ENTRY I50806 #type fragment
TITLE complement component C3 - Japanese lamprey (fragment)
ORGANISM #formal_name Lampetra japonica #common_name Japanese lamprey
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Aug-1998

ACCESSIONS I50806
#reference I50806
#authors Nonaka, M.; Takahashi, M.
#journal J. Immunol. (1992) 148:3290-3295
#title Complete complementary DNA sequence of the third component of complement of lamprey; implication for the evolution of thioester containing protein.
#cross-references MUID:92251197
#accession I50806
#status preliminary; translated from GB/EMBL/DBJ
#molecule-type mRNA
#residues 1-1673 #label NON
#cross-references GB:D10087; NID:g222887; PID:g222888
#classification #superfamily alpha-2-macroglobulin
#summary #length 1673 #checksum 8983

Query Match 77.8%; Score 49; DB 2; Length 1673;
Best Local Similarity 75.0%; Pred. No. 4.67e+00;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 443 OKYASAPY 450
| | | | |
| | | | |
QY 1 OKYASAPY 8

RESULT 8
ENTRY S42466 #type complete

ig kappa chain V region - mouse
#formal_name Mus musculus #common_name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

ACCESSIONS S42466
#reference S42466
#authors Shlyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
#submission submitted to the EMBL Data Library, March 1994
#accession S42466
#status preliminary
#molecule-type mRNA
#residues 1-117 #label SHI
#cross-references EMBL:X78108; NID:g460824; PID:g460825
#classification #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
#keywords #length 117 #molecular-weight 12860 #checksum 7634
#summary

Query Match 74.6%; Score 47; DB 2; Length 117;
Best Local Similarity 77.8%; Pred. No. 1.20e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 99 OKYSSAPY 107
| | | | |
| | | | |
QY 1 OKYSSAPY 9

RESULT 9
ENTRY F69362 #type complete
TITLE conserved hypothetical protein AF0902 - Archaeoglobus fulgidus
ORGANISM #formal_name Archaeoglobus fulgidus
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998

ACCESSIONS F69362
#reference A69250
#authors Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.R.; Peterson, J.D.; Richardson, D.L.; Kervatage, A.R.; Graham, D.E.; Kyriades, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirsch, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kane, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
#journal Nature (1997) 390:364-370
#title The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus.
#cross-references MUID:98049343
#accession F69362
#status preliminary; nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-270 #label KLE
#cross-references GB:AE001041; GB:AE000782; NID:g2689364; PID:g2649696; TIGR:AF0902

Query Match 74.6%; Score 47; DB 2; Length 270;
Best Local Similarity 66.7%; Pred. No. 1.20e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 19 EKYSSAPY 27
| | | | |
| | | | |
QY 1 OKYSSAPY 9

RESULT 10
ENTRY S72385 #type complete

TITLE hypothetical protein 9 - Enterococcus faecalis plasmid PAD1
ORGANISM #formal_name Enterococcus faecalis
DATE 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
05-Jun-1998

ACCESSIONS S72385
REFERENCE S72375
#authors Hirt, H.; Wirth, R.; Muscholl, A.
#journal Mol. Gen. Genet. (1996) 252:640-647
#title Comparative analysis of 18 sex pheromone plasmids from Enterococcus faecalis: detection of a new insertion element on pPD1 and implications for the evolution of this plasmid family

#cross-references MIMD:97074879
#accession S72385
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-278 #label HIR
#cross-references EMBL:X96977; NID:91279406; PID:e236596; PID:91279411
#experimental_source strain OG1x
#note the nucleotide sequence was submitted to the EMBL Data Library, February 1996

GENETICS
#genome plasmid PAD1
SUMMARY #length 278 #molecular-weight 30520 #checksum 877

Query Match 74.6%; Score 47; DB 2; Length 278;
Best Local Similarity 62.5%; Pred. No. 1.20e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 227 OKYGNAPF 234
|||:||||
QY 1 OKYSSAPY 8

RESULT 11
ENTRY T00829 #type complete
TITLE homeodomain transcription factor homolog - Arabidopsis thaliana
ALTERNATE_NAMES T13L16.3 protein; wuschel protein
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear cress
DATE 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
12-Feb-1999

ACCESSIONS T00829
REFERENCE 214205
#authors de la Bastide, M.; Hameed, A.; Gnoj, L.; Jensen, K.; Shohdy, N.; Gottesman, T.; Habermann, K.; Huang, E.N.; Schütz, K.; Kaplan, N.; Lohr, M.; Marre, M.; Dedhia, N.; Parnell, L.D.; Martienssen, R.; McCombie, W.R.
#submission submitted to the EMBL Data Library, January 1999
#description A. thaliana BAC T13L16 from chromosome IV, top arm.
#accession T00829
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-292 #label DEL
#cross-references EMBL:AC003932; NID:92708736; PID:92708739
#experimental_source cultivar Columbia

GENETICS
#map_position 2
#introns 166/1; 195/3
SUMMARY #length 292 #molecular-weight 33189 #checksum 7184

Query Match 74.6%; Score 47; DB 2; Length 292;
Best Local Similarity 75.0%; Pred. No. 1.20e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 215 HHYSAPY 222
:|||||
QY 1 OKYSSAPY 8

RESULT 12

ENTRY ABCBS #type complete
TITLE serum albumin precursor - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
05-Sep-1997

ACCESSIONS S15571; A05078; A13451
REFERENCE S15571
#authors Casasady, A.I.; Salikid, C.K.; Baverstock, P.; Wallace, J.C.
#submission submitted to the EMBL Data Library, July 1991
#accession S15571
#molecule_type mRNA
#residues 1-615 #label CAS
#cross-references EMBL:X60688; NID:963747; PID:963748
REFERENCE A05078
#authors Heche, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.
#journal J. Biol. Chem. (1983) 258:4556-4564
#title The 5' noncoding and flanking regions of the avian very low density apolipoprotein II and serum albumin genes. Homologies with the egg white protein genes.

#cross-references MIMD:83161037
#accession A05078
#molecule_type DNA
#residues 1-28 #label HAC
#cross-references GB:V00381; NID:963038; PID:963039
REFERENCE A13451
#authors Rosen, A.M.; Geller, D.M.
#journal Biochem. Biophys. Res. Commun. (1977) 78:1060-1066
#title Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.
#cross-references MIMD:78019943
#accession A13451
#molecule_type protein
#residues 19-23, 'M', 25-30 #label ROS
COMMENT Serum albumin is synthesized in the liver as preproalbumin. It binds copper, nickel, calcium (weakly, at 2-3 sites), and protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (weak bonds with these hormones promote their transfer across the membranes), thyroxine, and triiodothyronine.

CLASSIFICATION #superfamily serum albumin; serum albumin repeat homology
KEYWORDS carrier protein; duplication; metal binding; plasma
FEATURES
1-18 #domain signal sequence #status predicted #label SIG
19-26 #domain propeptide #status predicted #label PRO
27-613 #product serum albumin #status predicted #label MAT
32-206 #domain serum albumin repeat homology #label SA1
225-398 #domain serum albumin repeat homology #label SA2
417-596 #domain serum albumin repeat homology #label SA3
30 #binding_site copper (His) #status predicted
80-89, 102-118,
117-128, 152-197,
196-205, 228-274,
273-281, 293-307,
306-317, 344-389,
388-397, 420-466,
465-476, 489-505,
504-515, 542-587,
586-595
#disulfide_bonds #status predicted
SUMMARY #length 615 #molecular-weight 69918 #checksum 4822

Query Match 74.6%; Score 47; DB 1; Length 615;
Best Local Similarity 55.6%; Pred. No. 1.20e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 249 OKYKAPFS 257
|||:||||
QY 1 OKYSSAPY 9

RESULT 13
ENTRY SA1028 #type complete
TITLE hypothetical protein K03H1.4 - Caenorhabditis elegans
ORGANISM #formal_name Caenorhabditis elegans

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
ACCESSIONS S41028
REFERENCE S41024
#authors Smith, M.; Ainscough, R.
#submission Submitted to the EMBL Data Library, January 1994
#accession S41028
#status Preliminary
#molecule_type DNA
#residues 1-1409 #label SMI
#cross-references EMBL:229560

GENETICS
#introns 44/3; 189/3; 223/3; 319/3; 340/3; 375/2; 493/3; 517/3; 591/2;
662/3; 852/2; 928/1; 988/1; 1104/1; 1202/1; 1324/2
SUMMARY #length 1409 #molecular_weight 161796 #checksum 2817

Query Match 74.6%; Score 47; DB 2; Length 1409;
Best Local Similarity 50.0%; Pred. No. 1.20e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

821 HRYGAPY 828
:::||||
QY 1 QKYSAPY 8

RESULT 14
ENTRY S37524 #type fragment
TITLE Ig kappa chain V region (V-kappa 3) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
08-Sep-1997

ACCESSIONS S37524
REFERENCE S37501
#authors Klein, U.; Kuipers, R.; Rajewsky, K.
#submission Submitted to the EMBL Data Library, September 1993
#description Human IgM(+)19d(+) cells, the major B cell subset in the peripheral blood, expresses V(kappa) genes with no or little somatic mutation throughout life.

#accession S37524
#status Preliminary
#molecule_type mRNA
#residues 1-92 #label KLE
#cross-references EMBL:226620; NID:9405690; PID:9405691
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 92 #checksum 5958

Query Match 73.0%; Score 46; DB 2; Length 92;
Best Local Similarity 55.6%; Pred. No. 1.91e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 73 QQYSSPFT 81
| | | | |
QY 1 QKYSAPY 9

RESULT 15
ENTRY A49138 #type fragment
TITLE IgA kappa rheumatoid factor variable - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1998

ACCESSIONS A49138
REFERENCE A49138
#authors Gause, A.; Koppers, R.; Mierau, R.
#journal Clin. Exp. Immunol. (1992) 88:430-434
#title A somatically mutated V kappa IV gene encoding a human rheumatoid factor light chain.
#cross-references MVID:92298590
#accession A49138
#status Preliminary
#molecule_type DNA
#residues 1-106 #label GAU

#cross-references GB:S37926; NID:9298207; PID:9298208
#note
#note sequence inconsistent with the nucleotide translation
sequence extracted from NCBI backbone (NCBI:106633,
NCBI:106637)
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 106 #checksum 7525

Query Match 73.0%; Score 46; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 1.91e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 98 QQYSSPFT 106
| | | | |
QY 1 QKYSAPY 9

Search completed: Thu Sep 2 11:35:21 1999
Job time : 16 secs.

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 W E S T
 (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:35:38 1999; Maspar time 2.09 Seconds
 on output not generated. 121.628 Million cell updates/sec

Title: >US-08-599-226-14
 Description: (1-9) from US08599226.pep
 Perfect Score: 63
 Sequence: 1 OKYSAPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 22.644; Variance 24.519; scale 0.924

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	52	82.5	138	1	KV3K_HUMAN	IG KAPPA CHAIN PRECURSOR	2.94e+01
2	49	77.8	1673	1	CO3_LAMJA	COMPLEMENT C3 PRECURSOR	1.50e+00
3	47	74.6	615	1	ALBU_CHICK	SERUM ALBUMIN PRECURSOR	4.27e+00
4	47	74.6	1385	1	YMS5_CABEL	HYPOTHETICAL 159.2 KD	4.27e+00
5	46	73.0	108	1	KV3A_HUMAN	IG KAPPA CHAIN V-II R	7.12e+00
6	46	73.0	808	1	PLD_RICCO	PHOSPHOLIPASE D PRECUR	7.12e+00
7	46	73.0	808	1	PLD_TOBAC	PHOSPHOLIPASE D PRECUR	7.12e+00
8	46	73.0	809	1	PLD_VITON	PHOSPHOLIPASE D PRECUR	7.12e+00
9	46	73.0	812	1	PLD_ORYSA	PHOSPHOLIPASE D PRECUR	7.12e+00
10	46	73.0	812	1	PLD_MAIZE	PHOSPHOLIPASE D PRECUR	7.12e+00
11	46	73.0	1897	1	PTPF_HUMAN	LAR PROTEIN PRECURSOR	7.12e+00
12	45	71.4	510	1	EYAS_MOUSE	EYES ABSENT HOMOLOG 3.	1.18e+01
13	45	71.4	573	1	EYAS_HUMAN	EYES ABSENT HOMOLOG 3.	1.18e+01
14	44	69.8	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-I REG	1.93e+01
15	44	69.8	242	1	HELO_HELLO	HELOTERMINE PRECURSOR	1.93e+01
16	44	69.8	250	1	OCRC_BACST	MENAOQUINOL-CYTOCHROME	1.93e+01
17	44	69.8	252	1	YJG6_YEAST	HYPOTHETICAL 28.5 KD P	1.93e+01
18	44	69.8	335	1	PBGE_HUMAN	PREGNANCY-SPECIFIC BET	1.93e+01
19	44	69.8	360	1	DCAM_SOLTU	S-ADENOSINETHIONINE D	1.93e+01
20	44	69.8	362	1	DCAM_DATST	S-ADENOSINETHIONINE D	1.93e+01
21	44	69.8	417	1	PBG1_HUMAN	PREGNANCY-SPECIFIC BET	1.93e+01
22	44	69.8	419	1	PBGD_HUMAN	PREGNANCY-SPECIFIC BET	1.93e+01
23	44	69.8	428	1	PBGC_HUMAN	PREGNANCY-SPECIFIC BET	1.93e+01

Result ID	Query Match	Score	Length	ID	Description	Pred. No.	
24	44	69.8	500	1	AR08_YEAST	AROMATIC AMINO ACID AM	1.93e+01
25	44	69.8	790	1	SMY2_YEAST	SMY2 PROTEIN.	1.93e+01
26	44	69.8	945	1	SEN3_YEAST	26S PROTEASOME REGULAT	1.93e+01
27	44	69.8	1279	1	APU_THESA	ANTYDOPULULINASE PRECU	1.93e+01
28	44	69.8	1861	1	APU_THETU	ANTYDOPULULINASE PRECU	1.93e+01
29	44	69.8	2259	1	CB21_RABIT	BRAIN CALCIUM CHANNEL	1.93e+01
30	43	68.3	108	1	KV1O_HUMAN	IG KAPPA CHAIN V-I REG	3.14e+01
31	43	68.3	114	1	KV4A_HUMAN	IG KAPPA CHAIN V-IV RE	3.14e+01
32	43	68.3	251	1	YG64_HAEIN	HYPOTHETICAL PROTEIN H	3.14e+01
33	43	68.3	309	1	YAO8_SCHPO	HYPOTHETICAL 35.3 KD P	3.14e+01
34	43	68.3	378	1	MNT3_CANAL	PROBABLE MANNOsylTRANS	3.14e+01
35	43	68.3	689	1	YBP3_YEAST	HYPOTHETICAL 77.3 KD P	3.14e+01
36	43	68.3	818	1	PLD2_ORYSA	PHOSPHOLIPASE D 2 PREC	3.14e+01
37	43	68.3	942	1	YD73_SCHPO	HYPOTHETICAL 104.0 KD	3.14e+01
38	43	68.3	1060	1	YN18_YEAST	HYPOTHETICAL 118.3 KD	3.14e+01
39	43	68.3	1233	1	HCT1_OCTDO	HEMOCYANIN, UNITS ODE	3.14e+01
40	42	66.7	193	1	Y455_METJA	HYPOTHETICAL PROTEIN M	5.04e+01
41	42	66.7	303	1	Y440_MYCTU	HYPOTHETICAL TRANSPORT	5.04e+01
42	42	66.7	485	1	VST2_HEYRH	STRUCTURAL PROTEIN 2 (5.04e+01
43	42	66.7	573	1	YEF8_YEAST	HYPOTHETICAL 63.7 KD P	5.04e+01
44	42	66.7	660	1	VST2_HEYBU	STRUCTURAL PROTEIN 2 P	5.04e+01
45	42	66.7	660	1	VST2_HEYMT	STRUCTURAL PROTEIN 2 P	5.04e+01

ALIGNMENTS

RESULT 1
 ID KV3K_HUMAN STANDARD: PRT; 128 AA.

AC P06311;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-II REGION (IARC/BL41).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86041852.
 RA KLOBECK H.G., MEINDL A., CONERATO G., SOLOMON A., ZACHAU H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 III.";
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
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DR EMBL; Z00021; G33179; -
 DR PIR; A01899; K3H041.
 DR PFAM; PF00047; 19; 1.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL
 FT CHAIN
 FT DOMAIN
 FT DOMAIN
 FT DOMAIN
 FT DOMAIN
 FT DOMAIN
 FT DOMAIN
 FT DOMAIN
 FT DISULFID
 FT NON_TER
 FT SEQUENCE
 128 AA; 14070 MW; 318E08AF CRC32;

Query Match 82.5%; Score 52; DB 1; Length 128;
 Best Local Similarity 66.7%; Pred. No. 2.94e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 109 QOYSTSPYT 117
OY 1 OKXSAPYT 9

RESULT 2 STANDARD; PRT: 1673 AA.

AC 000685;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN] (FRAGMENT).
GN C3.
OS LAMPEPTRA JAPONICA (JAPANESE LAMPREY).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CEPHALASPIDOMORPHI;
OC PETROMYZONITIFORMES; PETROMYZONITIDAE; LAMPEPTRA.
RN [1]
RP SEQUENCE FROM N.A.

TISSUE=LIVER;
MEDLINE: 92251197.
NONAKA M., TAKAHASHI M.;
Complete complementary DNA sequence of the third component of complement of lamprey. Implication for the evolution of thioester containing proteins.;
J. IMMUNOL. 148:3290-3295(1992).
-1- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. AFTER ACTIVATION (C3B), IT CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. CYCLOSTOMATES C3 APPEARS TO REPRESENT THE COMMON ANCESTOR OF MAMMALIAN C3 AND C4, SHOWING SIMILARITIES TO BOTH PROTEINS.

-1- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
-1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.

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CC EMBL: D10087; G222888; -
DR PROSITE: PS00477; ALPHA-2-MACROGLOBULIN; 1.
DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
DR PFAM: PF00207; A2M; 1.
DR HSSP: P01024; 1C3D.
COMPLEMENT PATHWAY; PLASMA; INFLAMMATORY RESPONSE; GLYCOPROTEIN; SIGNAL.

FT NON_TER 1 13 POTENTIAL.
FT SIGNAL <1 13 COMPLEMENT C3.
FT CHAIN 14 1673 BETA CHAIN (BY SIMILARITY).
FT CHAIN 14 653 ALPHA CHAIN (BY SIMILARITY).
FT CHAIN 657 1375 GAMMA CHAIN (BY SIMILARITY).
FT CHAIN 1379 1673 C3A ANAPHYLATOXIN (BY SIMILARITY).
FT PEPTIDE 657 732 ANAPHYLATOXIN-LIKE.
FT DOMAIN 678 713 ANAPHYLATOXIN-LIKE.
FT DISULFID 678 705 BY SIMILARITY.
FT DISULFID 679 712 BY SIMILARITY.
FT DISULFID 682 713 BY SIMILARITY.
FT THIOLEST 986 990 BY SIMILARITY.
SQ SEQUENCE 1673 AA; 187767 MW; D857446F CRC32;

Query Match 77.88; Score 49; DB 1; Length 1673;
Best Local Similarity 75.08; Pred. No. 1.50e+00;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 443 OKXSASY 450
OY 1 OKXSAPY 8

RESULT 3 STANDARD; PRT: 615 AA.

AC ALBU.CHICK
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE SERUM ALBUMIN PRECURSOR.
GN ALB.
OS GALLUS GALUS (CHICKEN).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASININAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA CASSADY A.I., SALKILD C.K., BAYERSTOCK P., WALLACE J.C.;
RL SUBMITTED (JUL-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE: 83161037.
RA HACHE R.J.G., WISKOCIL R., VASA M., ROY R.N., LAU P.C.K., DEELEY R.G.;
RT "The 5' noncoding and flanking regions of the avian very low density apolipoprotein II and serum albumin genes. Homologies with the egg white protein genes.*";
J. BIOL. CHEM. 258:4556-4564(1983).
RN [3]
RP SEQUENCE OF 19-30.
RX MEDLINE: 78019943.
RA ROSEN A.M., GELLER D.M.;
RT "Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.*";
BIOCHEM. BIOPHYS. RES. COMMUN. 78:1060-1066(1977).

CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES, BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE COLLOIDAL OSMOTIC PRESSURE OF BLOOD.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.

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CC EMBL: X60688; G63748; -
DR EMBL: V00381; G63039; -
DR PIR: S15571; ABCS.
DR PROSITE: PS00212; ALBUMIN; 3.
DR PFAM: PF00273; transport_prot; 1.
DR HSSP: P02768; 1U0R.
KW PLASMA; METAL-BINDING; LIPID-BINDING; ALBUMIN; REPEAT; SIGNAL;
KW COPPER.

FT SIGNAL 1 18
FT CHAIN 19 23 SERUM ALBUMIN.
FT REPEAT 24 615
FT REPEAT 31 206
FT REPEAT 225 398
FT REPEAT 417 596
FT METAL 30 30 COPPER (BY SIMILARITY).
FT DISULFID 80 89 BY SIMILARITY.
FT DISULFID 102 118 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 152 197 BY SIMILARITY.
FT DISULFID 196 205 BY SIMILARITY.
FT DISULFID 228 274 BY SIMILARITY.
FT DISULFID 273 281 BY SIMILARITY.
FT DISULFID 293 307 BY SIMILARITY.
FT DISULFID 306 317 BY SIMILARITY.
FT DISULFID 344 389 BY SIMILARITY.

FT DISULFID 388 397 BY SIMILARITY.
 FT DISULFID 420 466 BY SIMILARITY.
 FT DISULFID 465 476 BY SIMILARITY.
 FT DISULFID 489 505 BY SIMILARITY.
 FT DISULFID 504 515 BY SIMILARITY.
 FT DISULFID 542 587 BY SIMILARITY.
 FT DISULFID 586 595 BY SIMILARITY.
 FT CARBOHYD 500 500 POTENTIAL.
 FT CONFLICT 24 24 F -> M (IN REF. 3).
 SQ SEQUENCE 615 AA; 69918 MW; DC5EEEA CRC32;

Query Match 74.6%; Score 47; DB 1; Length 615;
 Best Local Similarity 55.6%; Pred. No. 4.27e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 249 QKYSAPY 257
 QY 1 QKYSAPY 9

RESULT 4 STANDARD; PRT; 1385 AA.
 AC P34501;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOTHEICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III.
 GN K03H1.5.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEIA; RHABDITIA; RHABDITIDA;
 OC RHABDITIA; RHABDITIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA CAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
 RA FULTON L., GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M.,
 RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
 RA LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFEEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMER E., STADEN R.,
 RA SOUTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
 RA WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
 RA WOLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RT NATURE 368:32-38(1994).

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CC EMBL; Z29560; E1347842; -;
 CC DR PIR; S41028; S41028;
 CC DR MORPEP; K03H1.5; CE03459.
 CC PRAM; PF00084; suh1; 1.
 CC KW HYPOTHEICAL PROTEIN.
 CC SQ SEQUENCE 1385 AA; 159181 MW; A2134063 CRC32;

Query Match 74.6%; Score 47; DB 1; Length 1385;
 Best Local Similarity 50.0%; Pred. No. 4.27e+00;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 797 HRYGAPY 804
 QY 1 QKYSAPY 8

RESULT 5 STANDARD; PRT; 108 AA.
 AC P01619;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-III REGION (B6).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE.
 RA MISTEIN C.;
 RT "The basic sequences of immunoglobulin kappa chains: sequence studies
 of Bence Jones proteins Rad, F4 and B6.";
 RL FEBS LETT. 2:301-304(1969).
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01891; K3H086.
 DR PRAM; PF00047; 19; 1.
 DR HSP; P01789; 2MCP.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11635 MW; 46D6B68E CRC32;

Query Match 73.0%; Score 46; DB 1; Length 108;
 Best Local Similarity 55.6%; Pred. No. 7.12e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 90 QOYGSPY 98
 QY 1 QKYSAPY 9

RESULT 6 STANDARD; PRT; 808 AA.
 AC Q41142; P93507;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (P4D) (CHOLINE PHOSPHATASE)
 DE (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D).
 OS RICINUS COMMUNIS (CASTOR BEAN).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC EUPHORBIALES; EUPHORBIACEAE; RICINUS.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-CV. HALE; TISSUE-ENDOSPERM;
 RX MEDLINE; 94327597.
 RA WANG X., XU L., ZHENG L.;
 RT "Cloning and expression of phosphatidylcholine-hydrolyzing
 phospholipase D from Ricinus communis L.";
 RT J. BIOL. CHEM. 269:20312-20317(1994).
 RN [2]
 RP SEQUENCE FROM N.A.

CC TISSUE-LEAF;
 CC RX MEDLINE; 97134969.
 CC RA XU L., ZHENG L., COUGHLAN S.J., WANG X.;
 CC "Structure and analysis of phospholipase D gene from Ricinus communis
 L.";
 CC PLANT MOL. BIOL. 32:767-771(1996).
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN CELLULAR PATHWAYS INCLUDING
 CC SIGNAL TRANSDUCTION PATHWAYS.
 CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = CHOLINE + A
 CC PHOSPHATIDATE.
 CC -1- COFACTOR: CALCIUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: MOSTLY EXPRESSED IN VACUOLES, ENDOPLASMIC
 CC RETICULUM, A FEW IN PLASTIDS AND PLASMA MEMBRANE. EXPRESSION IS
 CC HIGHER IN RADICLE THAN IN ENDOSPERM.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.
 CC -----

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CC EMBL: L33686; G1438075; -

DR EMBL: U72693; G1698844; -

DR PROSITE: PSS0004; C2_DOMAIN_2; 1.

DR PFAM: PF00614; PLDC; 1.

DR HYDROLASE: LIPID DEGRADATION: CALCIUM.

FT PROPEP 1 30 PHOSPHOLIPASE D.

FT CHAIN 31 808 C2 DOMAIN.

FT DOMAIN 1 109 L->I (IN REF. 2).

FT CONFLICT 268 268

FT SEQUENCE 808 AA; 91992 MW; 13B746DA CRC32;

Query Match 73.0%; Score 46; DB 1; Length 808;

Best Local Similarity 62.5%; Pred. No. 7.12e+00;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 164 KYSGVPT 171

QY 2 KYSGVPT 9

RESULT 7 STANDARD; PRT; 808 AA.

AC P33400; P93399; DT 15-DEC-1998 (REL. 37, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (PLD) (CHOLINE PHOSPHATASE)

DE (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D).

OS NICOTIANA TABACUM (COMMON TOBACCO).

OC EUPHAROTIA: VIRIDIPALANAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;

CC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS;

CC ASTERIDAE: SOLANACEAE: SOLANALES: NICOTIANA.

CC [1]

RP SEQUENCE FROM N.A.

RA STRAIN-CV, SRI; TISSUE-LEAF;

RA LEIN W., SALBACH G.;

RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN CELLULAR PATHWAYS INCLUDING

CC SIGNAL TRANSDUCTION PATHWAYS.

CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O -> CHOLINE + A

CC PHOSPHATIDATE.

CC -1- COFACTOR: CALCIUM (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.

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Db 164 KYSGVPT 171

QY 2 KYSGVPT 9

RESULT 8 STANDARD; PRT; 809 AA.

AC P33400; P93399; DT 15-DEC-1998 (REL. 37, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (PLD) (CHOLINE PHOSPHATASE)

DE (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D).

OS VIGNA UNICULATA (COMPEL).

OC EUPHAROTIA: VIRIDIPALANAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;

CC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS; ROSIDAE;

CC FABACEAE; PAPILIONOIDEAE; VIGNA.

CC [1]

RP SEQUENCE FROM N.A.

RA STRAIN-CV, EPAGE-1; TISSUE-LEAF;

RA EL MAROUF H., PHAM THI A.T., GARELI M., D'ARCY-LAMETA A.,

RA ZUTY-FODIL Y.;

RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN CELLULAR PATHWAYS INCLUDING

CC SIGNAL TRANSDUCTION PATHWAYS.

CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O -> CHOLINE + A

CC PHOSPHATIDE.

CC -1- COFACTOR: CALCIUM (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: U92656; G1928979; -

DR PROSITE: PSS0004; C2_DOMAIN_2; 1.

DR PFAM: PF00168; C2; 1.

DR PFAM: PF00614; PLDC; 1.

DR HYDROLASE: LIPID DEGRADATION: CALCIUM.

FT PROPEP 1 809 POTENTIAL.

FT CHAIN 1 809 PHOSPHOLIPASE D.

FT DOMAIN 1 109 C2 DOMAIN.

FT SEQUENCE 809 AA; 91565 MW; 06597C1 CRC32;

Query Match 73.0%; Score 46; DB 1; Length 809;

Best Local Similarity 62.5%; Pred. No. 7.12e+00;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 164 KYSGVPT 171

QY 2 KYSGVPT 9

RESULT 9 STANDARD; PRT; 812 AA.

AC P33400; P93399; DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (PLD 1) (CHOLINE PHOSPHATASE

DE 1) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1).

OS ORYZA SATIVA (RICE).

OC EUPHAROTIA: VIRIDIPALANAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;

CC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA; LILIOPSIDA; POALES;

CC POACEAE; ORYZA.

CC [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN-CV. KOSHIIKARI;
 RA MEDLINE; 96012933.
 RA UKRI J., MORIOKA S., KOMARI T., KUMASHIRO T.;
 RT Purification and characterization of phospholipase D (PLD) from rice
 RT (Oryza sativa L.) and cloning of cDNA for PLD from rice and maize
 RT (Zea mays L.).
 RL PLANT CELL PHYSIOL. 36:903-914(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. KOSHIIKARI; TISSUE-LEAF;
 RA MORIOKA S., UKRI J., KOMARI T.;
 RT Characterization of two distinctive genomic clones for phospholipase
 RT D from rice.
 RL (IN) PLANT GENE REGISTER PGR97-076.
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN VARIOUS CELLULAR PROCESSES.
 CC THERMOSTABLE BETWEEN 4 AND 37 DEGREES CELSIUS, BUT ACTIVITY IS
 CC REDUCED TO ONE THIRD OF THE ORIGINAL LEVEL AFTER INCUBATION AT 50
 CC DEGREES CELSIUS FOR 30 MINUTES. OPTIMAL PH IS 6.0.
 CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O - CHOLINE + A
 CC PHOSPHATIDATE.
 CC -1- COFACTOR: CALCIUM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: EXPRESS IN LEAVES, ROOTS, DEVELOPING SEEDS AND
 CC CULTURED CELLS.
 CC -1- DEVELOPMENTAL STAGE: THE TRANSCRIPT BEGINS TO EMERGE IN SEEDS AS
 CC EARLY AS THE SECOND DAY AFTER IMBIBITION AND INCREASED AFTER
 CC RADICLE EMERGENCE ON THE THIRD DAY. STRONGLY EXPRESSED IN THE
 CC LEAVES, ROOTS AND RESIDUAL GRAIN OF SEEDLING EIGHT DAYS AFTER
 CC IMBIBITION. BELONGS TO THE PHOSPHOLIPASE D FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D73411; D1011797; -;
 DR EMBL; AB001920; D1020224; -;
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PFAM; PF00614; PLDC; 2.
 KM HYDROLASE; LIPID DEGRADATION; CALCIUM; MULTIGENE FAMILY.
 FT PROPEP 1 46
 FT CHAIN 47 812 PHOSPHOLIPASE D 1.
 FT DOMAIN 1 114 C2 DOMAIN.
 FT SEQUENCE 812 AA; 92209 MW; 4314CED1 CRC32;
 Query Match 73.0%; Score 46; DB 1; Length 812;
 Best Local Similarity 62.5%; Pred. No. 7.12e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 168 KYGPVPT 175
 OY 2 KYSSAPYT 9
 RESULT 10
 ID P.D. MAIZE STANDARD; PRT; 812 AA.
 AC Q43270;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (PLD) (CHOLINE PHOSPHATASE)
 DE (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D).
 OS ZEA MAYS (MAIZE).
 OS EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMEROPHYTES; TRACHEOPHYTES;
 OC EUPHYLOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; LILIOPSIDA; POALES;
 OC POACEAE; ZEA.
 OC [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. MO17;

RX MEDLINE; 96012933.
 RA UKRI J., MORIOKA S., KOMARI T., KUMASHIRO T.;
 RT Purification and characterization of phospholipase D (PLD) from rice
 RT (Oryza sativa L.) and cloning of cDNA for PLD from rice and maize
 RT (Zea mays L.).
 RL PLANT CELL PHYSIOL. 36:903-914(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. KOSHIIKARI; TISSUE-LEAF;
 RA MORIOKA S., UKRI J., KOMARI T.;
 RT Characterization of two distinctive genomic clones for phospholipase
 RT D from rice.
 RL (IN) PLANT GENE REGISTER PGR97-076.
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN VARIOUS CELLULAR PROCESSES.
 CC THERMOSTABLE BETWEEN 4 AND 37 DEGREES CELSIUS, BUT ACTIVITY IS
 CC REDUCED TO ONE THIRD OF THE ORIGINAL LEVEL AFTER INCUBATION AT 50
 CC DEGREES CELSIUS FOR 30 MINUTES. OPTIMAL PH IS 6.0.
 CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O - CHOLINE + A
 CC PHOSPHATIDATE.
 CC -1- COFACTOR: CALCIUM (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.
 CC
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 CC -----
 DR EMBL; D73410; D1011796; -;
 DR MAZEDB; 113853; -;
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PFAM; PF00614; PLDC; 2.
 KM HYDROLASE; LIPID DEGRADATION; CALCIUM.
 FT PROPEP 1 46
 FT CHAIN 47 812 PHOSPHOLIPASE D.
 FT DOMAIN 1 114 C2 DOMAIN.
 FT SEQUENCE 812 AA; 92242 MW; F535BF6B CRC32;
 Query Match 73.0%; Score 46; DB 1; Length 812;
 Best Local Similarity 62.5%; Pred. No. 7.12e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 168 KYGPVPT 175
 OY 2 KYSSAPYT 9
 RESULT 11
 ID P.P.F. HUMAN STANDARD; PRT; 1897 AA.
 AC P10586;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).
 DE P.P.R.F. OR LAR.
 GN GN HOMO SAPIENS (HUMAN).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 OC [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE-TONSIL;
 RC MEDLINE; 89035978.
 RA STREUBLI M., KRUEGER N.X., HALL L.R., SCHLOSSMAN S.F., SAITO H.;
 RT A new member of the immunoglobulin superfamily that has a
 RT cytoplasmic region homologous to the leukocyte common antigen.
 RT J. EXP. MED. 168:1523-1530(1988).
 RN [2]
 RP NOTAGNESIS.
 RP MEDLINE; 90046860.
 RA STREUBLI M., KRUEGER N.X., TSAI A.Y.M., SAITO H.;
 RT A family of receptor-linked protein tyrosine phosphatases in humans
 RT and Drosophila.
 RT PROC. NATL. ACADE. SCI. U.S.A. 86:8698-8702(1989).
 RN [3]
 RP NOTAGNESIS.
 RP MEDLINE; 90316093.
 RA STREUBLI M., KRUEGER N.X., THAI T., TANG M., SAITO H.;
 RT Distinct functional roles of the two intracellular phosphatase like
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and
 RT LAR.

RL EMBL J. 9:2399-2407(1990).
 CC -1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.
 CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
 CC (PTPASE).
 CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC THE FIRST ONE.
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
 CC LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS),
 CC AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
 CC -1- SIMILARITY: TO DPTP AND TO LAR.
 CC -----
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 CC -----
 CC EMBL: Y00815; G34267; -.
 CC PIR: S03841; TDHULK.
 CC DR MIM; 179590; -.
 CC DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 CC DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 CC DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 CC DR PRAM; PF00041; fn3; 7.
 CC DR PRAM; PF00047; 1g; 3.
 CC DR PRAM; PF00102; Y-phosphatase; 2.
 CC DR HSP; P18052; 1YFO.
 CC DR HYDROLASE; RECEPTOR; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE;
 CC CELL ADHESION; IMMUNOGLOBULIN FOLD; DUPLICATION.
 CC KW
 CC FT SIGNAL 1 16 POTENTIAL.
 CC FT CHAIN 17 1897 LAR PROTEIN.
 CC FT DOMAIN 17 1250 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 1251 1274 POTENTIAL.
 CC FT DOMAIN 1275 1897 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 1360 1606 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT DOMAIN 1649 1897 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 1538 1538 BY SIMILARITY.
 CC FT ACT_SITE 1829 1829 C->S: LOSS OF ACTIVITY.
 CC FT MOTAGEN 1538 1538 POTENTIAL.
 CC FT CARBOHYD 107 107 POTENTIAL.
 CC FT CARBOHYD 240 240 POTENTIAL.
 CC FT CARBOHYD 285 285 POTENTIAL.
 CC FT CARBOHYD 711 711 POTENTIAL.
 CC FT CARBOHYD 956 956 POTENTIAL.
 CC SQ SEQUENCE 1897 AA; 211844 MW; 40B63F08 CRC32;
 SQ
 Query Match 73.0%; Score 46; DB 1; Length 1897;
 Best Local Similarity 50.0%; Pred. No. 7.12e+00;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Db 1226 RYASSPYR 1233
 QY 2 KYSSAPY 9
 RESULT 12
 ID EYA3_MOUSE STANDARD; PRT; 510 AA.
 AC P97480; P97768;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE EYES ABSENT HOMOLOG 3.
 GN EYA3.
 OS MUS MUSCULUS (MUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MURINAE; MUS.
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-EMBRYO;
 RX MEDLINE: 97202104.
 RA ZIMMERMAN J.E., BUI Q.T., STEINGRIMSSON E., NAGLE D.L., FU W.,
 RA GERIN A., SPINNER N.B., COPELAND N.G., JENKINS N.A., BUCAN M.,
 RA BONINI N.M.;
 RT "Cloning and characterization of two vertebrate homologs of the
 RT Drosophila eyes absent gene";
 RL GENOME RES. 7:128-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-EMBRYO;
 RX MEDLINE: 97158722.
 RA XU P.-X., WOO I., HER H., BEIER D.R., MAAS R.L.;
 RT "House Eya homologues of the Drosophila eyes absent gene require Pax6
 RT for expression in lens and nasal placode";
 RL DEVELOPMENT 124:219-231(1997).
 CC -1- FUNCTION: MAY BE INVOLVED IN DEVELOPMENT OF THE EYE. MAY PLAY A
 CC ROLE IN MEDIATING THE INDUCTION AND DIFFERENTIATION OF CRANIAL
 CC PLACODES.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN, ISOFORMS 1 AND 2,
 CC MAY BE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE
 CC IS THAT OF ISOFORM 1.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRANCHIAL ARCHES, CNS AND
 CC DEVELOPING EYE.
 CC -1- SIMILARITY: TO DROSOPHILA EYES ABSENT.
 CC -----
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 CC -----
 CC EMBL: U01604; G1816533; -.
 CC DR EMBL; U01112; G1850335; -.
 CC DR MGI; 109339; EYA3.
 CC KW DEVELOPMENTAL PROTEIN; MULTIGENE FAMILY; ALTERNATIVE SPLICING.
 CC FT VARSPIC 1 105
 CC FT MOEPROTISOVNPPASDEKPTSLASLMSSEIMCT
 CC FT DTPRSNDTSMYSAKRAHLSVSTTTPGTOIOT
 CC FT LOOSOPVAVYPOATOTGTGLPPFA -> MIIHPKCILOT
 CC FT (IN ISOFORM 2).
 CC FT A -> V (IN REF. 2).
 CC FT CONFLICT 272 272
 CC SQ SEQUENCE 510 AA; 55945 MW; 84087104 CRC32;
 SQ
 Query Match 71.4%; Score 45; DB 1; Length 510;
 Best Local Similarity 55.6%; Pred. No. 1.18e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 54 OMYSAPYR 62
 QY 1 OYSSAPY 9
 RESULT 13
 ID EYA3_HUMAN STANDARD; PRT; 573 AA.
 AC Q99504; Q99813;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE EYES ABSENT HOMOLOG 3.
 GN EYA3.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-EMBRYO;
 RX MEDLINE: 97172972.
 RA ABDELHAK S., KALATZIS V., HELLIG R., COMPAIN S., SANSON D.,
 RA VINCENT C., WEIL D., GRUARD C., SAHLY I., LEIBOVICI M.,
 RA BITNER-GLINDZIC M., FRANCIS M., LACOMBE D., VIGNERON J.,

RA CHARACHON R., BOVEN K., BEDEDER P., VAN REGEMORTER N.,
 RA WEISENACH J., PETIT C.;
 RT "A human homologue of the Drosophila eyes absent gene underlies
 RT branchio-oto-renal (BOR) syndrome and identifies a novel gene
 RT family.";
 RL NAT. GENET. 15:157-164(1997).
 CC [2]
 CC SEQUENCE FROM N.A. (ISOFORM 2).
 CC TISSUE-RETINA:
 CC MEDLINE: 97202104.
 CC ZIMMERMAN J.E., BUT O.T., STEINGRIMSSON E., NAGLE D.L., FU W.,
 RA BONINI N.M.;
 RA SPINNER N.B., COPELAND N.G., JENKINS N.A., BOCAN M.,
 RT "Cloning and characterization of two vertebrate homologs of the
 RT Drosophila eyes absent gene.";
 RL GENOME RES. 7:128-141(1997).
 CC -1- FUNCTION: MAY BE INVOLVED IN DEVELOPMENT OF THE EYE.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN, ISOFORMS 1 AND 2,
 CC MAY BE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN HERE
 CC IS THAT OF ISOFORM 1.
 CC -1- SIMILARITY: TO DROSOPHILA EYES ABSENT.
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 CC -----
 CC EMBL: Y10262; E299512; -
 CC DR EMBL: U81602; G1816529; -
 CC DR MIM: 601655; -
 CC CC
 CC DR DEVELOPMENTAL PROTEIN, MULTIGENE FAMILY; ALTERNATIVE SPLICING.
 CC FT VARSPLIC 1 126 MISSING (IN ISOFORM 2).
 CC FT CONFLICT 142 142 H -> R (IN REF. 2).
 CC FT CONFLICT 151 151 L -> V (IN REF. 2).
 CC FT CONFLICT 253 253 K -> R (IN REF. 2).
 CC FT CONFLICT 268 268 T -> S (IN REF. 2).
 CC FT CONFLICT 283 283 N -> T (IN REF. 2).
 CC FT CONFLICT 290 290 K -> R (IN REF. 2).
 CC FT CONFLICT 305 305 V -> L (IN REF. 2).
 CC FT CONFLICT 345 345 K -> E (IN REF. 2).
 CC FT CONFLICT 357 357 S -> F (IN REF. 2).
 CC FT CONFLICT 361 361 K -> E (IN REF. 2).
 CC FT CONFLICT 373 374 PN -> SD (IN REF. 2).
 CC FT CONFLICT 376 376 K -> N (IN REF. 2).
 CC FT CONFLICT 379 379 N -> D (IN REF. 2).
 CC FT CONFLICT 381 381 N -> S (IN REF. 2).
 CC FT CONFLICT 388 388 N -> D (IN REF. 2).
 CC FT CONFLICT 447 447 K -> R (IN REF. 2).
 CC FT CONFLICT 449 449 K -> R (IN REF. 2).
 CC FT CONFLICT 457 457 N -> D (IN REF. 2).
 CC FT CONFLICT 473 473 K -> R (IN REF. 2).
 CC FT CONFLICT 480 480 L -> P (IN REF. 2).
 CC FT CONFLICT 487 487 L -> V (IN REF. 2).
 CC FT CONFLICT 500 500 K -> E (IN REF. 2).
 CC FT CONFLICT 524 526 TSL -> SF (IN REF. 2).
 CC FT CONFLICT 530 530 L -> V (IN REF. 2).
 CC SQ SEQUENCE 573 AA; 62411 MW; 630A47F3 CRC32;

DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (BAN).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 CC [1]
 CC SEQUENCE.
 CC MEDLINE: 86174817.
 RA DWULET F.E., O'CONNOR T.P., BENSON M.D.;
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
 RL MOL. IMMUNOL. 23:73-78(1986).
 DR PIR: A01878; KIHUBN.
 DR PIR: P00047; 15; 1.
 DR HSP: P80362; 1MTL.
 KW IMUNOGLOBULIN V REGION; AMYLOID.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 0D44DA0A CRC32;

Query Match 69.8%; Score 44; DB 1; Length 108;
 Best Local Similarity 66.7%; Pred. No. 1.93e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 89 QOYNSAPYT 97
 QY 1 QKXSSAPYT 9

RESULT 15
 ID HELD_HELHO STANDARD; PRT; 242 AA.
 AC Q91053;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HELOTHERMINE PRECURSOR
 OS HELODERMA HORRIDUM HORRIDUM (MEXICAN BEADED LIZARD).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPTODOSAURIA; SQUAMATA;
 CC SCLEROGLOSSA; ANGUIMORPHA; HELODERMATIDAE; HELODERMA.
 CC [1]
 CC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 CC TISSUE-SALIVARY GLAND;
 CC MEDLINE: 95375162.
 RA MORRISSETTE J., KRAETZSCHMAR J., HAENDLER B., EL-HAYER R.,
 RA MOCHCA-MORALES J., MARTIN B.M., PATEL J.R., MOSS R.L.;
 RA SCHLEUNING W.-D., CORONADO R., POSSANI L.D.;
 RT "Primary structure and properties of heliothermine, a peptide toxin
 RT that blocks ryanodine receptors.";
 RL BIOPHYS. J. 68:2280-2286(1995).
 CC -1- FUNCTION: PEPTIDE TOXIN THAT BLOCKS RYANODINE RECEPTORS.
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
 CC -----
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 CC -----
 CC EMBL: U13619; G606921; -
 CC DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
 CC DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; FALSE_NEG.
 CC PIR: P00188; SCP; 1.

DR HSSP; P04284; 1CFE.
 KW TOXIN; SIGNAL.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 242 HELOTHERMINE.
 SQ SEQUENCE 242 AA; 27493 MW; 9C89BARF CRC32;
 Query Match 69.88; Score 44; DB 1; Length 242;
 Best Local Similarity 85.7%; Pred. NO. 1.93e+01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Caps 0;
 Db 100 FSSAPYT 106
 QY 3 YSSAPYT 9

Search completed: Thu Sep 2 11:35:46 1999
 Job time : 8 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

On: Thu Sep 2 11:36:04 1999; Maspar time 4.41 Seconds
 111.375 Million cell updates/sec

Similar output not generated.

Title: >US-08-599-226-14
 Description: (1-9) from US08599226.pep
 Perfect Score: 63
 Sequence: 1 OKYSSAPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: sptrembl9
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 21.780; Variance 25.113; scale 0.867

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Hit No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	52	82.5	337	2	ORF40X1 PROTEIN.	6.35e-01
2	52	82.5	337	2	ORF139-17 PROTEIN.	6.35e-01
3	50	79.4	533	6	RETINAL PIGMENT EPITHE	1.83e+00
4	50	79.4	533	6	RETINAL PIGMENT EPITHE	1.83e+00
5	48	76.2	320	2	SITE-SPECIFIC RECOMBIN	5.12e+00
6	48	76.2	322	5	AMPHITOXUS OTX TRANSCR	5.12e+00
7	48	76.2	451	13	TRANSCRIPTION FACTOR (5.12e+00
8	48	76.2	533	4	RETINAL PIGMENT EPITHE	5.12e+00
9	48	76.2	560	5	KLID12.1 PROTEIN.	5.12e+00
10	48	76.2	653	11	REXO70.	5.12e+00
11	47	74.6	270	1	CONSERVED HYPOHETICAL	8.48e+00
12	47	74.6	278	2	PLASMODI PADL, OPEN REA	8.48e+00
13	47	74.6	292	10	PUTATIVE SERINE PROTEIN	8.48e+00
14	46	73.0	319	5	HYPOHETICAL 37.0 KD P	1.39e+01
15	46	73.0	496	2	HLA-KR21 RESTRICTION EN	1.39e+01
16	46	73.0	864	11	LEUCOCYTE COMMON ANTIG	1.39e+01
17	46	73.0	1290	11	LEUCOCYTE COMMON ANTIG	1.39e+01
18	46	73.0	1898	11	LEUCOCYTE COMMON ANTIG	1.39e+01
19	46	73.0	3082	14	POLYPROTEIN.	1.39e+01
20	45	71.4	305	5	ZK1010.2 PROTEIN.	2.28e+01

21	45	71.4	342	6	018744	LU-ECAM-1.	2.28e+01
22	45	71.4	448	5	002441	GDP-DISSOCIATION INHIB	2.28e+01
23	45	71.4	697	11	035250	EXO70 PROTEIN.	2.28e+01
24	45	71.4	734	4	075112	KIA0613 PROTEIN (FRAG	2.28e+01
25	45	71.4	794	6	018742	LU-ECAM-1.	2.28e+01
26	45	71.4	820	6	018743	LU-ECAM-1.	2.28e+01
27	45	71.4	905	6	018741	LU-ECAM-1.	2.28e+01
28	44	69.8	298	5	061731	NON-RECEPTOR PROTEIN-T	3.69e+01
29	44	69.8	333	4	075238	PSG IIA-D.	3.69e+01
30	44	69.8	335	4	075237	PSG IIA-C.	3.69e+01
31	44	69.8	336	5	044833	FS4D12.8 PROTEIN.	3.69e+01
32	44	69.8	350	1	P95976	RIBOSOMAL PROTEIN S15.	3.69e+01
33	44	69.8	352	4	008266	PREGNANCY-SPECIFIC BET	3.69e+01
34	44	69.8	417	4	075236	PBG1 HUMAN.	3.69e+01
35	44	69.8	426	4	060410	F19434.2.	3.69e+01
36	44	69.8	426	4	016660	PREGNANCY-SPECIFIC BET	3.69e+01
37	44	69.8	426	4	015243	PREGNANCY-SPECIFIC GLY	3.69e+01
38	44	69.8	428	4	016557	PREGNANCY-SPECIFIC BET	3.69e+01
39	44	69.8	428	4	008265	PREGNANCY-SPECIFIC BET	3.69e+01
40	44	69.8	450	2	050511	ZINC PROTEASE.	3.69e+01
41	44	69.8	542	14	084357	REGULATORY PROTEIN E2.	3.69e+01
42	44	69.8	759	5	020429	SIMILAR TO TRANSCRIPT	3.69e+01
43	44	69.8	1042	1	060295	PUTATIVE TYPE I RESTRI	3.69e+01
44	44	69.8	1095	5	019132	F07A11.4 PROTEIN.	3.69e+01
45	44	69.8	2312	4	015878	VOLTAGE-OPERATED CALCI	3.69e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	337 AA.
AC	034232			
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)		
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)		
DE	ORF40X1 PROTEIN.			
OS	VIBRIO CHOLERAE.			
OC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-AI-1837;			
RC	MEDLINE: 97252505.			
RA	STROEHER U.H., PARASIVAM G., DREDGE B.K., MANNING P.A.;			
RT	"Novel Vibrio cholerae O139 genes involved in lipopolysaccharide			
RT	biosynthesis.";			
RL	J. BACTERIOL. 179:2740-2747(1997).			
DR	EMBL: Y07786; E274650; -			
SQ	SEQUENCE 337 AA; 40132 MM; 2D4A7939 CRC32;			

Query Match 82.5%; Score 52; DB 2; Length 337;
 Best Local Similarity 87.5%; Pred. No. 6.35e-01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB	147 OKYSSAPY 154
QY	1 OKYSSAPY 8
RESULT	2
ID	087136; PRELIMINARY; PRT; 337 AA.
AC	087136;
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE	ORF139-17 PROTEIN.
OS	VIBRIO CHOLERAE.
OC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-MO45;
RC	YANASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,
RA	TAREDA Y.;
RT	"The genes responsible for O-antigen synthesis of Vibrio cholerae

RT 0139 are closely related to those of Vibrio cholerae 022.
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567; -
 SO SEQUENCE 337 AA; 40147 MW; 1768468B CRC32;

Query Match 82.5% Score 52; DB 2; Length 337;
 Best Local Similarity 87.5% Pred. No. 6.35e-01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 147 OKYSAPY 154
 ||| |||
 QY 1 OKYSAPY 8

RESULT 3 PRELIMINARY; PRT; 533 AA.
 ID 028175;
 AC 028175;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 RETINAL PIGMENT EPITHELIUM-SPECIFIC PROTEIN.
 BOS TAURUS (BOVINE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 93340181.

RA HAMEL C.P., TSILIOU E., PEEFER B.A., HOOKS J.J., DETRICK B.,
 REDMOND T.;
 RT Molecular cloning and expression of RPE65, a novel retinal pigment
 epithelium-specific microsome protein that is post-translationally
 regulated in vitro.
 RL J. BIOL. CHEM. 268:15751-15757(1993).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 9333190.

RA HAMEL C.P., TSILIOU E., HARRIS E.D., PEEFER B.A., HOOKS J.J.,
 DETRICK B., REDMOND T.;
 RT "A developmentally regulated microsome protein specific for the
 pigment epithelium of the vertebrate retina."
 RL J. NEUROSCI. RES. 34:414-423(1993).

DR EMBL: L11356; G163657; -
 KW PIGMENT.

SO SEQUENCE 533 AA; 60944 MW; 911D0716 CRC32;
 Query Match 79.4% Score 50; DB 6; Length 533;
 Best Local Similarity 66.7% Pred. No. 1.83e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 424 OKYGKPYT 432
 |||: |||
 QY 1 OKYSAPY 9

RESULT 4 PRELIMINARY; PRT; 533 AA.
 ID 005661;
 AC 005661;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 RETINAL PIGMENT EPITHELIUM MEMBRANE RECEPTOR P63.

DE BOS TAURUS (BOVINE).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.

RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 365-382 AND 407-423.
 RC STRAIN-STREINHOITZ; TISSUE-EYE;
 RX MEDLINE: 9338633.

RA BAVIK C.O., HELLMAN U., WERNSTEDT C., ERIKSSON U.;
 RT "The retinal pigment epithelial membrane receptor for plasma
 retinol-binding protein. Isolation and cDNA cloning of the 63-kDa

RT protein.";
 RL J. BIOL. CHEM. 268:20540-20546(1993).
 CC -1- FUNCTION: THIS RECEPTOR BINDS PLASMA RETINOL BINDING PROTEIN.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN RETINAL PIGMENT
 EPITHELIUM.

DR EMBL: X66277; G564; -
 KW RECEPTOR; RETINOL-BINDING; PLASMA; MEMBRANE.
 FT MOD_RES 71
 SO SEQUENCE 533 AA; 60970 MW; F7E22D7 CRC32;

Query Match 79.4% Score 50; DB 6; Length 533;
 Best Local Similarity 66.7% Pred. No. 1.83e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 424 OKYGKPYT 432
 |||: |||
 QY 1 OKYSAPY 9

RESULT 5 PRELIMINARY; PRT; 320 AA.
 ID 068847;
 AC 068847;

DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 SITE-SPECIFIC RECOMBINASE INT14.

GN INT14.
 OS VIBRIO CHOLERAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.

RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON-INTVCH;
 RX MEDLINE: 98221242.

RA MAZEL D., DYCHINCO B., WEBB V.A., DAVIES J.;
 RT "A distinctive class of integration in the Vibrio cholerae genome."
 RL SCIENCE 280:605-608(1998).
 DR EMBL: AF055586; G3095165; -

SO SEQUENCE 320 AA; 37505 MW; CBF0F9CD CRC32;
 Query Match 76.2% Score 48; DB 2; Length 320;
 Best Local Similarity 62.5% Pred. No. 5.12e+00;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 208 EKYPNAPY 215
 |||: |||
 QY 1 OKYSAPY 8

RESULT 6 PRELIMINARY; PRT; 322 AA.
 ID 045024;
 AC 045024;

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE AMPHILOXUS OTX TRANSCRIPTION FACTOR.

OS BRANCHIOSTOMA FLORIDAE (FLORIDA LANCELET) (AMPHIOXUS).
 OC EUKARYOTA; METAZOA; CHORDATA; CEPHALOCHORDATA; BRANCHIOSTOMIDAE;
 OC BRANCHIOSTOMA.

RN [1]
 RP SEQUENCE FROM N.A.
 RA WILLIAMS N.A., HOLLAND P.W.H.;
 RL MOL. BIOL. EVOL. 0:0-0(1998).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: AF043740; G2828716; -

DR PROSITE: PS00027; HOMEBOX_1;
 KW HOMEBOX; DNA-BINDING; NUCLEAR PROTEIN.

SO SEQUENCE 322 AA; 34715 MW; F0E80B18 CRC32;
 Query Match 76.2% Score 48; DB 5; Length 322;
 Best Local Similarity 75.0% Pred. No. 5.12e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 224 QYSPAPY 231
 1 11111
 QY 1 OKYSSAPY 8

RESULT 7
 ID 093374 PRELIMINARY: PRT: 451 AA.
 AC 093374;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 GN PAX8.
 OS FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
 OC TELOSTEII; EUTELEOSTEII; ACANTHOPTERYGII; PERCOMORPHA;
 OC TETRAODONTIFORMES; TETRAODONTIOIDEI; TETRAODONTIDAE; FUGU.
 RN [1]
 RS SEQUENCE FROM N.A.
 MEDLINE: 98337826.
 PF PEEFER P.L., GERSTER T., LUN K., BRAND M., BUSSENGER M.;
 RT "Characterization of three novel members of the zebrafish pax2/5/8
 family: dependency of pax3 and pax8 expression on the pax2.1 (nol)
 function.";
 RL DEVELOPMENT 125:3063-3074(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
 DR EMBL: AF072556; G3420029;-.
 DR PROSITE: PS00034; PAIRED_BOX: 1.
 DR PAIRED_BOX: DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN.
 FT NON_TER 1
 SQ SEQUENCE 451 AA; 48389 MW; 0081252D CRC32;

Query Match 76.2%; Score 48; DB 13; Length 451;
 Best Local Similarity 66.7%; Pred. No. 5.12e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 406 QYXSHSPYT 414
 1 11111
 QY 1 OKYSSAPY 9

RESULT 8
 ID 016518 PRELIMINARY: PRT: 533 AA.
 AC 016518;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 RS RETINAL PIGMENT EPITHELIUM-SPECIFIC 61 KDA PROTEIN.
 REE5.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 95359969.
 RA NICOLETTI A., WONG D.J., KAWASE K., GIBSON L.H., YANG-FENG T.L.,
 RA RICHARDS J.E., THOMPSON D.A.;
 RT "Molecular characterization of the human gene encoding an abundant 61
 kDa protein specific to the retinal pigment epithelium.";
 RL HUM. MOL. GENET. 4:641-649(1995).
 RN [2]
 RS SEQUENCE FROM N.A.
 RP MORIMURA H.;
 RA SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U18991; G675458;-.
 DR EMBL: U20510; G675485;-.
 DR EMBL: U20477; G675485; JOINED.
 DR EMBL: U20477; G675485; JOINED.
 DR EMBL: U20478; G675485; JOINED.
 DR EMBL: U20479; G675485; JOINED.

DR EMBL: U20481; G675485; JOINED.
 DR EMBL: U20482; G675485; JOINED.
 DR EMBL: U20484; G675485; JOINED.
 DR EMBL: U20485; G675485; JOINED.
 DR EMBL: U20486; G675485; JOINED.
 DR EMBL: AF039868; G2773292;-.
 DR EMBL: AF039865; G2773292; JOINED.
 DR EMBL: AF039856; G2773292; JOINED.
 DR EMBL: AF039857; G2773292; JOINED.
 DR EMBL: AF039858; G2773292; JOINED.
 DR EMBL: AF039859; G2773292; JOINED.
 DR EMBL: AF039860; G2773292; JOINED.
 DR EMBL: AF039861; G2773292; JOINED.
 DR EMBL: AF039862; G2773292; JOINED.
 DR EMBL: AF039863; G2773292; JOINED.
 DR EMBL: AF039864; G2773292; JOINED.
 DR EMBL: AF039865; G2773292; JOINED.
 DR EMBL: AF039866; G2773292; JOINED.
 DR EMBL: AF039867; G2773292; JOINED.
 SQ SEQUENCE 533 AA; 60947 MW; 088A41C3 CRC32;

Query Match 76.2%; Score 48; DB 4; Length 533;
 Best Local Similarity 66.7%; Pred. No. 5.12e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 424 QYXCGKPYT 432
 1 11111
 QY 1 OKYSSAPY 9

RESULT 9
 ID 044626 PRELIMINARY: PRT: 560 AA.
 AC 044626;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE K11D12.1 PROTEIN.
 GN K11D12.1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COSEY T., COOPER J., COULSON A.,
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKIN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SOLTSON J.,
 RA THIRRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL NATURE 368:32-38(1994).
 RN [2]
 RS SEQUENCE FROM N.A.
 RP STRAIN-BRISTOL N2;
 RA HENKHAUS J., WOHLDMANN P., GILLAM B.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RS SEQUENCE FROM N.A.
 RP STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF039047; G2736445;-.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2; 1.
 KW ZINC_FINGER; METAL-BINDING; DNA-BINDING.
 SQ SEQUENCE 560 AA; 61136 MW; 5906EB7D CRC32;

Query Match 76.2%; Score 48; DB 5; Length 560;
Best Local Similarity 75.0%; Pred. No. 5.12e+00;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 81 OKKRAPY 88
:|||||
QY 1 OKYSAPY 8

RESULT 10
ID 054922; PRELIMINARY; PRT; 653 AA.

AC 054922;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE REXO70.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCITURONGNATHI; MORIDA; MORINAE; RATTUS.
[1]
SEQUENCE FROM N.A.
AC TISSUE-BRAIN;
RX MEDLINE: 98070770.
RA KEE Y., YOO J.S., HAZUKA C.D., PETERSON K.E., HSU S.C.,
SCHELLER R.H.;
RT "Subunit structure of the mammalian exocyst complex."
RL PROOC. NATL. ACAD. SCI. U.S.A. 94:14438-14443(1997).
DR EMBL: AF032667; G2827160; -.
SO SEQUENCE 653 AA; 75045 MW; 0778EB24 CRC32;

Query Match 76.2%; Score 48; DB 11; Length 653;
Best Local Similarity 55.6%; Pred. No. 5.12e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 619 HRYSSVPT 627
:|||||
QY 1 OKYSAPY 9

RESULT 11
ID 029360; PRELIMINARY; PRT; 270 AA.

AC 029360;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN AF0902.
OS ARCHAEOGLOBUS FULGIDUS.
ACHERA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
ARCHAEOGLOBUS.
[1]
SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE: 98049343.
RA KLEIN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GINN N., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
REICHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLOBEK A., ZHOU L.,
OVERBEER K., GOGAINE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
COTTON M.D., SPRIGGS T., ARTACH P., RAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
NASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., MOSE C.R.,
VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic,
sulphate-reducing archaeon Archaeoglobus fulgidus."
RL NATURE 390:364-370(1997).
DR EMBL: AE001041; G2649696; -.
DR TIGR: AF0902; -.
KM HYPOTHETICAL PROTEIN.
SO SEQUENCE 270 AA; 30971 MW; 195DB20D CRC32;

Query Match 74.6%; Score 47; DB 1; Length 270;
Best Local Similarity 66.7%; Pred. No. 8.48e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 19 EKXSNPPT 27
:|||||
QY 1 OKYSAPY 9

RESULT 12
ID 047792; PRELIMINARY; PRT; 278 AA.

AC 047792;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PLASMID PAD1, OPEN READING FRAMES.
OS ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS).
OC PLASMID PAD1.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; ENTEROCOCCACEAE;
OC ENTEROCOCCUS.
[1]
SEQUENCE FROM N.A.
RC STRAIN-OG1;
RX MEDLINE: 97074879.
RA HIRT H., WIRTH R., MÜSCHOLL A.;
RT "Comparative analysis of 18 sex pheromone plasmids from Enterococcus
faecalis: detection of a new insertion element on pPD1 and
implications for the evolution of this plasmid family."
RL MOL. GEN. GENET. 252:640-647(1996).
DR EMBL: X96977; E236596; -.
KW PLASMID.
SO SEQUENCE 278 AA; 30520 MW; 67892F0F CRC32;

Query Match 74.6%; Score 47; DB 2; Length 278;
Best Local Similarity 62.5%; Pred. No. 8.48e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 227 OKXNAPF 234
:|||||
QY 1 OKYSAPY 8

RESULT 13
ID 048821; PRELIMINARY; PRT; 292 AA.

AC 048821;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE PUTATIVE SERINE PROTEINASE.
GN T13L16.3.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPRIFALES; BRASSICACEAE; ARABIDOPSIS.
[1]
SEQUENCE FROM N.A.
RA DE LA BASTIDE M., HAMEED A., GNOJ L., JENSEN K., SHOHDI N.,
GOTTSMAN T., HABERMANN K., HUANG E.N., SCHUTZ K., KARLAN N.,
LODHI M., MARRA M., DEDRA N., PARNELL L.D., MARTINSEN R.,
MCCOMBIE W.R.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AC003952; G2708739; -.
SO SEQUENCE 292 AA; 33189 MW; F69680E1 CRC32;

Query Match 74.6%; Score 47; DB 10; Length 292;
Best Local Similarity 75.0%; Pred. No. 8.48e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 215 HRYSSAPY 222
:|||||
QY 1 OKYSAPY 8

RESULT 14
 ID 015926 PRELIMINARY; PRT; 319 AA.
 AC 015926;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL. 37.0 KD PROTEIN.
 OS CRYPTOSPORIDIUM PARVUM.
 OC EUKARYOTA; ALVEOLATA; APICOMPLEXA; COCCIDIA; EIMERIIDA;
 CC CRYPTOSPORIDIIDAE; CRYPTOSPORIDIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KSU-1;
 RX MEDLINE: 98043502.
 RA KHRAMTSOV N.V., WOODS K.M., NESTERENKO M.V., DYKSTRA C.C.,
 UPTON S.J.;
 RT "Virus-like, double-stranded RNAs in the parasitic protozoan
 Cryptosporidium parvum."
 RL MOL. MICROBIOL. 26:289-300(1997).
 EMBL: U95996; G2465523; -.
 HYPOTHETICAL PROTEIN.
 SEQUENCE 319 AA; 37028 MW; 1362B027 CRC32;

Query Match 73.0%; Score 46; DB 5; Length 319;
 Best Local Similarity 62.5%; Pred. No. 1.39e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 250 RYTCAPYT 257
 :||:||||
 QY 2 KYSSAPYT 9

RESULT 15
 ID 087348 PRELIMINARY; PRT; 496 AA.
 AC 087348;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE LIAKR21 RESTRICTION ENZYME.
 GN LIAKR21R.
 OS LACTOCOCCUS LACTIS (STREPTOCOCCUS LACTIS).
 OG PLASMID PKR223.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 CC LACTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TWOMEY D.P., MCKAY L.L., O'SULLIVAN D.J.;
 RT "Molecular characterization of the lactococcus lactis LIAKR21
 restriction-modification system and effect of an IS982 element
 positioned between the restriction and modification genes.";
 J. BACTERIOL. 180:0-0(1998).
 DR EMBL: AF051563; G3702799; -.
 KW PLASMID.
 SQ SEQUENCE 496 AA; 58081 MW; A04BA2A9 CRC32;

Query Match 73.0%; Score 46; DB 2; Length 496;
 Best Local Similarity 62.5%; Pred. No. 1.39e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 33 EKXOSTPY 40
 :||:||||
 QY 1 QKXSAPY 8

Search completed: Thu Sep 2 11:36:26 1999
 Job time : 22 secs.

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CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 100.0%; Score 64; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.50e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|||||
 QY 1 QKINSAPPT 9

ULR 2
 W2570 standard; peptide: 9 AA.

AC W2570; (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-NOV-1997; U02219.
 PF 10-FEB-1997; US-031476.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASP AC.
 PI Allen DJ, Hoogenboom HRM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-413302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 67; 10pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 95.3%; Score 61; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 3.35e+00;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|||||
 QY 1 QKINSAPPT 9

RESULT 3
 W2573 standard; peptide: 9 AA.

AC W2573; (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-NOV-1997; U02219.
 PF 10-FEB-1997; US-031476.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASP AC.
 PI Allen DJ, Hoogenboom HRM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-413302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 68; 10pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, malignancy, pulmonary, intestinal,
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 93.8%; Score 60; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.38e+00;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|||||
 QY 1 QKINSAPPT 9

RESULT 4
 W2582 standard; peptide: 9 AA.

AC W2582; (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 bone resorption disease; inflammatory bone disorder; reperfusion injury;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 93.8%; Score 60; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.38e+00;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 qkynsdyt 9
 1 QKYNsAPYT 9

RESULT 5
 ID W2576 standard; peptide: 9 AA.
 AC W2576;
 DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).

PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 92.2%; Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.70e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 qkynsapy 8
 1 QKYNsAPYT 8

RESULT 6
 ID W2577 standard; peptide: 9 AA.
 AC W2577;
 DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 92.2%; Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.70e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsapyt 8
 |||||
 OY 1 QKYNsAPYT 8

RESULT 7
 ID W2575 standard; peptide: 9 AA.

AC W2575;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 92.2%; Score 59; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 5.70e+00;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapyt 9
 |||||
 OY 1 QKYNsAPYT 9

RESULT 8
 ID W2578 standard; peptide: 9 AA.

AC W2578;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain: complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 92.2%; Score 59; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 5.70e+00;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysapyt 9
 |||||
 OY 1 QKYNsAPYT 9

RESULT 9
ID W27583 standard; peptide: 9 AA.
AC W27583;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PS 14-AUG-1997.
PS 10-FEB-1997: U02219.
PS 25-NOV-1996: US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Markovitch JA, McGuiness BR, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 72; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:
Query Match 87.5%; Score 56; DB 27; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.26e+01;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 gkyisappt 9
Oy 1 OKYNSAPPT 9

RESULT 10
ID W27584 standard; peptide: 9 AA.
AC W27584;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PS 14-AUG-1997.
PS 10-FEB-1997: U02219.
PS 25-NOV-1996: US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Markovitch JA, McGuiness BR, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 72; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:
Query Match 87.5%; Score 56; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.26e+01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 gkyrnppt 9
Oy 1 OKYNSAPPT 9

RESULT 11
ID W27571 standard; peptide: 9 AA.
AC W27571;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PS 14-AUG-1997.
PS 10-FEB-1997: U02219.
PS 25-NOV-1996: US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Markovitch JA, McGuiness BR, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 72; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:
Query Match 87.5%; Score 56; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.26e+01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 gkyrnppt 9
Oy 1 OKYNSAPPT 9

PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 sclerostis, osteoarthritis, gouty arthritis, allergy, multiple
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 87.5%: Score 56: DB 27: Length 9;
 Best Local Similarity 77.8%: Pred. No. 1,26e+01;
 Matches 7: Conservative 1: Mismatches 1: Indels 0: Gaps 0;

DB 1 qkynrapya 9
 :||| |||
 QY 1 OKYNSAPYT 9

RESULT 12
 ID W27568 standard; Protein: 107 AA.
 AC W27568;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain variable region.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
 light chain; variable region; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.
 DR N-PSDB: T88403.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 15: Page 75: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spodylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerostis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 107 AA:

Query Match 87.5%: Score 56: DB 27: Length 107;
 Best Local Similarity 77.8%: Pred. No. 1,26e+01;
 Matches 7: Conservative 1: Mismatches 1: Indels 0: Gaps 0;

DB 89 qkynrapyt 97
 :||| |||
 QY 1 OKYNSAPYT 9

RESULT 13
 ID W27572 standard; peptide: 9 AA.
 AC W27572;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BAD) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68: 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC sclerostis, osteoarthritis, gouty arthritis, allergy, multiple
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 cardiac or inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 84.4%; Score 54; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2,11e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 qkyqrpyt 9
 ||| |||
 OY 1 OKYNSAPY 9

RESULT 14
 ID W27579 standard; peptide: 9 AA.
 AC W27579;

DE 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 DE light chain; complementarity determining region 3; inhibition;
 DE treatment; sepsis; disease; autoimmune disease; infectious disease;
 DE malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 DE cardiac disorder; inflammatory bone disorder; reperfusion injury;
 DE bone resorption disease; coagulation disturbance; burn; ELAM-1;
 DE keloid formation; scar tissue formation; pyrexia; HUVEC;
 DE periodontal disease; obesity; radiation toxicity;
 DE endothelial cell leukocyte adhesion molecule-1;
 DE Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-41302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical cell
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 84.4%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2,11e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkyqrpyt 8
 ||| |||
 OY 1 OKYNSAPY 8

RESULT 15
 ID W27580 standard; peptide: 9 AA.
 AC W27580;

DE 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 DE light chain; complementarity determining region 3; inhibition;
 DE treatment; sepsis; disease; autoimmune disease; infectious disease;
 DE malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 DE cardiac disorder; inflammatory bone disorder; reperfusion injury;
 DE bone resorption disease; coagulation disturbance; burn; ELAM-1;
 DE keloid formation; scar tissue formation; pyrexia; HUVEC;
 DE periodontal disease; obesity; radiation toxicity;
 DE endothelial cell leukocyte adhesion molecule-1;
 DE Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-41302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 84.4%; Score 54; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2,11e+01;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 qkynsaays 9
 ||| |||
 OY 1 OKYNSAPY 9

Search completed: Thu Sep 2 11:37:27 1999
 Job time : 19 secs.

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(TM)

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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:40:41 1999; MasPar time 1.38 Seconds
Regular output not generated. 66.028 Million cell updates/sec

Title: >US-08-599-226-15
Description: (1-9) from US08599226.pep
Perfect Score: 64
Sequence: 1 OKXNSAPYT 9

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfile1

Statistics: Mean 14.831; Variance 45.721; scale 0.334

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	52	81.3	107	3	PCT-US95-0	Sequence 87, Applicati	1.64e+01
2	52	81.3	107	1	US-08-276-	Sequence 87, Applicati	1.64e+01
3	52	81.3	107	2	US-08-899-	Sequence 87, Applicati	1.64e+01
4	52	81.3	107	2	US-08-899-	Sequence 87, Applicati	1.64e+01
5	50	78.1	109	2	US-07-934-	Sequence 3, Applicatio	2.73e+01
6	50	78.1	109	3	PCT-US93-0	Sequence 3, Applicatio	2.73e+01
7	49	76.6	533	1	US-08-488-	Sequence 6, Applicatio	3.52e+01
8	48	75.0	106	1	US-08-276-	Sequence 85, Applicati	4.52e+01
9	48	75.0	106	3	PCT-US95-0	Sequence 85, Applicati	4.52e+01
10	48	75.0	106	2	US-08-899-	Sequence 85, Applicati	4.52e+01
11	48	75.0	106	2	US-08-899-	Sequence 85, Applicati	4.52e+01
12	48	75.0	108	1	PCT-US95-0	Sequence 99, Applicati	4.52e+01
13	48	75.0	108	1	US-08-276-	Sequence 99, Applicati	4.52e+01
14	48	75.0	108	2	US-08-899-	Sequence 99, Applicati	4.52e+01
15	48	75.0	108	2	US-08-899-	Sequence 99, Applicati	4.52e+01
16	47	73.4	53	2	US-08-162-	Sequence 44, Applicati	5.81e+01
17	47	73.4	107	3	PCT-US95-0	Sequence 84, Applicati	5.81e+01
18	47	73.4	107	2	US-08-899-	Sequence 84, Applicati	5.81e+01
19	47	73.4	107	2	US-08-899-	Sequence 84, Applicati	5.81e+01
20	47	73.4	107	1	US-08-276-	Sequence 82, Applicati	5.81e+01
21	47	73.4	107	3	PCT-US95-0	Sequence 82, Applicati	5.81e+01
22	47	73.4	107	1	US-08-276-	Sequence 84, Applicati	5.81e+01
23	47	73.4	107	2	US-08-899-	Sequence 82, Applicati	5.81e+01

RESULT	ID	PCT-US95-08743-87	STANDARD:	PRT:	107 AA.
24	47	73.4	107	2	US-08-899- Sequence 84, Applicati
25	47	73.4	109	3	PCT-US93-0 Sequence 24, Applicati
26	47	73.4	109	2	US-08-162- Sequence 24, Applicati
27	46	71.9	52	2	US-08-162- Sequence 43, Applicati
28	46	71.9	106	2	US-08-202- Sequence 26, Applicati
29	46	71.9	109	3	PCT-US93-0 Sequence 23, Applicati
30	46	71.9	109	2	US-08-162- Sequence 23, Applicati
31	45	70.3	23	2	US-08-303- Sequence 9, Applicatio
32	45	70.3	107	2	US-08-561- Sequence 6, Applicatio
33	45	70.3	107	2	US-08-562- Sequence 6, Applicatio
34	45	70.3	107	3	PCT-US95-0 Sequence 84, Applicati
35	45	70.3	107	2	US-08-318- Sequence 8, Applicatio
36	45	70.3	107	2	US-08-561- Sequence 6, Applicatio
37	45	70.3	107	2	PCT-US95-0 Sequence 6, Applicatio
38	45	70.3	108	2	US-08-070- Sequence 7, Applicatio
39	45	70.3	126	2	US-08-202- Sequence 13, Applicati
40	45	70.3	126	2	US-08-202- Sequence 17, Applicati
41	45	70.3	126	2	US-08-202- Sequence 19, Applicati
42	45	70.3	126	2	US-08-202- Sequence 15, Applicati
43	45	70.3	131	2	US-08-202- Sequence 15, Applicati
44	45	68.8	106	2	US-08-899- Sequence 101, Applicat
45	44	68.8	106	2	US-08-899- Sequence 101, Applicat

ALIGNMENTS

RESULT	ID	PCT-US95-08743-87	STANDARD:	PRT:	107 AA.
XX	XXXXXX				
XX	Sequence 87, Application PC/TUS9508743				
CC	Sequence 87, Application PC/TUS9508743				
CC	GENERAL INFORMATION:				
CC	APPLICANT:				
CC	TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES				
CC	NUMBER OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS				
CC	NUMBER OF SEQUENCES: 170				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: FLOPPY disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: PCT/US95/08743				
CC	FILING DATE: 11-JUL-1995				
CC	PRIOR APPLICATION DATA:				
CC	APPLICATION NUMBER: US 08/276,852				
CC	FILING DATE: 18-JUL-1994				
CC	INFORMATION FOR SEQ ID NO: 87:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 107 amino acids				
CC	TYPE: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
CC	SEQUENCE 107 AA; 11654 MW; 62438 CN;				
CC	SEQUENCE 107 AA; 11654 MW; 62438 CN;				
DB	88 QOYHSSPYT 96				
DB	1 OKXNSAPYT 9				
QY	1 OKXNSAPYT 9				
RESULT	2				
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XX	XXXXXX				
AC	XXXXXX				

Query Match 81.3% Score 52; DB 3; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.64e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

[illegible]

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CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbás, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 NO. 5804440th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ
Query Match 81.3%; Score 52; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. NO. 1.6e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 88 QOYHSSPYT 96
| | : | : | | |
QY 1 QKYNAPYT 9

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Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 87 OKYNSVPH 95
||||| 1 1
1 OKYNSAPYT 9

RESULT 9
PCT-US95-08743-85 STANDARD: PRT: 106 AA.
xxxxxx

Sequence 85, Application PC/TUS9508743

CC Sequence 85, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 85:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 106 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 106 AA; 11406 MW; 64692 CN;

Query Match 75.0%; Score 48; DB 3; Length 106;
Best Local Similarity 77.8%; Pred. No. 4.52e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 87 OKYNSVPH 95
||||| 1 1
1 OKYNSAPYT 9

RESULT 10
ID US-08-899-575-85 STANDARD: PRT: 106 AA.
xxxxxx

Sequence 85, Application US/08899575

CC Sequence 85, Application US/08899575
CC Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8

CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentln Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 85:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 106 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 106 AA; 11406 MW; 64692 CN;

Query Match 75.0%; Score 48; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 4.52e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 87 OKYNSVPH 95
||||| 1 1
1 OKYNSAPYT 9

RESULT 11
ID US-08-899-575-85 STANDARD: PRT: 106 AA.
xxxxxx

Sequence 85, Application US/08899575

CC Sequence 85, Application US/08899575
CC Patent No. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA: US/08/899,575
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 85:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 106 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 106 AA: 11406 MW: 64692 CN:
SQ
Query Match 75.0%; Score 48; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 4.52e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 87 OKYNSAPYT 95
| | | | |
OY 1 OKYNSAPYT 9
RESULT 12
ID PCT-US95-08743-99 STANDARD: PRT: 108 AA.
XX xxxxxx
AC
XX
XX
DT
XX
XX
Sequence 99, Application PC/TUS9508743
GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN;
SQ

Query Match 75.0%; Score 48; DB 3; Length 108;
Best Local Similarity 55.6%; Pred. No. 4.52e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 88 QOYGTSPYT 96
| | | | |
OY 1 QOYGTSPYT 9
RESULT 13
ID US-08-276-852-99 STANDARD: PRT: 108 AA.
XX xxxxxx
AC
XX
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DT
XX
XX
Sequence 99, Application US/08276852
DE
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CC Sequence 99, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Bardas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11738 MW: 63142 CN;
SQ
Query Match 75.0%; Score 48; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 4.52e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 88 QOYGTSPYT 96
| | | | |

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 W P E S R E F
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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 Distribution rights by Oxford Molecular Ltd

Search: protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:38:39 1999; MasPar time 3.22 Seconds
 111.890 Million cell updates/sec
 Regular output not generated.

Title: >US-08-599-226-15
 Description: (1-9) from US08599226.pep
 Perfect Score: 64
 Sequence: 1 OKYNSAPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: PLR60
 1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 22.073; Variance 27.395; scale 0.806

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	50	78.1	91	2	S67940	Ig kappa chain V regl	2.98e+00
2	50	78.1	92	2	S37513	Ig kappa chain V regl	2.98e+00
3	50	78.1	109	2	H30601	Ig kappa chain V-III	2.98e+00
4	50	78.1	109	2	A30608	Ig kappa chain V-III	2.98e+00
5	49	76.6	128	1	K3H041	Ig kappa chain precu	4.81e+00
6	49	76.6	533	2	A47143	retinal pigment micro	4.81e+00
7	48	75.0	106	2	A49138	IgA kappa rheumatoid	7.72e+00
8	48	75.0	107	2	A28195	Ig kappa chain V regl	7.72e+00
9	48	75.0	108	2	PL0204	anti-DNA autoantibody	7.72e+00
10	48	75.0	108	1	K1HUBN	Ig kappa chain V-I re	7.72e+00
11	48	75.0	129	2	S40369	Ig kappa chain - huma	7.72e+00
12	48	75.0	500	2	S64220	hypothetical protein	1.23e+01
13	47	73.4	95	2	PH0863	Ig kappa chain V regl	1.23e+01
14	47	73.4	107	2	S40366	Ig kappa chain V regl	1.23e+01
15	47	73.4	1203	2	S27458	SMY2 protein - yeast	1.23e+01
16	47	73.4	1203	2	S27455	pullulanase - Thermo	1.23e+01
17	46	71.9	1673	2	I50806	complement component	1.95e+01
18	46	71.9	278	2	S72385	hypothetical protein	1.95e+01
19	46	71.9	846	2	S13795	neurotactin - fruit f	1.95e+01
20	46	71.9	846	2	S12005	neurotactin - fruit f	1.95e+01
21	46	71.9	1042	2	G64514	type I restriction en	1.95e+01
22	46	71.9	1409	2	S41028	hypothetical protein	1.95e+01
23	45	70.3	92	2	S37524	Ig kappa chain V regl	3.07e+01

24	45	70.3	109	2	G30607	Ig kappa chain V-III	3.07e+01
25	45	70.3	114	1	K1HURE	Ig kappa chain V-I re	3.07e+01
26	45	70.3	114	1	K4HULN	Ig kappa chain V-IV r	3.07e+01
27	45	70.3	216	2	JE0241	Ig kappa chain Am37 p	3.07e+01
28	45	70.3	259	2	H64699	hypothetical protein	3.07e+01
29	45	70.3	259	2	C71820	hypothetical protein	3.07e+01
30	45	70.3	376	2	S73941	oligopeptide transpor	3.07e+01
31	45	70.3	1139	2	S61918	protein kinase C (EC	3.07e+01
32	44	68.8	117	2	S42466	Ig kappa chain V regl	4.79e+01
33	44	68.8	138	2	PC1206	envelope protein - he	4.79e+01
34	44	68.8	270	2	F63362	conserved hypotherica	4.79e+01
35	44	68.8	292	2	T00829	homodomain transcrip	4.79e+01
36	44	68.8	376	2	S55149	hypothetical protein	4.79e+01
37	44	68.8	615	1	ABCHS	serum albumin precurs	4.79e+01
38	44	68.8	697	2	T03722	EXO70 protein - mouse	4.79e+01
39	44	68.8	794	2	T02171	hypothetical protein	4.79e+01
40	44	68.8	820	2	T02152	hypothetical protein	4.79e+01
41	44	68.8	905	2	T02205	Lu-ECAM-1 protein - b	4.79e+01
42	44	68.8	1260	2	S28407	guanine nucleotide-ex	4.79e+01
43	44	68.8	1290	2	A56493	leucocyte common anti	4.79e+01
44	44	68.8	1529	2	T02730	probable reverse tran	4.79e+01
45	44	68.8	2259	2	S29236	calcium channel prote	4.79e+01

ALIGNMENTS

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ENTRY	S67940	#type fragment	
TITLE	Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998		
ACCESSIONS	S67940		
REFERENCE	S67940		
#authors	Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.		
#journal	Autoimmunity (1992) 12:135-141		
#title	Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial approach.		
#cross-references	#cross-references M01D:92314301		
#accession	S67940		
#status	preliminary		
#molecule_type	mRNA		
#residues	1-91 #label HEX		
#cross-references	#cross-references EMBL:X73852		
CLASSIFICATION	#superfamily Immunoglobulin V region; immunoglobulin homology		
SUMMARY	#length 91 #checksum 3259		
Query Match	78.1%; Score 50; DB 2; Length 91;		
Best Local Similarity	66.7%; Pred. No. 2.98e+00;		
Matches	6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
Db	71 OKYNSAPYT 79		
Qy	1 OKYNSAPYT 9		
RESULT	2		
ENTRY	S37513	#type fragment	
TITLE	Ig kappa chain V region (V-kappa 3) - human (fragment)		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997		
ACCESSIONS	S37513		
REFERENCE	S37513		
#authors	Klein, U.; Kuempers, R.; Rajewsky, K.		
#submission	submitted to the EMBL Data Library, September 1993		
#description	Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood, expresses V(kappa) genes with no or little somatic mutation throughout life.		
#accession	S37513		

##status preliminary
 ##molecule-type mRNA
 ##residues 1-92 ##label KLE
 ##cross-references EMBL:226598; NID:9405668; PID:9405666
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 92 #checksum 6096

Query Match 78.1%; Score 50; DB 2; Length 92;
 Best Local Similarity 66.7%; Pred. No. 2.98e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 73 QOYSSPYT 81
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 QY 1 OKYNSAPYT 9

RESULT 3
 ENTRY H30601 #type fragment
 TITLE Ig kappa chain V-III region (Gar and Plo) - human (fragment)
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
 ACCESSIONS H30601; E30601
 REFERENCE A30601
 #authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.

#journal J. Immunol. (1989) 142:3158-3163
 #title Structural and idiotypic characterization of the L chains of human Igm autoantibodies with different specificities.
 #cross-references M0ID:89215279
 #accession H30601
 #status preliminary
 #molecule-type protein
 #accession E30601
 #residues 1-109 ##label GON1
 #status preliminary
 #molecule-type protein
 #residues 1-109 ##label GON2
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 109 #checksum 5951

Query Match 78.1%; Score 50; DB 2; Length 109;
 Best Local Similarity 66.7%; Pred. No. 2.98e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

90 QOYSSPYT 98
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 QY 1 OKYNSAPYT 9

RESULT 4
 ENTRY A30608 #type fragment
 TITLE Ig kappa chain V-III region (Son) - human (fragment)
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
 ACCESSIONS A30608
 REFERENCE A30601
 #authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.

#journal J. Immunol. (1989) 142:3158-3163
 #title Structural and idiotypic characterization of the L chains of human Igm autoantibodies with different specificities.
 #cross-references M0ID:89215279
 #accession A30608
 #status preliminary
 #molecule-type protein
 #residues 1-109 ##label GON
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 109 #checksum 6031

Query Match 78.1%; Score 50; DB 2; Length 109;
 Best Local Similarity 66.7%; Pred. No. 2.98e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 90 QOYSSPYT 98
 | | | | |
 QY 1 OKYNSAPYT 9

RESULT 5
 ENTRY K3H041 #type complete
 TITLE Ig kappa chain precursor V-III region (IARC/BL41) - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
 ACCESSIONS A01899
 REFERENCE A93588
 #authors Klobbeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zachau, H.G.

#journal Nucleic Acids Res. (1985) 13:6499-6513
 #title Human immunoglobulin kappa light chain genes of subgroups II and III.
 #cross-references M0ID:86041852
 #accession A01899
 #molecule-type DNA
 #residues 1-128 ##label K10
 #note the sequence was determined from the differentiated gene

GENETICS
 #gene GDB:IGKV3
 #cross-references GDB:136266
 #map_position 2p12-2p11
 #introns 17/1

COMPLEX
 An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 #superfamily immunoglobulin V region; immunoglobulin homology
 heterotetramer; immunoglobulin

CLASSIFICATION #status predicted #label SIG
 KEYWORDS #product Ig kappa chain V-III region (IARC/BL41) #status predicted #label MAT

FEATURE
 1-20
 21-128
 21-43 #region framework 1\
 44-54 #region complementarity-determining 1\
 55-69 #region framework 2\
 70-76 #region complementarity-determining 2\
 77-108 #region framework 3\
 109-117 #region complementarity-determining 3\
 118-128 #region framework 4\
 43-108 #disulfide_bonds #status predicted
 #length 128 #molecular_weight 14070 #checksum 5944

Query Match 76.6%; Score 49; DB 1; Length 128;
 Best Local Similarity 55.6%; Pred. No. 4.81e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 109 QOYSSPYT 117
 | | | | |
 QY 1 OKYNSAPYT 9

RESULT 6
 ENTRY A47143 #type complete
 TITLE retinal pigment microsome protein RPE65, epithelium-specific
 - bovine

ALTERNATE_NAMES membrane receptor p63; retinol-binding protein receptor
 ORGANISM #formal_name Bos primigenius taurus #common_name cattle
 DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change

10-Sep-1997
ACCESSIONS A47143; A48017; S28503
ENTRY A47143
TITLE Hamel, C.P.; Tsilou, E.; Pfeiffer, B.A.; Hooks, J.J.; Detrick, B.; Redmond, T.M.
ORGANISM J. Biol. Chem. (1993) 268:15751-15757
#journal Molecular cloning and expression of RPE65, a novel retinal pigment epithelium-specific microsomal protein that is post-translationally regulated in vitro.
#cross-references MUID:93340181
#accession A47143
#status preliminary
#molecule_type mRNA
#residues 1-533 #label HAM
#cross-references GB:L1356; NID:g163656; PID:g163657
REFERENCE A48017
#authors Baviik, C.O.; Levy, F.; Hellman, U.; Wernstedt, C.; Eriksson, U.
#journal J. Biol. Chem. (1993) 268:20540-20546
#title The retinal pigment epithelial membrane receptor for plasma retinol-binding protein. Isolation and cDNA cloning of the 63-kDa protein.
#cross-references MUID:93386633
#accession A48017
#status preliminary
#molecule_type mRNA
#residues 1-340, 'L', 342-533 #label BA2
#cross-references EMBL:X66277; NID:g563; PID:g564
KEYWORDS membrane protein
SUMMARY #length 533 #molecular-weight 60944 #checksum 3885

Query Match 76.6%; Score 49; DB 2; Length 533;
Best Local Similarity 66.7%; Pred. No. 4.81e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 424 QKYGKPYT 432
| | | | |
OY 1 QKYSAPYT 9

RESULT 7
ENTRY A49138 #type fragment
TITLE IGA kappa rheumatoid factor variable - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
ACCESSIONS A49138
REFERENCE A49138
#authors Gause, A.; Kupperts, R.; Mierau, R.
#journal Clin. Exp. Immunol. (1992) 88:430-434
#title A somatically mutated V kappa IV gene encoding a human rheumatoid factor light chain.
#cross-references MUID:92298590
#accession A49138
#status preliminary
#molecule_type DNA
#residues 1-106 #label GAV
#cross-references GB:S37926; NID:g298207; PID:g298208
#note sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:106633, NCBI:P:106637)
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 106 #checksum 7525

Query Match 75.0%; Score 48; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 7.72e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 98 QOYSTPYT 106
| | | | |
OY 1 QKYSAPYT 9

RESULT 8
ENTRY A28195 #type complete
TITLE Ig kappa chain V region (anti-haloperidol antibody A) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 08-Sep-1997
ACCESSIONS A28195
REFERENCE A28195
#authors Sherman, M.A.; Deans, R.J.; Bolger, M.B.
#journal J. Biol. Chem. (1988) 263:4059-4063
#title Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid sequence determination.
#cross-references MUID:88153717
#accession A28195
#status preliminary
#molecule_type mRNA
#residues 1-107 #label SHE
#cross-references GB:M19766; NID:g197039; PID:g197040
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 107 #molecular-weight 11782 #checksum 8207

Query Match 75.0%; Score 48; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 7.72e+00;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYSTPYT 97
| | | | |
OY 1 QKYSAPYT 9

RESULT 9
ENTRY P10204 #type fragment
TITLE anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-May-1996
ACCESSIONS P10204
REFERENCE P10198
#authors Smith, R.G.; Voss Jr., E.W.
#journal Mol. Immunol. (1990) 27:463-470
#title Variable region primary structures of monoclonal anti-DNA autoantibodies from NZB/NZW F1 mice.
#accession P10204
#molecule_type mRNA
#residues 1-108 #label SMT
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE 24-34 #region complementarity-determining 1\
50-56 #region complementarity-determining 2\
89-97 #region complementarity-determining 3\
96-108 #region JH region
SUMMARY #length 108 #checksum 3275

Query Match 75.0%; Score 48; DB 2; Length 108;
Best Local Similarity 77.8%; Pred. No. 7.72e+00;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYSTPYT 97
| | | | |
OY 1 QKYSAPYT 9

RESULT 10
ENTRY K1HDBN #type complete
TITLE Ig kappa chain V-I region (Ban) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 15-Aug-1997
ACCESSIONS A01878
REFERENCE A01878
#authors Dwaileh, F.E.; O'Connor, T.P.; Benson, M.D.
#journal Mol. Immunol. (1986) 23:73-78

#title Polymorphism in a kappa I primary (AL) amyloid protein (BAN).
#cross-references M01D:86174817
#accession A01878
#molecule-type protein
#residues 1-108 ##label DMU
GENETICS
#gene GDB:IGKV1
#cross-references GDB:136264
#map_position 2p12-2p12
COMPLEX
An immunoglobulin heterotrimer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology amyloid; heterotrimer; immunoglobulin
KEYWORDS
FEATURE
#region framework 1\
#domain immunoglobulin homology #label IMM\
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3\
#region framework 4\
#disulfide_bonds #status predicted
#length 108 #molecular_weight 11840 #checksum 3210
SUMMARY
Query Match 75.0%; Score 48; DB 1; Length 108;
Best Local Similarity 77.8%; Pred. No. 7.72e+00;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 89 QKNSAPYT 97
| | | | |
QY 1 QKNSAPYT 9
RESULT 11
ENTRY S40369 #type complete
TITLE Ig kappa chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 08-Sep-1997
ACCESSIONS S40369
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chl genes and their hypermutation.
#accession S40369
#status preliminary; translation not shown
#molecule-type mRNA
#residues 1-129 ##label KIE
#cross-references EMBL:X72479; NID:g441426; PID:g441427
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology heterotrimer; immunoglobulin
KEYWORDS
SUMMARY
#length 129 #molecular_weight 14063 #checksum 6277
Query Match 75.0%; Score 48; DB 2; Length 129;
Best Local Similarity 77.8%; Pred. No. 7.72e+00;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 110 QKNSAPYT 118
| | | | |
QY 1 QKNSAPYT 9
RESULT 12
ENTRY S64220 #type complete
TITLE hypothetical protein YGL202W - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein G1253

ORGANISM #formal_name Saccharomyces cerevisiae
DATE 17-May-1996 #sequence_revision 17-May-1996 #text_change 06-Feb-1998
ACCESSIONS S64220
REFERENCE S64218
#authors Bjorson, A.J.; McReynolds, A.D.K.; Wright, L.F.
#submission submitted to the Protein Sequence Database, May 1996
#accession S64220
#molecule-type DNA
#residues 1-500 ##label BJO
#cross-references EMBL:272724; NID:g1322833; PID:e243502; PID:g1322834; MIPS:YGL202W
#experimental_source strain S288C
GENETICS
#gene SCD:ARO8
#cross-references SGD:S0003170; MIPS:YGL202W
#map_position 7L
SUMMARY
#length 500 #molecular_weight 56177 #checksum 3537
Query Match 75.0%; Score 48; DB 2; Length 500;
Best Local Similarity 85.7%; Pred. No. 7.72e+00;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 415 KYNDDPY 421
| | | | |
QY 2 KYNDDPY 8
RESULT 13
ENTRY PH0863 #type fragment
TITLE Ig kappa chain V region (anti-DNA, IIT-2R) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
ACCESSIONS PH0863
REFERENCE PH0862
#authors Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
#journal J. Exp. Med. (1991) 174:1639-1652
#title Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.
#cross-references M01D:9207875
#accession PH0863
#molecule-type DNA
#residues 1-95 ##label MAN
COMMENT This antibody is produced by Epstein-Barr virus-transformed B cell that bears the Jt idiotype expressed on anti-DNA antibody.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology heterotrimer; immunoglobulin
KEYWORDS
FEATURE
#region framework 1\
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
#length 95 #checksum 6652
SUMMARY
Query Match 73.4%; Score 47; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.23e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 89 QKNSAP 95
| | | | |
QY 1 QKNSAP 7
RESULT 14
ENTRY S40366 #type complete
TITLE Ig kappa chain V-J region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-May-1994 #sequence_revision 26-May-1995 #text_change 20-Mar-1998


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ACCESSIONS      S40366
REFERENCE        S40312
#authors         Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal         Eur. J. Immunol. (1993) 23:3248-3271
#title           Expressed human immunoglobulin chl genes and their
#               hypermutation.
#accession       S40366
#status          Preliminary; translation not shown
#molecule_type mRNA
#residues        1-107 #label KLE
#cross-references EMBL:X72476; NID:9441420; PID:9441421
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS         heterotrimer; immunoglobulin
SUMMARY          #length 107 #molecular-weight 11556 #checksum 9149

Query Match      73.4%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.23e+01;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

101 OKNSAP 107
|||||
1 OKNSAP 7

RESULT 15
ENTRY      S27458 #type complete
TITLE      SMY2 protein - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein YBR123; protein YBR172c
ORGANISM   #formal_name Saccharomyces cerevisiae
DATE       28-May-1993 #sequence_revision 28-May-1993 #text_change
          06-Feb-1998
ACCESSIONS S27458; S36778; S46043; S37602
REFERENCE   S27458
#authors    Lillie, S.H.; Brown, S.S.
#submission submitted to the EMBL Data Library, April 1992
#description Characterization of a suppressor of the MYO2 gene in yeast.
#accession  S27458
#molecule_type DNA
#residues   1-790 #label LIL
#cross-references EMBL:M90654; NID:9172627; PID:9172628
REFERENCE     S36778
#authors      Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.;
#submission   submitted to the EMBL Data Library, July 1993
#description  Sequence and function analysis of a 4.3kb fragment of
#               saccharomyces cerevisiae Chromosome II including three open
#               reading frames.
#accession    S36778
#molecule_type DNA
#residues     323-790 #label SCH
#cross-references EMBL:X7437; NID:9402607; PID:9402610
REFERENCE     S46013
#authors      Enlian, K.D.; Koetter, P.; Rose, M.; Becker, J.; Grey, M.;
#               Li, Z.; Niegemann, E.; Schenk-Groeninger, R.; Servos, J.;
#               Wehner, E.; Wolter, R.; Brendel, M.; Baur, J.; Braun, H.;
#               Dern, K.; Duesterhus, S.; Gruenbein, R.; Hedges, D.;
#               Klesau, P.; Korol, S.; Krems, B.; Proft, M.; Siegers, K.;
#               Baur, A.; Boles, E.; Miosga, T.; Schaaff-Gerstenschlaeger,
#               I.; Zimmermann, F.K.
#submission   submitted to the Protein Sequence Database, August 1994
#accession    S46043
#molecule_type DNA
#residues     1-790 #label ENT
#cross-references EMBL:Z36041; NID:9536517; PID:9536518; MIPS:YBR172c
REFERENCE     S37600
#authors      Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.;
#               Zimmermann, F.K.
#journal      Yeast (1993) 9:915-921
#title        Yeast sequencing reports. Sequence and function analysis of a
#               4.3 kb fragment of Saccharomyces cerevisiae Chromosome II
#               including three open reading frames.
#accession    S37602
#molecule_type DNA

```

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#residues      323-358,'S',359-394,'S',395-430,'S',431-466,'S',467-502,
               'S',503-538,'S',539-573,'S',574-610,'S',611-646,'S',
               647-682,'S',683-718,'S',719-754,'S',755-790,'S'
#label         SC2
#note           In reference S46617 the authors state: In Fig. 3 the 'S'
               at the end of each line is not part of the amino acid
               sequence and has to be removed
REFERENCE       S46617
#authors        Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.;
               Zimmermann, F.K.
#journal        Yeast (1994) 10:1257
#title          Erratum to: sequence and function analysis of a 4.3 kb
               fragment of Saccharomyces cerevisiae Chromosome II
               including three open reading frames.
               annotation; erratum; correction to sequence display
GENETICS        #contents
#gene           SGD:SMY2
#cross-references SGD:S0000376; MIPS:YBR172c
#map_position   2R
SUMMARY         #length 790 #molecular-weight 87098 #checksum 5821

Query Match      73.4%; Score 47; DB 2; Length 790;
Best Local Similarity 44.4%; Pred. No. 1.23e+01;
Matches          4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db             318 EXYDPT 326
QY             1 OKNSAPIT 9

Search completed: Thu Sep 2 11:38:54 1999
Job time : 15 secs.

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 WISE (TM)

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MSearch protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:39:13 1999; Maspar time 2.22 Seconds
 Modular output not generated. 114.716 Million cell updates/sec

Title: >US-08-599-226-15
 Description: (1-9) from US08599226.pep
 Perfect Score: 64
 Sequence: 1 OKNSAPYT 9

Scoring table: PAW150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 22.646; Variance 24.608; scale 0.920

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	ID	Description	Pred. No.
1	76.6	128	1	KV3K_HUMAN IG KAPPA CHAIN PRECURS	1.55e+00
2	75.0	108	1	KV1V_HUMAN IG KAPPA CHAIN V-I REG	2.62e+00
3	75.0	500	1	AR08_YEAST AROMATIC AMINO ACID AM	4.39e+00
4	73.4	790	1	SMY2_YEAST SMY2 PROTEIN.	4.39e+00
5	73.4	1279	1	APU_THESA AMYLOBULIDULANASE PRECU	4.39e+00
6	73.4	1673	1	CO3_LAMIA COMPLEMENT C3 PRECURSO	4.39e+00
7	73.4	1861	1	APU_THESA AMYLOBULIDULANASE PRECU	4.39e+00
8	71.9	846	1	NRT_DROME NEUROACTIN.	7.31e+00
9	71.9	1385	1	YMS_CAEEL HYPOHETICAL.159.2 KD	7.31e+00
10	70.3	108	1	KV1O_HUMAN IG KAPPA CHAIN V-I REG	1.21e+01
11	70.3	108	1	KV3A_HUMAN IG KAPPA CHAIN V-III R	1.21e+01
12	70.3	114	1	KV4A_HUMAN IG KAPPA CHAIN V-IV RE	1.21e+01
13	70.3	376	1	OPPC_MYCPN OLIGOPEPTIDE TRANSPORT	1.21e+01
14	70.3	1139	1	KPCI_TREBE PROTEIN KINASE C-LIKE	1.21e+01
15	68.8	376	1	YNN4_YEAST HYPOHETICAL.41.2 KD P	1.98e+01
16	68.8	423	1	ARGD_KLULA ACETYLORITINE AMINOT	1.98e+01
17	68.8	517	1	TYR2_MOUSE DOPACHROME TAUOMERASE	1.98e+01
18	68.8	615	1	ALBU_CHICK SERUM ALBUMIN PRECURSO	1.98e+01
19	68.8	725	1	SPEI_DACA ARGININE DECARBOXYLASE	1.98e+01
20	68.8	1262	1	GNNP_MOUSE GUANINE NUCLEOTIDE REL	1.98e+01
21	68.8	1897	1	PTPF_HUMAN LAR PROTEIN PRECURSOR	1.98e+01
22	68.8	2259	1	CB21_RABIT BRAIN CALCIUM CHANNEL	1.98e+01
23	67.2	121	1	HV01_MOUSE IG HEAVY CHAIN V REGION	3.20e+01

Query	Match	Length	ID	Description	Pred. No.
24	67.2	392	1	YH8B_BACSU HYPOTHETICAL 45.3 KD P	3.20e+01
25	67.2	530	1	PRO9_YEAST PRE-MRNA SPLICING FACT	3.20e+01
26	67.2	591	1	EVAL_MOUSE EYES ABSENT HOMOLOG 1.	3.20e+01
27	67.2	592	1	EVAL_HUMAN EYES ABSENT HOMOLOG 1.	3.20e+01
28	67.2	808	1	PLD_TORAC PHOSPHOLIPASE D PRECUR	3.20e+01
29	67.2	808	1	PLD_RICCO PHOSPHOLIPASE D PRECUR	3.20e+01
30	67.2	809	1	PLD_VIGUN PHOSPHOLIPASE D PRECUR	3.20e+01
31	67.2	812	1	PLD_MAIZE PHOSPHOLIPASE D PRECUR	3.20e+01
32	67.2	812	1	PLD_ORYSA PHOSPHOLIPASE D 1 PREC	3.20e+01
33	67.2	1233	1	HCT_OCTDO HEMOCYTININ, UNITS ODE	3.20e+01
34	65.6	251	1	YGG4_HAEIN HYPOTHETICAL PROTEIN H	5.15e+01
35	65.6	252	1	YGG6_YEAST HYPOTHETICAL 28.5 KD P	5.15e+01
36	65.6	275	1	OMPS_VIBPA OUTER MEMBRANE PROTEIN	5.15e+01
37	65.6	309	1	YAOB_SCHPO HYPOTHETICAL 35.3 KD P	5.15e+01
38	65.6	340	1	YLS1_YEAST HYPOTHETICAL 39.8 KD P	5.15e+01
39	65.6	507	1	YGG6_YEAST HYPOTHETICAL 52.8 KD P	5.15e+01
40	65.6	573	1	EY43_HUMAN EYES ABSENT HOMOLOG 3.	5.15e+01
41	65.6	585	1	NEPU_THERV NEOPILULANASE (EC 3.2	5.15e+01
42	65.6	588	1	NEPU_BACST NEOPILULANASE (EC 3.2	5.15e+01
43	65.6	899	1	PMAL_KLULA PLASMA MEMBRANE ATPASE	5.15e+01
44	65.6	947	1	PMAL_YEAST PLASMA MEMBRANE ATPASE	5.15e+01
45	65.6	1389	1	TIM_DROME TIMELESS PROTEIN.	5.15e+01

ALIGNMENTS

RESULT 1
 ID KV3K_HUMAN STANDARD; PRT; 128 AA.
 AC P06311;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 NC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 86041852.
 RX KLOBECK H.G., METINDL A., COMBRIATO G., SOLOMON A., ZACHAU H.G.;
 RT "Human Immunoglobulin kappa light chain genes of subgroups II and
 III.";
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
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 CC EMBL; 200021; G33179; -
 DR PIR; A01899; K3H041.
 DR PFAM; PF00047; Ig; 1.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL
 FT CHAIN
 FT 1 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
 FT 21 128 FRAMEWORK 1.
 FT 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT 55 69 FRAMEWORK 2.
 FT 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT 77 108 FRAMEWORK 3.
 FT 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT 118 128 JKI SEGMENT.
 FT 128 128 BY SIMILARITY.
 FT NON TER
 FT 128 128
 SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match 76.6%; Score 49; DB 1; Length 128;
 Best Local Similarity 55.6%; Pred. No. 1.55e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 109 QOYSTSPYT 117
 QY 1 QKYNAPYT 9

RESULT 2
 ID KVIY_HUMAN STANDARD; PRT; 108 AA.
 AC P04450;

DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (BAN).

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RP SEQUENCE.

RX MEDLINE: 86174817.

RA DMULT F.E., O'CONNOR T.P., BENSON M.D.;
 "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
 MOL. IMMUNOL. 23:73-78(1986).
 PIR: A01878; KIHUBN.

DR HSSP: P80047; 19; 1.
 DR HSSP: P80362; 1WT.

KM IMMUNOGLOBULIN V REGION; AMYLOID.
 FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 49 FRAMEWORK 2.

FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 78 FRAMEWORK 3.

FT DOMAIN 6 89 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 0D44DA0A CRC32;

Query Match 75.0%; Score 48; DB 1; Length 108;

Best Local Similarity 77.8%; Pred. No. 2.62e+00;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYSTSPYT 97
 QY 1 QKYNAPYT 9

RESULT 3
 ID ARO8_YEAST STANDARD; PRT; 500 AA.
 AC P53080;

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE AROMATIC AMINO ACID AMINOTRANSFERASE I (EC 2.6.1.-).
 GN ARO8 OR YGL202W.

OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCCHAROMYCETALES;
 OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.

RP SEQUENCE FROM N.A.
 RC STRAIN-SIGNA 1278B;

RX MEDLINE: 98151783

RA TRAQUI I., VISSERS S., CARTIAUX M., URRESTARAZU A.;
 "Characterisation of Saccharomyces cerevisiae ARO8 and ARO9 genes
 encoding aromatic aminotransferases I and II reveals a new
 aminotransferase subfamily.";

RT MOL. GEN. GENET. 257:238-248(1998).
 RL [2]

RP SEQUENCE FROM N.A.

RA BJOUSON A.-J., MCREYNOLDS A.D.K., WRIGHT L.F.;
 SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

- I - SIMILARITY: TO YEAST ARO9.

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CC -----
 DR EMBL: Y13624; E321594; -.
 DR EMBL: 272724; E243502; -.
 DR SGD: L0003949; ARO8.
 KM TRANSFERASE; AMINOTRANSFERASE.
 SO SEQUENCE 500 AA; 56177 MW; B42B3B5 CRC32;

Query Match 75.0%; Score 48; DB 1; Length 500;
 Best Local Similarity 85.7%; Pred. No. 2.62e+00;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 415 KYNSDPY 421
 QY 2 KYNSAPY 8

RESULT 4
 ID SMY2_YEAST STANDARD; PRT; 790 AA.
 AC P32909;

DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)

DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE SMY2 PROTEIN.

GN SMY2 OR YBR172C OR YBR1233.

OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCCHAROMYCETALES;
 OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.

RP SEQUENCE FROM N.A.
 RA LITTE S.H., BROWN S.S.;

RL SUBMITTED (APR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]

RN SEQUENCE OF 323-790 FROM N.A.
 RC STRAIN-S288C;

RX MEDLINE: 94025982.

RA SCHAFF-GERSTENSLAGER I., BAUER A., BOLES E., ZIMMERMANN F.K.;
 "Sequence and function analysis of a 4.3 kb fragment of Saccharomyces
 cerevisiae chromosome II including three open reading frames.";

RT YEAST 9:915-921(1993).
 RL [3]

RN SEQUENCE FROM N.A.
 RP STRAIN-S288C;

RC EYTLIN K.-D., KOETTER P., ROSE M., BECKER J., GREY M., LI Z.,
 RA NIEGEMANN E., SCHENK-GROENINGER R., SERVOS J., WEHNER E.,
 RA WOLTER R., BRENDL M., BAUER J., BRAUN H., DERN K., DUESTERHUS S.,
 RA GRUBERBEIN R., HEDGES D., KIESAU P., KOROL S., KREMS B., PROFIT M.,
 RA SIEGERS K., BAUR A., BOLES E., MIOGA T.,
 RA SCHAFF-GERSTENSLAGER I., ZIMMERMANN F.K.;

RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [1- FUNCTION: SUPPRESSOR OF THE MYO2 GENE.

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CC -----
 DR EMBL: M80654; G172628; -.
 DR EMBL: X74437; G402610; -.
 DR EMBL: Z36041; G536518; -.
 DR PIR: S27458; S27458.
 DR SGD: L0001941; SMY2.

SO SEQUENCE 790 AA; 87098 MW; E3543AC2 CRC32;

Query Match 73.4%; Score 47; DB 1; Length 790;
 Best Local Similarity 44.4%; Pred. No. 4.39e+00;

Matches 4: Conservative 4: Mismatches 1: Indels 0: Gaps 0:
 Db 318 EXYDTPFT 326
 :||:|:|:
 QY 1 QKXNSAPYT 9

RESULT 5
 ID APU_THESA STANDARD: PRT: 1279 AA.
 AC P36905:
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE AMYLOPULULANASE PRECURSOR (ALPHA-AMYLASE/PULULANASE) (EC 3.2.1.1) /
 (EC 3.2.1.41) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (ALPHA-DEXTRIN
 DE ENDO-1,6-ALPHA-GLUCOSIDASE).
 GN APU.
 OS THERMOANEROBACTER SACCHAROLYTICUM.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
 THERMOANEROBACTER GROUP: THERMOANEROBACTERIUM.
 [1]
 [1] SEQUENCE FROM N.A.
 RC STRAIN-B6A-RI;
 RX MEDLINE: 94161525.
 RA RAMESH M.V., PODKOYEV S.M., LOWE S.E., ZEIRUS J.G.;
 RT "Cloning and sequencing of the Thermoanaerobacterium saccharolyticum
 RT B6A-RI apu gene and purification and characterization of the
 RT amylopullulanase from Escherichia coli";
 RT APPL. ENVIRON. MICROBIOL. 60:94-101(1994).
 RN [2]
 RP IDENTIFICATION OF PROBABLE VECTOR CONTAMINATION.
 RA ROBISON K.;
 RL UNPUBLISHED OBSERVATIONS (NOV-1994).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDOLYZES
 CC (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULULAN AND STARCH TO
 CC FORM MALTOSE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN BY THE PRESENCE OF
 CC AN EXTRA C-TERMINAL SEGMENT OF 9 RESIDUES THAT SEEMS TO ORIGINATE
 CC FROM A PUC-TYPE VECTOR.
 CC -----
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 CC -----
 CC EMBL: L07762; G154620; ALT_SEQ.
 CC DR PFAM: PF00041; fn3; 2.
 CC DR PFAM: PF00128; alpha-amyase; 1.
 CC KM HYDROLASE: GLYCOSIDASE; CARBOHYDRATE METABOLISM; SIGNAL; REPEAT;
 CC MULTIFUNCTIONAL ENZYME.
 CC FT SIGNAL 1 35 POTENTIAL.
 CC FT CHAIN 36 1279 AMYLOPULULANASE.
 CC FT ACT_SITE 629 629 BY SIMILARITY.
 CC FT ACT_SITE 658 658 BY SIMILARITY.
 CC FT ACT_SITE 735 735 BY SIMILARITY.
 CC FT DOMAIN 929 1017 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 1156 1248 FIBRONECTIN TYPE-III.
 CC SQ SEQUENCE 1279 AA; 142430 MW; DA982B83 CRC32;

Query Match 73.4% Score 47; DB 1; Length 1279;
 Best Local Similarity 55.6% Pred. No. 4.39e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 485 HKYDTADYT 493
 :||:|:|:

QY 1 QKXNSAPYT 9

RESULT 6
 ID CO3_LAMJA STANDARD: PRT: 1673 AA.
 AC 000685;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN] (FRAGMENT).
 GN C3.
 OS LAMPETRA JAPONICA (JAPANESE LAMPREY).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CEPHALASPIDOMORPHI;
 OC PETROMYZONIFORMES; PETROMYZONITIDAE; LAMPETRA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 92251197.
 RA NONAKA M., TAKAHASHI M.;
 RT "Complete complementary DNA sequence of the third component of
 RT complement of lamprey. Implication for the evolution of thioester
 RT containing proteins";
 RL J. IMMUNOL. 148:3290-3295(1992).
 CC -1- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
 CC COMPLEMENT SYSTEM. AFTER ACTIVATION (C3B), IT CAN BIND COVALENTLY,
 CC VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR
 CC IMMUNE AGGREGATES. CYCLOSTOMATIDS C3 APPEARS TO REPRESENT THE
 CC COMMON ANCESTOR OF MAMMALIAN C3 AND C4, SHOWING SIMILARITIES TO
 CC BOTH PROTEINS.
 CC -1- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D10087; G222888;
 CC DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 CC DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 CC DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 CC DR PFAM: PF00207; A2M; 1.
 CC DR HSSP: P01024; IC3D.
 CC KM COMPLEMENT PATHWAY; PLASMA; INFLAMMATORY RESPONSE; GLYCOPROTEIN;
 CC SIGNAL.
 CC FT NON_TER 1 1
 CC FT SIGNAL <1 13
 CC FT CHAIN 14 1673
 CC FT CHAIN 14 653
 CC FT CHAIN 657 1375
 CC FT CHAIN 1379 1673
 CC FT CHAIN 1673 1673
 CC FT PEPTIDE 657 732
 CC FT DOMAIN 678 713
 CC FT DISULFID 678 705
 CC FT DISULFID 679 712
 CC FT DISULFID 692 713
 CC FT THIOLEST 986 990
 CC SQ SEQUENCE 1673 AA; 187767 MW; D857446F CRC32;

Query Match 73.4% Score 47; DB 1; Length 1673;
 Best Local Similarity 75.0% Pred. No. 4.39e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 443 QKXASAY 450
 :||:|:|:
 QY 1 QKXNSAPYT 8
 :||:|:|:
 RESULT 7
 ID APU_THETA STANDARD: PRT: 1861 AA.

AC P38536; 01-OCT-1994 (REL. 30, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE AMYLOPULULANASE PRECURSOR (ALPHA-AMYLASE/PULULANASE) (EC 3.2.1.1) /
 (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN GLUCANOHIDROLASE) (ALPHA-DEXTRIN
 ENDO-1,6-ALPHA-GLUCOSIDASE) (PULULANASE TYPE II).
 GN AMYB.
 OS THERMOANAEROBACTER THERMOSULFURGENES (CLOSTRIDIUM
 THERMOSULFURGENES).
 OC BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP:
 THERMOANAEROBACTER GROUP; THERMOANAEROBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DSM 3896 / EML;
 RX MEDLINE: 94252998.
 RA MATUSCHER M., BURCHARDT G., SAHM K., BAH L. H.;
 RT "Pululanase of Thermoanaerobacterium thermosulfurigenes EML
 (Clostridium thermosulfurigenes): molecular analysis of the gene,
 composite structure of the enzyme, and a common model for its
 attachment to the cell surface.";
 J. BACTERIOL. 176:3295-3302(1994).
 RL [1]
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES
 (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULULAN AND STARCH TO
 FORM MALTOSE.
 CC -1- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN
 S-LAYER ANCHOR.
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
 CC -----
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 CC -----
 DR EMBL: M57692; G1235795; -;
 DR PROSITE: PS01072; SLH_DOMAIN; 3.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00128; alpha-amylase; 1.
 DR PFAM: PF00395; SLH; 3.
 CC HYDROLASE; GLYCOSIDASE; CARBOHYDRATE METABOLISM; SIGNAL; REPEAT;
 MULTIFUNCTIONAL ENZYME; GLYCOPROTEIN.
 FT SIGNAL 1 35
 FT CHAIN 36 1861
 FT ACT_SITE 628 628
 FT ACT_SITE 657 657
 FT ACT_SITE 734 734
 FT DOMAIN 928 1018
 FT DOMAIN 1157 1248
 FT DOMAIN 1681 1739
 FT DOMAIN 1740 1803
 FT DOMAIN 1804 1861
 FT CONFLICT 1734 1734
 FT SEQUENCE 1861 AA: 206104 MW; AHC2A80B CRC32;
 Query Match 73.4%; Score 47; DB 1; Length 1861;
 Best Local Similarity 55.6%; Pred. No. 4,39e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

ID NRT_DROME STANDARD; PRT; 846 AA.
 AC P23654;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEUROTACTIN.
 GN NRT.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA: METAZOA: ARTHROPODA: TRACHEATA: HEXAPODA: INSECTA:
 OC PTERYGOTA: DIPTERA: BRACHYCERA: MUSCOMORPHA: EPHYDROIDEA:
 OC DROSOPHILINAE: DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91301057.
 RA HORTSCH M., PATEL N.P., BIEBER A.J., TRAUQUINA Z.R., GOODMAN C.S.;
 RT "Drosophila neurotactin, a surface glycoprotein with homology to
 serine esterases, is dynamically expressed during embryogenesis.";
 DEVELOPMENT 110:1327-1340(1990).
 RL [2]
 CC -1- SEQUENCE FROM N.A.
 CC STRAIN-OREGON-R; TISSUE-EMBRYO;
 RX MEDLINE: 91006059.
 RA DE LA ESCALERA S., BOCKAMP E.O., MOYA F., PIOVANT M., JIMENEZ F.;
 RT "Characterization and gene cloning of neurotactin, a Drosophila
 transmembrane protein related to cholinesterases.";
 EMBO J. 9:3593-3601(1990).
 RN [3]
 RP FUNCTION.
 RX MEDLINE: 91006060.
 RA BARTHALAY Y., HIEPAU-JACQUOTTE R., DE LA ESCALERA S., JIMENEZ F.,
 RA PIOVANT M.;
 RT "Drosophila neurotactin mediates heterophilic cell adhesion.";
 EMBO J. 9:3603-3609(1990).
 RL [1]
 CC -1- FUNCTION: MAY MEDIATE OR MODULATE CELL ADHESION BETWEEN EMBRYONIC
 CELLS DURING DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN MEMBRANES DURING EMBRYOGENESIS
 AND THEN ACCUMULATES IN CNS AND PNS.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY
 IN THE EXTRACELLULAR DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X53837; G8288; -;
 DR EMBL: X54999; G8280; -;
 DR PIR: S12005; S12005.
 DR PIR: S13795; S13795.
 DR FLYBASE: FBgn0004108; Nrt.
 DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
 DR PFAM: PF00135; Coesterase; 1.
 DR HSSP: P21836; 1MAH.
 CC CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; PHOSPHORYLATION;
 KW SIGNAL-ANCHOR.
 FT DOMAIN 1 324
 FT TRANSMEM 325 346
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 347 846
 FT SIMILAR 351 846
 FT MOD_RES 28 28
 FT MOD_RES 75 75
 FT MOD_RES 103 103
 FT MOD_RES 169 169
 FT MOD_RES 186 186
 FT DISULFID 422 437
 FT DISULFID 600 605
 FT DISULFID 738 830
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT CARBOHYD 410 410 POTENTIAL.
 FT CARBOHYD 417 417 POTENTIAL.
 FT CARBOHYD 428 428 POTENTIAL.
 FT CARBOHYD 636 636 POTENTIAL.
 FT CARBOHYD 691 691 POTENTIAL.
 FT CARBOHYD 720 720 POTENTIAL.
 FT CARBOHYD 250 250 G -> S (IN REF. 2).
 FT CONFLICT 250 250 S -> T (IN REF. 2).
 FT CONFLICT 555 555 F -> Y (IN REF. 2).
 FT CONFLICT 567 567
 SQ SEQUENCE 846 AA; 92745 MW; AC82B36D CRC32;

Query Match 71.9%; Score 46; DB 1; Length 846;
 Best Local Similarity 44.4%; Pred. No. 7.31e+00;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 717 EKVYASPT 725
 QY 1 OKYNSAPYT 9

AC P34501; STANDARD; PRT; 1385 AA.
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III.
 GN K03H1.5.
 OS CAENORHABDITIS ELEGANS.
 OC ECAKAROTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL NZ;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
 RA FULTON L., GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M.,
 RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
 RA LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEFEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
 RA SULLSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
 RA WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
 RA WOLDMAN P.;
 RA *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans*;
 SQ NATURE 368:32-38(1994).

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CC EMBL: Z29560; E1347842; -
 CC DR PIR: S41028; S41028;
 CC DR WORMPEP: K03H1.5; CE03459.
 CC DR PFAM: PF00084; susn1.1.
 CC HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 1385 AA; 159181 MW; A2134063 CRC32;

Query Match 71.9%; Score 46; DB 1; Length 1385;
 Best Local Similarity 50.0%; Pred. No. 7.31e+00;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 797 HRYGAPY 804
 QY 1 OKYNSAPYT 8

RESULT 10
 ID RY10_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (REL).
 OS HOMO SAPIENS (HUMAN).
 OC ECAKAROTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]

RP SEQUENCE.
 RX MEDLINE: 76023758.
 RA PALM W., HILSCHEMANN N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); isolation
 RT and characterization of the tryptic peptides; the complete amino acid
 RT sequence of the protein; a contribution to the elucidation of the
 RT three-dimensional structure of antibodies, in particular their
 RT combining site.";
 RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 356:167-191(1975).
 RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE: 76039968.
 RA EPP O., LATMAN E.E., SCHIFFER M., HUBER R., PALM W.;
 RT "The molecular structure of a dimer composed of the variable portions
 RT of the Bence-Jones protein Rel refined at 2.0-A resolution.";
 RL BIOCHEMISTRY 14:4943-4952(1975).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01873; K1HDE.
 DR PDB: 1REI; 17-FEB-84.
 DR PFAM: PF00047; 19; 1.

KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 35 FRAMEWORK 2.
 FT DOMAIN 4 36 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 37 FRAMEWORK 3.
 FT DOMAIN 6 38 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 7 39 FRAMEWORK 4.
 FT DISULFID 23 88
 FT NON_TER 108 108

FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 98 98
 FT STRAND 102 106
 SQ SEQUENCE 108 AA; 11902 MW; D08F51A4 CRC32;

Query Match 70.3%; Score 45; DB 1; Length 108;
 Best Local Similarity 66.7%; Pred. No. 1.21e+01;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 89 QOYOSLPYT 97
 QY 1 OKYNSAPYT 9

```

RESULT 11
ID KV3A_HUMAN STANDARD: PRT: 108 AA.
AC P01619;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (B6).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PR PRIMATES; CATHARTINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE.
RA MILSTEIN C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, F4 and B6."
RL FEBS LETT. 2:301-304(1983).
CC -1- THIS IS A BENGE-JONES PROTEIN.
PFAM: A01891; K3H0B6.
HSSP: P01789; 2MCP.
IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11635 MW: 46D6B68E CRC32:

Query Match 70.3%; Score 45; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 1.21e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 90 QOYGSSEPT 98
1 1 1 1 1 1
1 OKYNSAPYT 9

RESULT 12
ID KV4A_HUMAN STANDARD: PRT: 114 AA.
AC P01625;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-IV REGION (LEN).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PR PRIMATES; CATHARTINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE.
RA MEDLINE: 76004342.
RA SCHNEIDER M., HILSCHMANN N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
subgroup IV of the kappa type (Bence-Jones protein Len.).";
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA SALOMON A.;
RA SUBMITTED (AUG-1996) TO THE SWISS-PROT DATA BANK.
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENGE-JONES PROTEIN.
PFAM: A01903; KAHULN.
HSSP: P01789; 2MCP.
IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 41 55 FRAMEWORK 2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 63 94 FRAMEWORK 3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 113 FRAMEWORK 4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA: 12640 MW: E1CE0BB CRC32:

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Query Match 70.3%; Score 45; DB 1; Length 114;
Best Local Similarity 55.6%; Pred. No. 1.21e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 95 QOYSTPYIS 103
1 1 1 1 1 1
1 OKYNSAPYT 9

RESULT 13
ID OPFC_MYCPN STANDARD: PRT: 376 AA.
AC P75553;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPFC.
GN OPFC.
OS MYCOPLASMA PNEUMONIAE.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLICUTES;
OC MYCOPLASMATACEAE; MYCOPLASMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129.
RX MEDLINE: 97105885.
RA HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
RA HERRMANN R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
pneumoniae";
RL NUCLEIC ACIDS RES. 24:4420-4449(1996).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF
THE SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPFC
SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000058; G1674317; -
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER: 1.
DR PFAM: PF00528; BPD_TRANSP: 1.
KW TRANSPORT; PEPTIDE TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
FT TRANSMEM 341 361 POTENTIAL.
SQ SEQUENCE 376 AA: 41233 MW: 151AF8C3 CRC32:

Query Match 70.3%; Score 45; DB 1; Length 376;
Best Local Similarity 85.7%; Pred. No. 1.21e+01;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 134 KYNIAPY 140
1 1 1 1 1 1
2 KYNSAPY 8

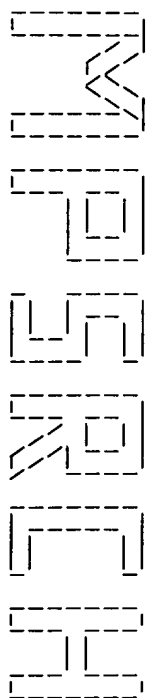
RESULT 14
ID KPCL_TRIPE STANDARD: PRT: 1139 AA.
AC Q99014;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

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DE PROTEIN KINASE C-LIKE (EC 2.7.1.-).
 GN PKC1.
 OS TRICHODERMA RESEI (HYPOCREA JECORINA).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
 CC HYPOCREALES; HYPOCREACEAE; HYPOCREA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-QM9414 / RUT C-30;
 RX MEDLINE: 96158841.
 RA MORAMETZ R., LENDENFELD T., MISCHAR H., MOHLBAUER M., GRUBER F.,
 RA KUBICEK C.P.;
 RT "Cloning and characterisation of genes (pkc1 and pkca) encoding
 RT protein kinase C homologues from Trichoderma reesei and Aspergillus
 RT niger.";
 RL MOL. GEN. GENET. 250:17-28(1996).
 CC -1- ENZYME REGULATION: STIMULATED ABOUT TWOFOOLD BY PHOSPHOLIPIDS OR
 CC PHORBOL ESTERS.
 CC -1- SIMILARITY: CONTAINS TWO COPIES OF THE ZINC-DEPENDENT PHORBOL-
 CC ESTER AND DAG BINDING DOMAIN.
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
 CC PROTEIN KINASES. BELONGS TO THE PKC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U10016; G501075; -
 CC DR PROSITE: PS00107; PROTEIN_KINASE_APP; 1.
 CC DR PROSITE: PS00479; DAG_PE_BINDING_DOMAIN; 2.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC DR PFAM: PF00069; pkinese; 1.
 CC DR PFAM: PF00130; DAG_PE-bind; 2.
 CC DR PFAM: PF00433; pkinese_C; 1.
 CC DR HSSP: O63450; 1A06
 CC TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING; ZINC;
 CC PHORBOL-ESTER BINDING; DUPLICATION.
 CC KW DOMAIN 455 502
 CC FT PHORBOL-ESTER AND DAG BINDING (BY
 CC FT SIMILARITY).
 CC FT DOMAIN 523 572
 CC FT PHORBOL-ESTER AND DAG BINDING (BY
 CC FT SIMILARITY).
 CC FT DOMAIN 814 1073
 CC FT NP_BIND 820 828
 CC FT BINDING 843 843
 CC FT ACT_SITE 939 939
 CC ACT_SITE 939 939
 CC BY SIMILARITY.
 CC SEQUENCE 1139 AA; 126055 MW; 2AF00B6 CRC32;
 CC -----
 CC Query Match 70.3%; Score 45; DB 1; Length 1139;
 CC Best Local Similarity 55.6%; Pred. No. 1.21e+01;
 CC Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC Db 707 HKYNPADYA 715
 CC QY 1 QKYNAPYT 9
 CC -----
 CC RESULT 15
 CC ID YNNA YEAST STANDARD; PRT; 376 AA.
 CC AC P53912;
 CC DT 01-OCT-1996 (REL. 34, CREATED)
 CC DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 CC DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 CC DE HYPOTHETICAL 41.2 KD PROTEIN IN FPR1-TOM22 INTERGENIC REGION.
 CC GN YNL134C OR N1214 OR N1847.
 CC OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
 CC OC SACCHAROMYCETACEAE; SACCHAROMYCETES.
 CC RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE: 96109932.
 RA MALLLET L., BUSSEMAN F., JACQUET M.;
 RT "A 43.5 Kb segment of yeast chromosome XIV, which contains MEA2,
 RT MEP2, CAP/SRV2, NAM9, FRB1/EPRI/RBP1, MOM22 and CPT1, predicts an
 RT adenosine deaminase gene and 14 new open reading frames.";
 RL YEAST 11:1195-1209(1995).
 CC -1- SIMILARITY: BELONGS TO THE YCR102C/YLR460C/YNL134C FAMILY.
 CC -----
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 CC -----
 CC EMBL: 246843; G854503; -
 CC DR EMBL: 271410; E239806; -
 CC DR PFAM: PF00107; adh_zinc; 1.
 CC KW HYPOTHETICAL PROTEIN.
 CC SQ SEQUENCE 376 AA; 41164 MW; 2523FEB4 CRC32;
 CC -----
 CC Query Match 68.8%; Score 44; DB 1; Length 376;
 CC Best Local Similarity 71.4%; Pred. No. 1.98e+01;
 CC Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC Db 239 KYNINPY 245
 CC QY 2 KYNAPYT 8
 CC -----
 CC Search completed: Thu Sep 2 11:39:24 1999
 CC Job time : 11 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:39:42 1999; Maspar time 4.30 Seconds
114.292 Million cell updates/sec

ular output not generated.

Title: >US-08-599-226-15
Description: (1-9) from US08599226.pep
Perfect Score: 64
Sequence: 1 OKNSAPYT 9

Scoring table: PAM 150
Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Databases:

sptrembl9
1:sp_archae 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mnc 8:sp_orcanelle
9:sp_phase 10:sp_plant 11:sp_protent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 21.769; Variance 24.891; scale 0.875

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	56	87.5	337	2	034232	ORF40X1 PROTEIN.	6.38e-02
2	56	87.5	337	2	087136	ORF139-17 PROTEIN.	6.38e-02
3	50	78.1	560	5	044626	KLID12.1 PROTEIN.	1.68e+00
4	49	76.6	533	6	028175	RETINAL PIGMENT EPITHE	2.83e+00
5	49	76.6	533	6	005661	RETINAL PIGMENT EPITHE	2.83e+00
6	48	75.0	496	2	087348	LAKR21 RESTRICTION EN	4.74e+00
7	47	73.4	16	14	079461	LIGHT-CHAIN COMPLEMENA	7.88e+00
8	47	73.4	16	14	079455	LIGHT-CHAIN COMPLEMENA	7.88e+00
9	47	73.4	450	2	050511	ZINC PROTEASE.	7.88e+00
10	47	73.4	856	4	076022	ELB-55KDA-ASSOCIATED P	1.88e+00
11	46	71.9	131	8	035865	NADH DEHYDROGENASE SUB	1.30e+01
12	46	71.9	278	2	047792	PUTATIVE PAD1, OPEN REA	1.30e+01
13	46	71.9	1042	1	060295	PUTATIVE TYPE I RESTRI	2.13e+01
14	45	70.3	259	2	025981	HYPOTHETICAL 29.4 KD P	2.13e+01
15	45	70.3	330	2	068847	SITE-SPECIFIC RECOMBIN	2.13e+01
16	45	70.3	332	5	045024	AMPHIOXUS ORX TRANSCRI	2.13e+01
17	45	70.3	451	13	093374	TRANSCRIPTION FACTOR (2.13e+01
18	45	70.3	653	11	054922	REXO70.	2.13e+01
19	45	70.3	758	2	066007	OUTER MEMBRANE PROTEIN	2.13e+01
20	45	70.3	758	2	P94930	OUTER MEMBRANE PROTEIN	2.13e+01

21	45	70.3	759	2	066006	OUTER MEMBRANE PROTEIN	2.13e+01
22	45	70.3	759	2	049099	MAJOR OUTER MEMBRANE P	2.13e+01
23	45	70.3	767	2	066008	OUTER MEMBRANE PROTEIN	2.13e+01
24	44	68.8	16	14	079456	LIGHT-CHAIN COMPLEMENA	3.47e+01
25	44	68.8	109	14	089863	(HHV-6).	3.47e+01
26	44	68.8	138	14	081372	POLYPROTEIN (FRAGMENT)	3.47e+01
27	44	68.8	257	14	098624	MATRIX PROTEIN.	3.47e+01
28	44	68.8	270	1	029360	CONSERVED HYPOTHETICAL	3.47e+01
29	44	68.8	292	10	048821	PUTATIVE SERINE PROTEI	3.47e+01
30	44	68.8	319	5	015926	HYPOTHETICAL 37.0 KD P	3.47e+01
31	44	68.8	342	6	018744	LU-ECAM-1.	3.47e+01
32	44	68.8	448	5	002441	GDP-DISSOCIATION INHIB	3.47e+01
33	44	68.8	564	5	045494	F3982.1 PROTEIN.	3.47e+01
34	44	68.8	697	11	035250	EXO70 PROTEIN.	3.47e+01
35	44	68.8	725	10	004429	ARGININE DECARBOXYLASE	3.47e+01
36	44	68.8	768	2	P94931	OUTER MEMBRANE PROTEIN	3.47e+01
37	44	68.8	794	6	018742	LU-ECAM-1.	3.47e+01
38	44	68.8	820	6	018743	LU-ECAM-1.	3.47e+01
39	44	68.8	864	11	063294	LEUCOCYTE COMMON ANTIG	3.47e+01
40	44	68.8	905	6	018741	LEUCOCYTE COMMON ANTIG	3.47e+01
41	44	68.8	1280	11	063295	LEUCOCYTE COMMON ANTIG	3.47e+01
42	44	68.8	1529	10	081068	PUTATIVE REVERSE TRANS	3.47e+01
43	44	68.8	2098	5	P91443	SIMILAR TO MYOSIN.	3.47e+01
44	44	68.8	2270	4	014581	DIHYDROPYRIDINE-SENSIT	3.47e+01
45	44	68.8	2312	4	015878	VOLTAGE-OPERATED CALCI	3.47e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	337 AA.
AC	034232			
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	ORF40X1 PROTEIN.			
OS	VIBRIO CHOLERAE.			
OC	BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: VIBRIONACEAE: VIBRIO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-AI-1837;			
RX	MEDLINE: 97252505.			
RA	STROEHER U.H., PARASIVAM G., DREDGE B.K., MANNING P.A.:			
RT	*Novel Vibrio cholerae O139 genes involved in lipopolysaccharide			
RT	biosynthesis.*;			
RL	J. BACTERIOL. 179:2740-2747(1997).			
RL	EMBL: Y07786; E274690; -			
SQ	SEQUENCE 337 AA: 40132 MW: 204A7939 CRC32:			

Query Match 87.5%; Score 56; DB 2: Length 337;
Best Local Similarity 87.5%; Pred. No. 6.38e-02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB	147 OKNSAPY 154
QY	1 OKNSAPY 8
RESULT	2
ID	087136
AC	087136
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE	ORF139-17 PROTEIN.
OS	VIBRIO CHOLERAE.
OC	BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: VIBRIONACEAE: VIBRIO.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-MO45;
RA	YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,
RA	TAKEDA Y.;
RT	*The genes responsible for O-antigen synthesis of Vibrio cholerae

RT 0139 are closely related to those of *Vibrio cholerae* 022.*;
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567; -
 SQ SEQUENCE 337 AA; 40147 MW; 176B46DB CRC32;

Query Match 87.5% Score 56; DB 2; Length 337;
 Best Local Similarity 87.5% Pred. No. 6.38e-02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 147 QKYSAPY 154
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 QY 1 QKYSAPY 8

RESULT 3 PRELIMINARY; PRT; 560 AA.
 ID 044626;
 AC 044626;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 K11D12.1 PROTEIN.
 K11D12.1.
 OS CAENORHABDITIS ELIGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITIDA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 CRAXTON M., DEAR S., DU 2., DURBIN R., FAVELLO A., FULTON L.,
 GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,
 SMALLDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,
 THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.*;
 RT elegans.*;
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA HENKHAUS J., WOHLDMANN P., GILLAM B.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF039047; G2736445; -
 DR PROSITE: PS00028; ZINC_FINGER_C2H2. 1.
 KW ZINC-FINGER; METAL-BINDING; DNA-BINDING.
 SQ SEQUENCE 560 AA; 61136 MW; 5906EBD CRC32;

Query Match 78.1% Score 50; DB 5; Length 560;
 Best Local Similarity 75.0% Pred. No. 1.68e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 81 QKGRAPY 88
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 QY 1 QKYSAPY 8

RESULT 4 PRELIMINARY; PRT; 533 AA.
 ID 028175;
 AC 028175;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE RETINAL PIGMENT EPITHELIUM-SPECIFIC PROTEIN.

OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 93340181.
 RA HAMEL C.P., TSILIOU E., PEEFER B.A., HOOKS J.J., DETRICK B.,
 RA REDMOND T.;
 RT "Molecular cloning and expression of RPE65, a novel retinal pigment
 epithelium-specific microsomal protein that is post-transcriptionally
 regulated in vitro.*";
 RL J. BIOL. CHEM. 268:15751-15757(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 93233190.
 RA HAMEL C.P., TSILIOU E., HARRIS E.D., PEEFER B.A., HOOKS J.J.,
 RA DETRICK B., REDMOND T.;
 RT "A developmentally regulated microsomal protein specific for the
 pigment epithelium of the vertebrate retina.*";
 RL J. NEUROSCI. RES. 34:414-425(1993).
 DR EMBL: L11356; G163657; -
 KW PIGMENT.
 SQ SEQUENCE 533 AA; 60944 MW; 911D0716 CRC32;

Query Match 76.6% Score 49; DB 6; Length 533;
 Best Local Similarity 66.7% Pred. No. 2.83e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 424 QKYGKPYT 432
 |||:||||
 QY 1 QKYSAPY 9

RESULT 5 PRELIMINARY; PRT; 533 AA.
 ID 005661;
 AC 005661;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE RETINAL PIGMENT EPITHELIUM MEMBRANE RECEPTOR P63.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 365-382 AND 407-423.
 RC STRAIN-STEINHOLTZ; TISSUE-EYE;
 RX MEDLINE: 93388633.
 RA BAYR C.O., HELLMAN U., WERNSTEDT C., ERIKSSON U.;
 RT "The retinal pigment epithelial membrane receptor for plasma
 retinol-binding protein. Isolation and cDNA cloning of the 63-kDa
 protein.*";
 RL J. BIOL. CHEM. 268:20540-20546(1993).
 CC -1- FUNCTION: THIS RECEPTOR BINDS PLASMA RETINOL BINDING PROTEIN.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN RETINAL PIGMENT
 EPITHELIUM.
 DR EMBL: X66277; G564; -
 KW RECEPTOR; RETINOL-BINDING; PLASMA; MEMBRANE.
 FT MOD_RES 71 71 BLOCKED.
 SQ SEQUENCE 533 AA; 60970 MW; F77E22D7 CRC32;

Query Match 76.6% Score 49; DB 6; Length 533;
 Best Local Similarity 66.7% Pred. No. 2.83e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 424 QKYGKPYT 432
 |||:||||
 QY 1 QKYSAPY 9

RESULT 6

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ID 087348 PRELIMINARY; PRT; 496 AA.
AC 087348:
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LIAKR21 RESTRICTION ENZYME.
GN LIAKR21R.
OS LACTOCOCCUS LACTIS (STREPTOCOCCUS LACTIS).
OC PLASMID FMR223.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC LACTOCOCCUS.
RN 11
RP SEQUENCE FROM N.A.
RA THOMEY D.P., MCKAY L.L., O'SULLIVAN D.J.;
RT "Molecular characterization of the Lactococcus lactis LIAKR21
RT restriction-modification system and effect of an IS982 element
RT positioned between the restriction and modification genes.";
RL J. BACTERIOL. 180:0-0(1998).
DR EMBL: AF051563; G3702799; -.
PLASMID.
SEQUENCE 496 AA; 58081 MW; A04BA2A9 CRC32;

Query Match 75.0%; Score 48; DB 2; Length 496;
Best Local Similarity 62.5%; Pred. No. 4.74e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 33 EKYOSTPY 40
:| | | |
:| | | |
OY 1 OKYNSAPY 8

RESULT 7 PRELIMINARY; PRT; 16 AA.
ID 079461
AC 079461:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LIGHT-CHAIN COMPLEMENTARITY-DETERMINING REGION 3 MRNA
DE (CLONE 31), PARTIAL CDS (FRAGMENT).
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE; 92032225.
RX BUTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
RA LERNER R.A.;
RT "A large array of human monoclonal antibodies to type 1 human
RT immunospecificity virus from combinatorial libraries of asymptomatic
RT seropositive individuals.";
PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
DR EMBL: M80726; G327954; -.
FT NON TER 1
FT NON TER 1
FT NON TER 16
FT NON TER 16
SO SEQUENCE 16 AA; 1883 MW; 5462CBDD CRC32;

Query Match 73.4%; Score 47; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.88e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 OKYNSAP 10
|||||
|||||
OY 1 OKYNSAP 7

RESULT 8 PRELIMINARY; PRT; 16 AA.
ID 079455
AC 079455:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LIGHT-CHAIN COMPLEMENTARITY-DETERMINING REGION 3 MRNA
DE (CLONE 14), PARTIAL CDS (FRAGMENT).
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).

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OC VIRUSES, RETROID VIRUSES, RETROVIRIDAE, LENTIVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92052225.
RA BURTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
  LEINER R.A.;
RT "A large array of human monoclonal antibodies to type 1 human
  immunodeficiency virus from combinatorial libraries of asymptomatic
  seropositive individuals.";
  PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
RL EMBL; M80720; G327942; -.
DR EMBL; M80720; G327942; -.
FT NON_TER 1 1
FT NON_TER 16 16
FT SEQUENCE 16 AA; 1883 MW; 5462C8DD CRC32;
SQ
  Query Match 73.4%; Score 47; DB 14; Length 16;
  Best Local Similarity 100.0%; Pred. No. 7,88e+00;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Db 4 OKYNSAP 10
  Oy 1 OKYNSAP 7

RESULT 9
ID 050511; PRELIMINARY; PRT; 450 AA.
AC 050511;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ZINC PROTEASE.
GN SC9B10.04.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
  ACINOMYCETALES; STREPTOMYCINAE; STREPTOMYCEACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
  OLIVER K., HARRIS D.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
  OLIVER K., HARRIS D.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-A3(2);
RX MEDLINE; 97000351.
RA REDEBNACH M., KIESER H.M., DENAPATTE D., EICHNER A., CULLUM J.,
  KINASH H., HOPWOOD D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
  the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
  MOL. MICROBIOL. 21:77-96(1998).
DR EMBL; AL009204; E1202335; -.
KV PROTEASE.
SQ SEQUENCE 450 AA; 49045 MW; 3E30B71A CRC32;
  Query Match 73.4%; Score 47; DB 2; Length 450;
  Best Local Similarity 50.0%; Pred. No. 7,88e+00;
  Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
  Db 147 OKYDVPY 154
  Oy 1 OKYNSAP 8

RESULT 10
ID 076022; PRELIMINARY; PRT; 856 AA.
AC 076022;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

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DE E1B-55KDA-ASSOCIATED PROTEIN.
 GN E1B-AP5.
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98406198.
 RA GABLER S., SCHUETT H., GROITL P., WOLF H., SHENK T., DOBNER T.;
 RT "E1B-55kDa-Associated protein: A cellular protein with
 RT RNA-binding activity implicated in nucleocytoplasmic transport of
 RT adenovirus and cellular mRNAs.";
 RL J. VIROL. 72:7960-7971(1998).
 DR EMBL; AJ007509; E1311327; -.
 SQ SEQUENCE 856 AA; 95809 MW; 5130EC97 CRC32;

Query Match 73.4%; Score 47; DB 4; Length 856;
 Best Local Similarity 85.7%; Pred. No. 7.8e+00;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

792 YNPAPYT 798
 11:1111
 3 YNSAPYT 9

RESULT 11
 ID Q35865 PRELIMINARY; PRT; 131 AA.
 AC Q35865;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE NADH DEHYDROGENASE SUBUNIT 5 (ND5) (FRAGMENT).
 OS STRONGYLOCENTROTUS INTERMEDIUS.
 CC MITOCHONDRION.
 OC EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA; EUECHINOIDEA;
 OC ECHINACCA; ECHINOIDA; STRONGYLOCENTROTIDAE; STRONGYLOCENTROTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91175684.
 RA THOMAS W.K., MAJ J., WILSON A.C.;
 RT "Shifting constraints on tRNA genes during mitochondrial DNA
 RT evolution in animals.";
 RL NEW BIOL. 1:93-100(1989).
 DR EMBL; M27670; E183877; -.
 KW MITOCHONDRION.
 FT NON_TER 131
 SQ SEQUENCE 131 AA; 14311 MW; E0BB7988 CRC32;

Query Match 71.9%; Score 46; DB 8; Length 131;
 Best Local Similarity 62.5%; Pred. No. 1.30e+01;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 60 KYNSGPPA 67
 11111111
 2 KYNSAPYT 9

RESULT 12
 ID Q47792 PRELIMINARY; PRT; 278 AA.
 AC Q47792;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PLASMID PAD1, OPEN READING FRAMES.
 OS ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS).
 CC PLASMID PAD1.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; ENTEROCOCCACEAE;
 CC ENTEROCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-OG1X;
 RC MEDLINE; 97074879.
 RA HIRT H., WIRTH R., MOSCHOLL A.;

RT "Comparative analysis of 18 sex pheromone plasmids from Enterococcus
 RT faecalis: detection of a new insertion element on pPDI and
 RT implications for the evolution of this plasmid family.";
 RL MOL. GEN. GENET. 252:640-647(1996).
 DR EMBL; X96977; E236596; -.

KW PLASMID.
 SQ SEQUENCE 278 AA; 30520 MW; 67892F0F CRC32;

Query Match 71.9%; Score 46; DB 2; Length 278;
 Best Local Similarity 62.5%; Pred. No. 1.30e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 227 QKXNAPF 234
 111111
 1 QKXNAPYT 8

RESULT 13
 ID Q60295 PRELIMINARY; PRT; 1042 AA.
 AC Q60295;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PUTATIVE TYPE I RESTRICTION ENZYME R PROTEIN (EC 3.1.21.3).
 GN MCEC140.
 OS METHANOCOCCUS JANNASCHII.
 OC ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
 OC METHANOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96337999.
 RA BOLT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
 RA KUTSON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
 RA KERLAVALGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
 RA OVERBEER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
 RA SCOTT J.L., GEORGE N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
 RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SAOUM P.W., HANNA M.C.,
 RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKI M.,
 RA KLENN H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL SCIENCE 273:1058-1073(1996).
 CC -1- FUNCTION: SUBUNIT R IS REQUIRED FOR BOTH NUCLEASE AND ATPASE
 CC ACTIVITIES, BUT NOT FOR MODIFICATION (BY SIMILARITY).
 CC -1- TYPE I RESTRICTION AND MODIFICATION ENZYMES ARE COMPLEX,
 CC MULTI-FUNCTIONAL SYSTEMS WHICH REQUIRE ATP, S-ADENOSYL METHIONINE
 CC AND MG(2+) AS CO-FACTORS AND, IN ADDITION TO THEIR
 CC ENDOCYTOLYTIC AND METHYLASE ACTIVITIES, ARE POTENT
 CC DNA-DEPENDENT ATPASES (BY SIMILARITY).
 CC -1- SUBUNIT: THE TYPE I RESTRICTION & MODIFICATION SYSTEM IS COMPOSED
 CC OF THREE POLYPEPTIDES R/M AND S (BY SIMILARITY).
 CC -1- SIMILARITY: WITH ATPASES.
 DR EMBL; L77118; G1522673; -.
 DR PFAM; PF00271; heliCase.C; 1.
 KW HYPOTHETICAL PROTEIN; RESTRICTION SYSTEM; DNA-BINDING; ATP-BINDING.
 SQ SEQUENCE 1042 AA; 121522 MW; 9FAF7E8 CRC32;

Query Match 71.9%; Score 46; DB 1; Length 1042;
 Best Local Similarity 62.5%; Pred. No. 1.30e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 262 KYKGNPYT 269
 11111111
 2 KYNSAPYT 9

RESULT 14
 ID Q25981 PRELIMINARY; PRT; 259 AA.
 AC Q25981;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 29.4 KD PROTEIN.

GN HP1440.
 OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
 OC BACTERIA: PROTEOBACTERIA: EPSILON SUBDIVISION: HELICOBACTER GROUP:
 OC HELICOBACTER.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-26695;
 RX MEDLINE: 97394467.
 RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
 RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
 RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
 RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODER A.,
 RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
 RA BERG D.E., GOCCAYNE J.D., UTERBACK T.R., PETERSON J.D., KELLEY J.M.,
 RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., MATTHEY L., WALLIN E.,
 RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori[*published erratum appears in Nature 1997 Sep*
 RT 25:389(6649):412. "];
 RT NATURE 388:539-547(1997).
 RT EMBL: AE000644; G2314621; -.
 RT TIGR: HP1440; -.
 RT HYPOTHETICAL PROTEIN.
 RT SEQUENCE 259 AA; 29361 MW; 59460701 CRC32;

Query Match 70.3% Score 45; DB 2; Length 259;
 Best Local Similarity 55.6%; Pred. No. 2.13e+01;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 148 QTFHNPYT 156
 QY 1 QKXNSAPY 9

RESULT 15
 ID 068847 PRELIMINARY; PRT; 320 AA.
 AC 068847;
 DT 01-AUG-1998 (TREMBLER. 07, CREATED)
 DT 01-AUG-1998 (TREMBLER. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLER. 08, LAST ANNOTATION UPDATE)
 DE SITE-SPECIFIC RECOMBINASE INT14.
 GN INT14.
 OS VIBRIO CHOLERAE.
 OC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: VIBRIONACEAE; VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TRANSPOSON-INVCB;
 RP MEDLINE: 98221242.
 RP MAZEL D., DYCHINCO B., WEBB V.A., DAVIES J.;
 RP "A distinctive class of integron in the *Vibrio cholerae* genome.";
 RP SCIENCE 280:605-608(1998).
 RP EMBL: AF035586; G3095165; -.
 RP DR EMBL: AF035586; G3095165; -.
 RP SEQUENCE 320 AA; 37505 MW; CBF0F9CD CRC32;

Query Match 70.3% Score 45; DB 2; Length 320;
 Best Local Similarity 62.5%; Pred. No. 2.13e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 208 EKYPNAPY 215
 QY 1 QKXNSAPY 8

Search completed: Thu Sep 2 11:40:23 1999
 Job time : 41 secs.

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Best Local Similarity 87.5%; Pred. No. 4.74e-02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 81 OKYRABY 88
1 OKYRABY 8

RESULT 2
ID Q44677 PRELIMINARY; PRT; 521 AA.
AC Q44677;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE NEUTRAL PROTEASE.
OS BACILLUS AMYLOLIOFACIENS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.

[1]
SEQUENCE FROM N.A.
SHIMADA H., HONJO M., MITA I., NAKAYAMA A., AKAOKA A., MANABE K.,
FURUTANI Y.,
RL J. BIOTECHNOL. 2:75-85(1985).
DR EMBL: M36723; GI43353; -.
DR PFAM: PF00099; zn-protease; 1.
KW PROTEASE.
SQ SEQUENCE 521 AA; 56725 MW; 64AFRE5F CRC32;

Query Match 76.8%; Score 53; DB 2; Length 521;
Best Local Similarity 75.0%; Pred. No. 1.69e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 308 OKYRABY 315
1 OKYRABY 8

RESULT 3
ID Q36979 PRELIMINARY; PRT; 3082 AA.
AC Q36979;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE POLYPROTEIN.
OS ZOCCCHINI YELLOW MOSAIC VIRUS (ZYMV).
OC VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
OC POTYVIRUS.
[1]
SEQUENCE FROM N.A.
STRAIN-SINGAPORE;
LEE R.C., WONG S.M.,
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF014811; G2462849; -.
DR PFAM: PF00271; helicase_C; 1.
DR PFAM: PF00680; RNA_dep_RNA_pol; 1.
DR PFAM: PF00767; Poly_coat; 1.
DR PFAM: PF00851; Peptidase_C6; 1.
DR PFAM: PF00863; Peptidase_C4; 1.
KW POLYPROTEIN.

FT CHAIN 1 313 P1.
FT CHAIN 314 769 HELPER COMPONENT-PROTEINASE.
FT CHAIN 770 1115 P3.
FT CHAIN 1116 1167 6K1.
FT CHAIN 1168 1801 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1802 1854 6K2.
FT CHAIN 1855 2044 SMALL NUCLEAR INCLUSION-GENOME LINKED
VPg.
FT CHAIN 2045 2287 SMALL NUCLEAR INCLUSION-PROTEINASE.
FT CHAIN 2288 2803 LARGE NUCLEAR INCLUSION.
FT CHAIN 2804 3082 COAT PROTEIN.
SQ SEQUENCE 3082 AA; 350508 MW; 43030AF1 CRC32;
Query Match 76.8%; Score 53; DB 14; Length 3082;

Best Local Similarity 75.0%; Pred. No. 1.69e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 279 OKYRABY 286
1 OKYRABY 8

RESULT 4
ID Q21017 PRELIMINARY; PRT; 509 AA.
AC Q21017;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE COSMID F58H12.
GN F58H12.1.
OS CAENORHABDITIS ELEGANS.
OC EURKOTIA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA.
OC RHABDITINA; RHABDITIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
[1]
SEQUENCE FROM N.A.
RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY I., COOPER J., COULSON A.,
RA GRAYSON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STURSTON J.,
RA THIERRY-WIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL NATURE 368:32-38(1994).

[2]
SEQUENCE FROM N.A.
RA MILLER N.,
RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
[3]
SEQUENCE FROM N.A.

RA WATERSTON R.,
RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U40416; G1065490; -.
SQ SEQUENCE 509 AA; 55953 MW; D0EC1387 CRC32;

Query Match 75.4%; Score 52; DB 5; Length 509;
Best Local Similarity 62.5%; Pred. No. 2.76e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 268 RYORTPYT 275
2 KYNRAPYT 9

RESULT 5
ID Q74961 PRELIMINARY; PRT; 231 AA.
AC Q74961;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 25.6 KD PROTEIN (FRAGMENT).
GN SPC736.16.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EURKOTIA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
OC SCHIZOSACCHAROMYCETACEAE; SCHIZOSACCHAROMYCETACEAE;
OC SCHIZOSACCHAROMYCES.
[1]
SEQUENCE FROM N.A.
RN STRAIN-972H-;
RC WOOD V., RAJANBHAM M.A., BARRELL B.G., MURPHY L., HARRIS D.,
RA SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AL023705; E1294543; -.

RESULT 10
ID 042265; PRELIMINARY; PRT; 260 AA.
AC 042265;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-NOV-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE 205 PROTEASOME SUBUNIT C2.
GN CC2.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGATIAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RA SINGH I., WAGNER B.J.;
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF027978; G3136063; -;
PFAM: PF00227; proteasome; 1.
PROTEASOME.
SEQUENCE 260 AA; 28925 MW; EF38499F CRC32;

Query Match 71.0%; Score 49; DB 13; Length 260;
Best Local Similarity 62.5%; Pred. No. 1.16e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 120 QRYGRPY 127
1:1:1:1
QY 1 QKYNRAPY 8

RESULT 11
ID 002441; PRELIMINARY; PRT; 448 AA.
AC 002441;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GDP-DISSOCIATION INHIBITOR.
GN GDI.
OS GEODIA CYDONIUM (SPONGE).
OC EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; TETRACINOMORPHA;
OC ASTROPHORIDA; GEODIIDEA; GEODIA.
RN [1]
RP SEQUENCE FROM N.A.
RA KRASNO A., SCHEFFER U., KOZIOL C., PANCER Z., BATEL R., BADRIA F.A.,
RA MUELLER W.E.G.;
RL AQUATIC TOXICOL. 37:157-168(1997).
EMBL: Y94983; E218570; -;
PFAM: PF00996; GDI; 1.
SEQUENCE 448 AA; 50215 MW; 848511EC CRC32;

Query Match 71.0%; Score 49; DB 5; Length 448;
Best Local Similarity 50.0%; Pred. No. 1.16e+01;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 217 QRYGKSPY 224
1:1:1:1
QY 1 QKYNRAPY 8

RESULT 12
ID 093374; PRELIMINARY; PRT; 451 AA.
AC 093374;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TRANSCRIPTION FACTOR (FRAGMENT).
GN PAX8.
OS FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES);
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELEOSTEI; EUTLEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;
OC TETRAODONTIFORMES; TETRAODONTIOIDEI; TETRAODONTIDAE; FUGU.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE: 98337826.
RA PEEPER P.L., GERSTER T., LUN K., BRAND M., BUSSENGER M.;
RT "Characterization of three novel members of the zebrafish Pax2/5/8
RT family: dependency of Pax5 and Pax8 expression on the Pax2.1 (nol)
RT function."
RL DEVELOPMENT 125:3063-3074(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
DR EMBL: AF072556; G3420029; -;
DR PROSITE: PS00034; PAIRED_BOX; 1.
KW PAIRED BOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN.
FT NON_TER
SQ SEQUENCE 451 AA; 48389 MW; 0081252D CRC32;

Query Match 71.0%; Score 49; DB 13; Length 451;
Best Local Similarity 55.6%; Pred. No. 1.16e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 406 QRYSHSPY 414
1:1:1:1
QY 1 QKYNRAPY 9

RESULT 13
ID 017517; PRELIMINARY; PRT; 1277 AA.
AC 017517;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ZC132.5 PROTEIN.
GN ZC132.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITIOIDEA; RHABDITIDAE; PLODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA BRADSHAW H., DEVLIN K.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF014939; G2275629; -;
SQ SEQUENCE 1277 AA; 146496 MW; 8A6DB899 CRC32;

Query Match 71.0%; Score 49; DB 5; Length 1277;
Best Local Similarity 85.7%; Pred. No. 1.16e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 877 QRYNRAP 883
1:1:1:1
QY 1 QKYNRAP 7

```

RESULT 14
ID 049246 PRELIMINARY; PRT; 43 AA.
AC 049246;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN RT.
OS ALSTROEMERIA INODORA.
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; LILIALES;
OC ALSTROEMERIACEAE; ALSTROEMERIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P002; TISSUE-YOUNG LEAVES;
RC TRANSPOSON-TY1-COPIA-LIKE RETROTRANSPOSON;
RA KUIPERS A.G.J., HESLOP-HARRISON J.S., JACOBSEN E.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DB EMBL; AJ223610; E1252160; -.
DB RNA-DIRECTED DNA POLYMERASE.
FT NON_TER 1 43
SQ SEQUENCE 43 AA; 5333 MW; E61D18CF CRC32;

Query Match
Best Local Similarity 83.3%; Score 48; DB 10; Length 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 14 YNRSpy 19
   |||:|
OY 3 YNRApy 8

RESULT 15
ID 049247 PRELIMINARY; PRT; 44 AA.
AC 049247;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN RT.
OS ALSTROEMERIA INODORA.
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; LILIALES;
OC ALSTROEMERIACEAE; ALSTROEMERIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P002; TISSUE-YOUNG LEAVES;
RC TRANSPOSON-TY1-COPIA-LIKE RETROTRANSPOSON;
RA KUIPERS A.G.J., HESLOP-HARRISON J.S., JACOBSEN E.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DB EMBL; AJ223611; E1252162; -.
DB RNA-DIRECTED DNA POLYMERASE.
FT NON_TER 1 44
SQ SEQUENCE 44 AA; 5477 MW; 70CA73A1 CRC32;

Query Match
Best Local Similarity 83.3%; Score 48; DB 10; Length 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 14 YNRSpy 19
   |||:|
OY 3 YNRApy 8

Search completed: Thu Sep 2 11:44:17 1999
Job time : 25 secs.

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Molecular output not generated.

(TM)

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March 1999 protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 11:42:53 1999; MasPar time 3.02 Seconds
119.594 Million cell updates/sec

Title: >US-08-599-226-16
Description: (1-9) from US08559226.pep
Perfect Score: 69
Sequence: 1 OKNRAPYT 9

Scoring table: PAM 150
Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: p1r60
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 22.906; Variance 29.489; scale 0.777

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	54	78.3	1260	2	S28407	1.10e+00
2	53	76.8	521	2	I39556	1.76e+00
3	52	75.4	279	1	SNF5K	2.81e+00
4	52	75.4	360	2	S28047	2.81e+00
5	52	75.4	360	2	S52662	2.81e+00
6	50	72.5	689	2	S45901	7.06e+00
7	49	71.0	263	1	SNR7C2	1.11e+01
8	49	71.0	269	2	JC1445	1.11e+01
9	49	71.0	615	1	ABCHS	1.11e+01
10	48	69.6	239	2	G02630	1.73e+01
11	48	69.6	287	2	JH0332	1.73e+01
12	48	69.6	367	2	S49009	1.73e+01
13	48	69.6	370	2	S49008	1.73e+01
14	48	69.6	419	3	JE0389	1.73e+01
15	48	69.6	490	2	E71486	1.73e+01
16	48	69.6	491	2	JC1390	1.73e+01
17	48	69.6	521	1	HRBSN	1.73e+01
18	48	69.6	790	2	S77032	1.73e+01
19	48	69.6	3973	2	B1612	1.73e+01
20	47	68.1	321	2	B1854	2.68e+01
21	47	68.1	340	2	S65000	2.68e+01
22	47	68.1	342	2	H71258	2.68e+01
23	47	68.1	342	2	S76447	2.68e+01

24	47	68.1	355	2	S76940	hypothetical protein	2.68e+01
25	47	68.1	361	2	T01934	adenosylmethionine de	2.68e+01
26	47	68.1	421	2	TC5323	anthranilate synthase	2.68e+01
27	47	68.1	440	2	F70792	hypothetical protein	2.68e+01
28	47	68.1	530	2	S38903	hypothetical protein	2.68e+01
29	47	68.1	1708	2	A43100	ataxia telangiectasia	2.68e+01
30	46	66.7	89	2	C47759	retrovirus-related re	4.13e+01
31	46	66.7	101	2	B37262	Ig kappa chain V-regi	4.13e+01
32	46	66.7	210	2	S05981	repB protein - Strept	4.13e+01
33	46	66.7	210	2	B23599	repB protein - Strept	4.13e+01
34	46	66.7	241	2	B55549	endothelial cell prot	4.13e+01
35	46	66.7	254	2	S28362	coat protein - beet c	4.13e+01
36	46	66.7	488	1	RKPRLE	ribulose-bisphosphate	4.13e+01
37	46	66.7	488	1	RKPRLE	ribulose-bisphosphate	4.13e+01
38	46	66.7	626	2	A42891	beta-galactosidase (E	4.13e+01
39	46	66.7	788	2	A26547	platelet glycoprotein	4.13e+01
40	46	66.7	903	2	T00358	hypothetical protein	4.13e+01
41	46	66.7	1013	2	S65195	probable membrane pro	4.13e+01
42	45	65.2	109	2	A30608	Ig kappa chain V-IIi	6.32e+01
43	45	65.2	215	2	JE0242	Ig kappa chain NIG26	6.32e+01
44	45	65.2	4957	2	T03455	ALR protein - human	6.32e+01
45	45 <th>65.2</th> <th>5262</th> <th>2</th> <th>T03454</th> <th>ALR protein - human</th> <th>6.32e+01</th>	65.2	5262	2	T03454	ALR protein - human	6.32e+01

ALIGNMENTS

RESULT 1
ENTRY S28407 #type complete
TITLE guanine nucleotide-exchange activator CDC25 homolog - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 10-Sep-1997

ACCESSIONS S28407; S22693; B46199; S20730
REFERENCE S28407
#authors Cen, H.; Papageorge, A.G.; Zippel, R.; Lowy, D.R.; Zhang, K.
#journal EMBO J. (1992) 11:4007-4015
#title Isolation of multiple mouse cDNAs with coding homology to
Saccharomyces cerevisiae CDC25. Identification of a region
related to Bcr, Vav, Dbl and CDC24.

#cross-references MOID:93010996
#accession S28407
#status not compared with conceptual translation

#molecule_type mRNA
#residues 1-1260 ##label CEN

REFERENCE

#authors Martegani, E.; Vanoni, M.; Zippel, R.; Cocchetti, P.;
Brambilla, R.; Ferrari, C.; Sturani, E.; Alberghina, U.

#journal EMBO J. (1992) 11:2151-2157
#title Cloning by functional complementation of a mouse CDNA
encoding a homologue of CDC25, a Saccharomyces cerevisiae

RAS activator.

#cross-references MOID:92289680

#accession S22693

#molecule_type mRNA

#residues 789-1260 ##label MAR

#cross-references EMBL:X59868; NID:950357; PID:950358

REFERENCE A46199

#authors Wei, W.; Mosteller, R.D.; Sanyal, P.; Gonzales, E.; McKinney,
D.; Dasgupta, C.; Li, P.; Liu, B.X.; Brock, D.

#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104
#title Identification of a mammalian gene structurally and
functionally related to the CDC25 gene of Saccharomyces
cerevisiae.

#cross-references MOID:92357779

#accession B46199

#status preliminary

#molecule_type nucleic acid

#residues 1029-1030, 'D', 1032-1224 ##label WEI

##experimental_source fetus
##note sequence extracted from NCBI backbone (NCBIN:111101,
NCBIP:111102)

CLASSIFICATION #superfamily CDC25-type guanine nucleotide exchange activator
homology; CDC24 homology; pleckstrin repeat homology

FEATURE
242-428 #domain CDC24 homology #label CD24\
1021-1257 #domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
SUMMARY #length 1260 #molecular-weight 143900 #checksum 9725

Query Match
Best Local Similarity 62.5%; Score 54; DB 2; Length 1260;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1058 EXERTPY 1065
1:1:1:1:1
QY 1 OKYNRAPY 8

RESULT 2
ENTRY I39956 #type complete
TITLE neutral proteinase (EC 3.4.24.-) - Bacillus amyloliquefaciens
ORGANISM #formal_name Bacillus amyloliquefaciens
KEYWORDS 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 18-Mar-1997
SUMMARY I39956
#accession I39956
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-521 #label RES
#cross-references GB:M36723; NID:g143352; PID:g143353

GENETICS
#start_codon GTG
#classification #superfamily thermolysin
#keywords hydrolase; metalloproteinase
SUMMARY #length 521 #molecular-weight 56725 #checksum 6816

Query Match
Best Local Similarity 76.8%; Score 53; DB 2; Length 521;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 308 OKYNRSY 315
1:1:1:1:1
QY 1 OKYNRAPY 8

RESULT 3
ENTRY SNF5K #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) 35K chain
- fruit fly (Drosophila melanogaster)
ALTERNATE_NAMES 19S cylinder particle 35K chain; multicatalytic proteinase
ORGANISM 35K chain; prosome 35K chain; proteasome 35K chain
#formal_name Drosophila melanogaster
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Sep-1997
SUMMARY S23450; S05507; A38761
#accession S23450
#status
REFERENCE S23450
#authors Frentzel, S.; Troxell, M.; Haass, C.; Pesold-Hurt, B.; Glaetzer, K.H.; Klotzel, P.M.
#journal Eur. J. Biochem. (1992) 205:1043-1051
#title Molecular characterization of the genomic regions of the Drosophila alpha-type subunit proteasome genes PROS-Dm28.1 and PROS-Dm35
#cross-references NUID:92249308
#accession S23450
#molecule_type DNA
#residues 1-279 #label FREN
#cross-references EMBL:X62285; NID:g8387; PID:g8388
#experimental_source strain Canton S
REFERENCE S05507
#authors Haass, C.; Pesold-Hurt, B.; Multhaup, G.; Beyreuther, K.;

#journal Klotzel, P.M.
#title EMO J. (1989) 8:2373-2379
The PROS-35 gene encodes the 35 kD protein subunit of Drosophila melanogaster proteasome.
#cross-references NUID:9005444
#accession S05507
#molecule_type mRNA
#residues 1-279 #label HAA
#cross-references EMBL:X15497; NID:g8381; PID:g8382
#accession A38761
#molecule_type protein
#residues 4-18;194-206 #label HAA2

GENETICS
#gene PROS-35
#cross-references FlyBase:FBgn0003151
#map_position 89F-90A
#introns 1/3; 211/3
CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9
KEYWORDS hydrolase; phosphoprotein; proteinase
SUMMARY #length 279 #molecular-weight 31058 #checksum 365

Query Match
Best Local Similarity 75.4%; Score 52; DB 1; Length 279;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 121 OKYDRPY 128
1:1:1:1:1
QY 1 OKYNRAPY 8

RESULT 4
ENTRY S28047 #type complete
TITLE TUB13 protein - potato
ORGANISM #formal_name Solanum tuberosum #common_name potato
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
SUMMARY S28047
#accessions S28047
#status
#authors Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flavell, A.J.
#journal Plant Mol. Biol. (1992) 20:641-651
#title Expression and sequence analysis of cDNAs induced during the early stages of tuberisation in different organs of the potato plant (Solanum tuberosum L.).
#accession S28047
#molecule_type mRNA
#residues 1-360 #label TAY
#cross-references EMBL:Z11680; NID:g21484; PID:g21485

GENETICS
#gene TUB13
SUMMARY #length 360 #molecular-weight 39726 #checksum 7941

Query Match
Best Local Similarity 75.4%; Score 52; DB 2; Length 360;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 332 OKYTRPY 339
1:1:1:1:1
QY 1 OKYNRAPY 8

RESULT 5
ENTRY S52662 #type complete
TITLE S-adenosylmethionine decarboxylase (SAMDC) - potato
ORGANISM #formal_name Solanum tuberosum #common_name potato
DATE 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
SUMMARY S52662
#accessions S52662
#status
#authors Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.; Burch, L.R.; Davies, H.V.; Stark, M.D.R.; Kumar, A.
#journal Plant Mol. Biol. (1994) 26:327-338
#title Characterisation of the S-adenosylmethionine decarboxylase

(SANDC) gene of potato.

#accession S52662
#status Preliminary
#molecule_type DNA
#residues 1-360 #label ARI

SUMMARY #length 360 #molecular-weight 39724 #checksum 8045

Query Match 75.4%; Score 52; DB 2; Length 360;
Best Local Similarity 62.5%; Pred. No. 2,81e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 332 OKYRAPPY 339
1:1:11
QY 1 OKYRAPPY 8

RESULT 6
ENTRY S45901 #type complete
TITLE Probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae)
#protein_hypothesis YBR043c
#formal_name Saccharomyces cerevisiae
#formal_name Saccharomyces cerevisiae
26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 04-Sep-1998

ACCESSIONS S45901
REFERENCE S45893
#authors Andre, B.; Czlepuch, C.; Hein, C.; Jaundaux, J.C.; Urrestarazu, A.; Vissers, S.
#submission submitted to the Protein Sequence Database, August 1994
#accession S45901
#molecule_type DNA
#residues 1-689 #label AND
#cross-references EMBL:Z35912; NID:9536267; PID:9536268; MIPS:YBR043C
#experimental_source strain 5288C

GENETICS
#map_position 2R
CLASSIFICATION #superfamily yeast probable membrane protein YBR043c
KEYWORDS transmembrane protein
FEATURES

108-124 #domain transmembrane #status predicted #label TM1
140-161 #domain transmembrane #status predicted #label TM2
177-193 #domain transmembrane #status predicted #label TM3
239-256 #domain transmembrane #status predicted #label TM4
265-287 #domain transmembrane #status predicted #label TM5
476-493 #domain transmembrane #status predicted #label TM6
513-529 #domain transmembrane #status predicted #label TM7
535-579 #domain transmembrane #status predicted #label TM8
587-603 #domain transmembrane #status predicted #label TM9
623-645 #domain transmembrane #status predicted #label TM10
648-670 #domain transmembrane #status predicted #label TM11
SUMMARY #length 689 #molecular-weight 77300 #checksum 8706

Query Match 72.5%; Score 50; DB 2; Length 689;
Best Local Similarity 71.4%; Pred. No. 7.06e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 500 KYSRAPPY 506
1:1:11
QY 2 KYNRAPPY 8

RESULT 7
ENTRY SNR7C2 #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2
#protein_hypothesis SNR7C2
#formal_name multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 17-Oct-1997

ACCESSIONS A32968; A38799; S09741
REFERENCE A32968
#authors Fujiwara, T.; Tanaka, K.; Kumatori, A.; Shin, S.; Yoshimura, T.; Ichihara, A.; Tokunaga, F.; Aruga, R.; Iwanaga, S.;

#journal Kakiyama, A.; Nakanishi, S.
#title Biochemistry (1989) 28:7332-7340
#protein_hypothesis Molecular cloning of cDNA for proteasomes (multicatalytic proteinase complexes) from rat liver: primary structure of the largest component (C2).

#cross-references MIM:90057428

#accession A32968

#molecule_type mRNA

#residues 1-263 #label FUJ1

#cross-references EMBL:M29859; NID:9206381; PID:9206382

#accession A38799

#molecule_type protein

#residues 2-25;42-58;63-74,'X',76-79,'X',81;116-135;190-203;218-226,'XX',229,'X',231;244-246,'X',248-262 #label FUJ2

REFERENCE S09741
#authors Tokunaga, F.; Aruga, R.; Iwanaga, S.; Tanaka, K.; Ichihara, A.; Takao, T.; Shimonishi, Y.
#journal FEBS Lett. (1990) 263:373-375
#title The NH2-terminal residues of rat liver proteasome (multicatalytic proteinase complex) subunits, C2, C3 and C8, are N-alpha-acetylated.

#cross-references MIM:90243011

#accession S09741

#molecule_type protein

#residues 1-30 #label TOK

CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9

KEYWORDS #acetylated amino end; hydrolase; proteinase

FEATURES 1-263

#product multicatalytic endopeptidase complex chain C2

#status experimental #label MAY

#modified site acetylated amino end (Met) #status experimental

SUMMARY #length 263 #molecular-weight 29517 #checksum 9238

Query Match 71.0%; Score 49; DB 1; Length 263;
Best Local Similarity 62.5%; Pred. No. 1.11e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 121 OKYRAPPY 128
1:1:11
QY 1 OKYRAPPY 8

RESULT 8
ENTRY JCI445 #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2, long splice form - human
#protein_hypothesis JCI445
#formal_name multicatalytic endopeptidase complex HC2
macropain nu chain; multicatalytic endopeptidase complex nu chain;
chain; multicatalytic endopeptidase complex nu chain;
multicatalytic proteinase chain C2; prosome 30-33K chain;
prosome alpha 1 subunit; proteasome chain C2; proteasome nu chain

CONTAINS multicatalytic endopeptidase complex chain C2, short splice form

ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997

ACCESSIONS JCI445; S15897; S25410; PC2321

REFERENCE JCI445
#authors Pereira, I.S.; Bey, F.; Coux, O.; Scherrer, K.

#journal Gene (1992) 120:235-242

#title Two mRNAs exist for the Hs PROS-30 gene encoding a component of human prosome.

JCI445

#accession JCI445

#molecule_type mRNA

#residues 1-269 #label PER

#cross-references GB:M64992

REFERENCE S15897

#authors Tamura, T.; Lee, D.H.; Osaka, F.; Fujiwara, T.; Shin, S.; Chung, C.H.; Tanaka, K.; Ichihara, A.

#journal Biochim. Biophys. Acta (1991) 1089:95-102

#title Molecular cloning and sequence analysis of cDNAs for five

```

major subunits of human proteasomes (multi-catalytic
proteasome complexes).
#cross-references EMBL:D00759; NID:g220021; PID:d100114; PID:g220022
#accession S15897
#molecule_type mRNA
#residues 'M',8-269 ##label TAM
#cross-references EMBL:D00759; NID:g220021; PID:d100114; PID:g220022
#accession S17520
#authors Dekartino, G.N.; Orch, K.; McCullough, M.L.; Lee, L.W.; Munn,
T.Z.; Moorman, C.R.; Dawson, P.A.; Slaughter, C.A.
#journal Blochim. Biophys. Acta (1991) 1079:23-38
#title The primary structures of four subunits of the human,
high-molecular-weight proteinase, macropain (proteasome),
are distinct but homologous.
#cross-references MVID:91363412
#accession S17520
#status not compared with conceptual translation
#molecule_type mRNA
#residues 'M',8-269 ##label DEM
#cross-references GB:X61969; NID:g296737; PID:g296738
#accession S25410
#molecule_type protein
#residues 10-40;46-61;68-75;89-95;103-128;132-148;164-168;176-195;
203-223;225-267 ##label DE2
#cross-references GDB:134040
#map_position 11q-11q
#classification #superfamily multicatalytic endopeptidase complex chain C9
#features hydrolyase; phosphoprotein; proteinase
2-269
#product multicatalytic endopeptidase complex chain C2,
long splice form #status predicted #label MATV
8-269 #product multicatalytic endopeptidase complex chain C2,
short splice form #status predicted #label MATS\
binding-site phosphate (Tyr) (covalent) #status
predicted
230 #length 269 #molecular-weight 30239 #checksum 5946
SUMMARY
Query Match 71.0%; Score 49; DB 2; Length 269;
Best Local Similarity 62.5%; Pred. No. 1.11e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 127 QRYGRAPY 134
QY 1 QKYNRABY 8
RESULT 9
ENTRY ABCHS #type complete
TITLE serum albumin precursor - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
05-Sep-1997
ACCESSIONS S15571; A05078; A13451
REFERENCE Casady, A.I.; Salikild, C.K.; Bayerstock, P.; Wallace, J.C.
#authors submitted to the EMBL Data Library, July 1991
#accession S15571
#molecule_type mRNA

```

```

#residues 1-615 ##label CAS
#cross-references EMBL:X60688; NID:g63747; PID:g63748
#accession A05078
#authors Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau,
P.C.K.; Deeley, R.G.
#journal J. Biol. Chem. (1983) 258:4556-4564
#title The 5' noncoding and flanking regions of the avian very low
density apolipoprotein II and serum albumin genes.
Homologues with the egg white protein genes.
#cross-references MVID:83161037
#accession A05078
#molecule_type DNA
#residues 1-28 ##label HAC
#cross-references GB:V00381; NID:g63038; PID:g63039
#accession A13451
#authors Rosen, A.M.; Geller, D.M.
#journal Biochem. Biophys. Res. Commun. (1977) 78:1060-1066
#title Chicken microsomal albumin: amino terminal sequence of
chicken proalbumin.
#cross-references MVID:78019943
#accession A13451
#molecule_type protein
#residues 19-23,'M',25-30 ##label ROS
#COMMENT Serum albumin is synthesized in the liver as preproalbumin. It
binds copper, nickel, calcium (weakly, at 2-3 sites), and
protoporphyrin, long-chain fatty acids, prostaglandins, steroid
hormones (weak bonds with these hormones promote their transfer
across the membranes), thyroxine, and triiodothyronine.
#superfamily serum albumin; serum albumin repeat homology
carrier protein; duplication; metal binding; plasma
FEATURE
1-18 #domain signal sequence #status predicted #label SIG\
19-26 #domain propeptide #status predicted #label PRO\
27-613 #product serum albumin #status predicted #label MATV\
32-206 #domain serum albumin repeat homology #label SA1\
225-398 #domain serum albumin repeat homology #label SA2\
417-596 #domain serum albumin repeat homology #label SA3\
30 #binding-site copper (His) #status predicted\
80-89,102-118,
117-128,152-197,
196-205,228-274,
273-281,293-307,
306-317,344-389,
388-397,420-466,
465-476,489-505,
504-515,542-587,
586-595
#disulfide_bonds #status predicted
SUMMARY
#length 615 #molecular-weight 69918 #checksum 4822
Query Match 71.0%; Score 49; DB 1; Length 615;
Best Local Similarity 55.6%; Pred. No. 1.11e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 249 QKYPKAPFS 257
QY 1 QKYNRABYT 9
RESULT 10
ENTRY G02630 #type complete
TITLE FcalphaRb - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
17-Jul-1998
ACCESSIONS G02630
REFERENCE H01508
#authors van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.;
Raaijmakers, J.A.M.; Lammers, J.
#submitted to the EMBL Data Library, April 1996
#accession G02630
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-239 ##label VAN

```

```
##cross-references EMBL:U56236; NID:g1326228; PID:g1326229
#length 239 #molecular-weight 26996 #checksum 5338
```

Query Match	69.68;	Score 48;	DB 2;	Length 239;
Best Local Similarity	83.38;	Pred. No. 1.73e+01;		
Matches	5;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

Db	197	YNRSPY	202
		:	
QY	3	YNRAPY	8

RESULT	ENTRY	11
TITLE	JH0332	#type complete
ALTERNATE_NAMES	IGa (Fc) receptor, myeloid cell (CD89) precursor - human	
ORGANISM	myeloid glycoprotein CD89	
DATE	#formal name Homo sapiens	#common name man
	12-Feb-1993	#sequence revision 12-Feb-1993
	1993	#text change

#authors Maliszewski, C.R.; March, C.J.; Schoenborn, M.A.; Gimpel, S.
Shen, L.
#journal J. Exp. Med. (1990) 172:1665-1672
#title Expression cloning of a human Fc receptor for IgA.
#cross-references MURD:91079769
#accession JH0332

```
##cross-references GB:X54150: NID:G31329; PID:g31330
##experimental_source cell_liver V937
REFERENCE
#authors J37224
#journal De Wit, T.P.; Morton, H.C.; Capel, P.J.; van de Winkel, J.G.
#journal J Immunol. (1995) 155:1203-1209
#title Structure of the gene for the human myeloid Iga Fc receptor
# (CD89).
#cross-references MUID:95363085
#accession I37224
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Query Match	69.6%;	Score 48;	DB 2;	Length 287;
Best Local Similarity	83.3%;	Pred. NO. 1.73e+01;		
Matches	5;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;

Db	197	YNRSPY	202
		:	
QY	3	YNRAPY	8

RESULT	12
ENTRY	S49009
TITLE	#type complete fork head protein 2 - african clawed frog
ORGANISM	#formal_name xenopus laevis #common_name African clawed frog
DATE	07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
ACCESSIONS	S49009

REFERENCE	S49008
#authors	Lef, J.; Clement, J.H.; Oswald, R.; Koester, M.; Knoechel

#journal Mech. Dev. (1994) 45:117-126
#title Spatial and temporal transcription patterns of the forkhead
related XFD-2/XFD-2' genes in *Xenopus laevis* embryos.
#cross-references MUID:94257528
#accession S49009

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128-219  #domain fork head DNA-binding domain homology #label FHD
SUMMARY  #length 367  #molecular-weight 40971  #checksum 6845

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Query Match	69.6%	Score 48;	DB 2;	Length 367;
Best Local Similarity	83.3%	Pred. No. 1.73e+01;		
Matches	5;	Conservative	0;	Indels 0;
		Mismatches	0;	Gaps 0;

Db 337 YNRSPY 34Z
|||:|
QY 3 YNRAPY 8

RESULT	13
ENTRY	549008
TITLE	fork head protein - African clawed frog
ORGANISM	#formal_name Xenopus laevis #common_name African clawed frog
DATE	07-May-1995 #sequence_revision 21-Jul-1995 #text-change 17-Mar-1999
ACCESSIONS	549008; B56556
REFERENCES	549008

#journal Mech. Dev. (1994) 45:117-126
#title Spatial and temporal transcription patterns of the forkhead related XFD-2/XFD-2' genes in *Xenopus laevis* embryos.
#cross-references MUID:94257528
#id 94000

#authors Knochei, S.; Ieff, J.; Clement, J.; Locke, B.; Hille, S.;
#journal Roster, M.; Knochei, W.
#title Mech. Dev. (1992) 38:157-165
#title Activin A induced expression of a fork head related gene in
posterior chordamesoderm (notochord) of *Xenopus laevis*
embryos.
#cross-references MUID:93041288
#accession B56556

```

FEATURE
127-218      #domain fork head DNA-binding domain homology #label FHD
SUMMARY      #length 370 #molecular-weight 41388 #checksum 6542

```

Query Match	69.6%	Score 48	DB 2	Length 370
Best Local Similarity	83.3%	Pred. No.	1.73e+01	
Matches	5	Mismatches	0	Indels 0
		Conservative		Gaps 0
Db	335 YNRSPY 340			
	:			
QY	3 YNRAPY 8			

Db 335 YNRSPY 34C
|||: ||
QY 3 YNRAPY 8

```

RESULT      14
ENTRY
TITLE      JE0389      #type complete
            catabolite repressor protein - Imperfect fungus (Humicola
            grisea)
ORGANISM    #formal_name Humicola grisea
DATE        13-Feb-1999 #sequence_revision 13-Feb-1999 #text_change
            13-Feb-1999
ACCESSIONS  JE0389
REFERENCE    JE0389
#authors    Takashima, S.; Nakamura, A.; Hidaka, M.; Masaki, H.; Uozumi,
            T.
#journal    Biosci. Biotechnol. Biochem. (1998) 62:2364-2370
#title      Isolation of the creA gene from the cellulolytic fungus
            Humicola grisea and analysis of CreA binding sites upstream
            from the cellulase genes.
#accession  JE0389
#status     preliminary
#residues   1-419 #label TAK
#cross-references DDBJ:AB003106
SUMMARY     #length 419 #molecular-weight 45852 #checksum 2179

Query Match      69.6%: Score 48; DB 3; Length 419;
Best Local Similarity 71.4%: Pred. No. 1,73e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db      188 YSRAPYS 194
|:||||:
QY      3 YNRAPYT 9

RESULT      15
ENTRY
TITLE      E71486      #type complete
            probable s/t protein kinase - Chlamydia trachomatis (serotype
            D, strain UW3/Cx)
ORGANISM    #formal_name Chlamydia trachomatis.
DATE        13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
            21-Nov-1998
ACCESSIONS  E71486
REFERENCE    A71570
#authors    Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe,
            R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov,
            R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W.
            Science (1998) 282:754-759
            Genome sequence of an obligate intracellular pathogen of
            humans: Chlamydia trachomatis.
            #cross-references KUID:99000809
            #accession E71486
            #status     preliminary
            #molecule_type DNA
            #residues   1-490 #label ARN
            #cross-references GB:AE001337; GB:AE001273; NID:93329113; PID:93329124
            #experimental_source serotype D, strain UW-3/Cx
GENETICS     pkn5
SUMMARY     #length 490 #molecular-weight 55926 #checksum 6253

Query Match      69.6%: Score 48; DB 2; Length 490;
Best Local Similarity 62.5%: Pred. No. 1,73e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      472 OKYRSLY 479
|:||||:
QY      1 OKYRAPY 8

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Search completed: Thu Sep 2 11:43:10 1999
 Job time : 17 secs.

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DR EMBL: L20899: G388347; -
 DR EMBL: X59868: G50358; -
 DR PIR: S20730; S20730.
 DR PIR: S22693; S22693.
 DR MGI: 99694; RASGRF1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR PROSITE: PS00741; GDS_CDC24; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PIR: P500159; PH; 2.
 DR PIR: P500612; IQ; 1.
 DR PIR: P500617; RASGEF; 1.
 DR PIR: P500618; RASGEFN; 1.
 DR PIR: P500621; RHOGEF; 1.
 DR KW: GUANTINE-NUCLEOTIDE RELEASE FACTOR.
 DR DOMAIN: 22 130 PH.
 DR CONFILCT 1033 1033 E -> D (IN REF. 3).
 DR SEQUENCE 1262 AA; 144101 MW; 021C787F CRC32;

Query Match 78.3%; Score 54; DB 1; Length 1262;
 Best Local Similarity 62.5%; Pred. No. 3,30e-01;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1060 EKYRTPY 1067
 QY 1 QKYNRPY 8

RESULT 2
 ID PRC2_DROME STANDARD; PRT; 279 AA.
 AC P12881;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROTEASOME 29 KD SUBUNIT (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE
 DE COMPLEX 35 KD SUBUNIT).
 GN PROS35 OR PROS-35.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PERICOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
 OC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-18 AND 194-206.
 RA STRAIN-OREGON-R;
 RA MEDLINE: 90005444.
 RA HAASS C., PESOLD-HURT B., MÜLTHAUP G., BEYREUTHER K.,
 RA KLOETZEL P.-M.;
 RT "The PROS-35 gene encodes the 35 kd protein subunit of Drosophila
 RT melanogaster proteasome";
 RL EMBO J. 8:2373-2379(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-OREGON-R;
 RA MEDLINE: 92249308.
 RA FRENZEL S., TROXELL M., HAASS C., PESOLD-HURT B., GLAETZER K.H.,
 RA KLOETZEL P.-M.;
 RT "Molecular characterization of the genomic regions of the Drosophila
 RT alpha-type subunit proteasome genes PROS-Dm28.1 and PROS-Dm35.";
 RL EUR. J. BIOCHEM. 205:1043-1051(1992).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH. THE 35 KD SUBUNIT IS PROBABLY A
 CC REGULATORY SUBUNIT. THE PROTEASOME HAS AN ATP-DEPENDENT
 CC PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.

CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.

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DR EMBL: X15497; G8382; -
 DR EMBL: X62285; G8388; -
 DR PIR: S05507; SNPEFSK.
 DR PIR: S23450; S23450.
 DR FIVEBASE: FBgn0003151; PROS35.
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PIR: P500227; Proteasome; 1.
 DR HSSP: P25156; 1PMA.
 DR PROTEASOME; HYDROLASE; PROTEASE; PHOSPHORYLATION
 DR MOD_RES 103 103 PHOSPHORYLATION (POTENTIAL).
 DR SEQUENCE 279 AA; 31058 MW; A418BDE CRC32;

Query Match 75.4%; Score 52; DB 1; Length 279;
 Best Local Similarity 62.5%; Pred. No. 9,36e-01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 121 QKYNRPY 128
 QY 1 QKYNRPY 8

RESULT 3
 ID DCAM_SOLTU STANDARD; PRT; 360 AA.
 AC Q04694;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETDC)
 DE (SAMDC) (INDUCED STOLEN TIP PROTEIN TUB13).
 GN SAMDC OR TUB13.
 OS SOLANUM TUBEROSUM (POTATO).
 OC EUKARYOTA; VIRIDIPHYTES; EMBRYOPHYTES; TRACHEOPHYTES;
 OC EUPHYPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; EUDICOTYLEDONS;
 OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; SOLANUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. RECORD; TISSUE-STOLON TIP;
 RA MEDLINE: 93081725.
 RA TAYLOR M.A., MAD ARIFF S.A., KUMAR A., DAVIES H.V., SCOBIE L.A.,
 RA PEARCE S.R., FLAVELL A.J.;
 RT "Expression and sequence analysis of cDNAs induced during the early
 RT stages of tuberisation in different organs of the potato plant
 RT (Solanum tuberosum L.).";
 RL PLANT MOL. BIOL. 20:641-651(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. DESIREE;
 RA MEDLINE: 95036004.
 RA MAD ARIFF S.A., TAYLOR M.A., GEORGE L.A., BUTLER A.R., BURCH L.R.,
 RA DAVIES H.V., STARK M.J., KUMAR A.;
 RT "Characterisation of the S-adenosylmethionine decarboxylase (SAMDC)
 RT gene of potato.";
 RL PLANT MOL. BIOL. 26:337-338(1994).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE = (5-DEOXY-5-ADENOSYL)
 CC (3-AMINOPROPYL)METHYLSULFONIUM SALT + CO(2).
 CC -1- COFACTOR: THIS ENZYME REQUIRES A PYRUVYL GROUP FOR ITS ACTIVITY.
 CC -1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
 CC AMINOPROPYL MOIETY REQUIRED FOR SPERMATIDINE AND SPERMINE
 CC BIOSYNTHESIS FROM PUTRESCINE.
 CC -1- TISSUE SPECIFICITY: STOLON, ALSO EXPRESSED IN LEAVES, STEMS

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CC ANDROOTS.
CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING THE
CC EARLY STAGES OF TUBERIZATION. MAXIMUM EXPRESSION WAS IN NON-
CC SMELLING STOLON TIPS FROM STAGE B, AND LEVEL DECLINED AS THE
CC TUBER INCREASED IN SIZE.
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CC DR EMBL; Z11680; G21485; -.
CC DR EMBL; S74514; G807094; -.
CC DR PIR; S28047; S28047.
CC KW SPERMIDINE BIOSYNTHESIS; LYASE: DECARBOXYLASE; PYRUVATE; ZYMOMEN.
CC FT CHAIN 1 72 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
CC CHAIN 73 360 CHAIN (BY SIMILARITY).
CC FT SITE 72 73 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
CC FT MOD_RES 73 73 CHAIN (BY SIMILARITY).
CC FT ACT_SITE 13 13 CLEAVAGE (NONHYDROLYTICAL)
CC FT ACT_SITE 16 16 (BY SIMILARITY).
CC FT ACT_SITE 87 87 CONVERTED TO A PYRUVYL GROUP
CC FT ACT_SITE 87 87 (BY SIMILARITY).
CC FT CONFLICT 174 174 IMPORTANT FOR CATALYTIC ACTIVITY (BY
CC CONFLICT 257 257 SIMILARITY).
CC FT CONFLICT 291 291 IMPORTANT FOR CATALYTIC ACTIVITY (BY
CC FT CONFLICT 305 305 SIMILARITY).
CC SQ SEQUENCE 360 AA; 39726 MW; 42929EB4 CRC32.
CC -----
CC Query Match 75.4%; Score 52; DB 1; Length 360;
CC Best Local Similarity 62.5%; Pred. No. 9.36e-01;
CC Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC Db 332 OKFTTPY 339
CC 1: 1:11
CC 1 OKYNRAPY 8
CC -----
CC RESULT 4 STANDARD: PRT: 544 AA.
CC H15_DROME Q94890.
CC 01-NOV-1997 (REL. 35, CREATED)
CC 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
CC 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CC T-BOX PROTEIN H15.
CC H15.
CC OS DROSOPHILA MELANOGASTER (FRUIT FLY).
CC OC EUKARYOTA; METAEOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
CC CC PTERYCOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;
CC CC DROSOPHILIDAE; DROSOPHILA.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE-EYE;
CC RA BROOK W.U.; COHEN S.M.;
CC RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC CC -1- SIMILARITY: CONTAINS A T-BOX DOMAIN.
CC -----
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CC
DR EMBL; X98766; E255227; -.
DR FLXBASE; FB9n0016660; H15.
DR PROSITE; PS01264; TBOX_2; FALSE_NEG.
DR PROSITE; PS01283; TBOX_1; 1.
DR PFAM; PF00907; T-box; 1.
DR HSSP; P24781; 1XBR.
DR DNA-BINDING; NUCLEAR PROTEIN.
KW DOMAIN
FT DOMAIN 56 59 POLY-ALA.
FT DOMAIN 83 91 POLY-GLN.
FT DOMAIN 118 125 POLY-PRO.
FT DNA_BIND 170 356 T-BOX.
FT DOMAIN 242 245 POLY-PRO.
FT DOMAIN 436 443 POLY-PRO.
SQ SEQUENCE 544 AA; 60010 MW; 701FD98D CRC32;

Query Match 73.9%; Score 51; DB 1; Length 544;
Best Local Similarity 55.6%; Pred.No.1.56e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 414 OMEGRSPYT 422
Qy 1 OKYNRAPYT 9

RESULT 5
ID YBP3_YEAST STANDARD; PRT; 689 AA.
AC P38227;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHEETICAL 77.3 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.
GN YBR043C OR YBR0413.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOTECES; SACCCHAROMYCETALES;
OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RA ANDRE B., CZIEPLUCH C., HEIN C., JANUNIX J.C., URRESTARAZU A.,
RA VISSERS S.;
RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE
CC CARL/CYHR SUBFAMILY.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC
DR EMBL; Z35912; G536268; -.
DR PIR; S45901; S45901.
KW HYPOTHETICAL PROTEIN; TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 109 131 POTENTIAL.
FT TRANSMEM 140 163 POTENTIAL.
FT TRANSMEM 176 193 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 266 283 POTENTIAL.
FT TRANSMEM 476 493 POTENTIAL.
FT TRANSMEM 511 532 POTENTIAL.
FT TRANSMEM 559 577 POTENTIAL.
FT TRANSMEM 587 609 POTENTIAL.
FT TRANSMEM 625 642 POTENTIAL.
FT TRANSMEM 649 668 POTENTIAL.
SQ SEQUENCE 689 AA; 77300 MW; 3616EDAE CRC32;

Query Match 72.5%; Score 50; DB 1; Length 689;

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GN PSMAL.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MORIAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=LIVER;
RX MEDLINE: 90057428.
RA FUJIMURA T., TANAKA K., KUMATORI A., SHIN S., YOSHIMURA T.,
RA ICHIHARA A., TOKUNAGA F., ARUGA R., IWANAGA S., KATZOKA A.,
RA NAKANISHI S.;
RT "Molecular cloning of cDNA for proteasomes (multicatalytic proteinase
RT complexes) from rat liver: primary structure of the largest component
RT (C2).";
RL BIOCHEMISTRY 28:7332-7340(1989).
RN [2]
RP SEQUENCE OF 1-30.
RC TISSUE=LIVER;
RX MEDLINE: 90243011.
RA TOKUNAGA F., ARUGA R., IWANAGA S., TANAKA K., ICHIHARA A., TAKAO T.,
RA SHIMONISHI Y.;
RT "The N2-terminal residues of rat liver proteasome (multicatalytic
RT proteinase complex) subunits, C2, C3 and C8, are N
RT alpha-acetylated.";
RL FEBS LETT. 263:373-375(1990).
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC ARG. PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC PROTEOLYTIC ACTIVITY.
CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
CC PROTEOLYTIC PATHWAY.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC ALSO IN THE NUCLEUS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL RAT TISSUES.
CC -1- PTM: ITS C-TERMINAL EXTENSION IS PARTIALLY CLEAVED OFF BY LIMITED
CC PROTEOLYSIS LEADING TO A CONVERSION OF THE PROTEASOME FROM ITS
CC LATENT INTO ITS ACTIVE FORM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A, ALSO KNOWN AS THE
CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
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DR EMBL: M29859; G206382; -;
DR EMBL: D90265; G220877; -;
DR PIR: A32968; SNR1C2.
DR PROSITE: PS00388; PROTEASOME_A; 1.
DR PFAM: PF00227; proteasome; 1.
DR HSSP: P25156; 1PMA.
KW PROTEASOME; HYDROLASE; PROTEASE; ACETYLATION.
FT MOD_RES 1 1 ACETYLATION.
FT SEQUENCE 263 AA; 29517 MW; 01D55620 CRC32;
Query Match 71.0%; Score 49; DB 1; Length 263;
Best Local Similarity 62.5%; Pct. No. 4.35e+00;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE SERUM ALBUMIN PRECURSOR.
GN ALB.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOCORNITHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA CASSADY A.I., SALKELD C.K., BAYENSTOCK P., WALLACE J.C.;
RL SUBMITTED (JUL-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE: 83161037.
RA HACHE R.J.G., WISKOCIL R., VASA M., ROY R.N., LAU P.C.K., DEBELEY R.G.;
RT "The 5' noncoding and flanking regions of the avian very low density
RT apolipoprotein II and serum albumin genes. Homologues with the egg
RT white protein genes.";
RL J. BIOL. CHEM. 258:4556-4564(1983).
RN [3]
RP SEQUENCE OF 19-30.
RX MEDLINE: 78019943.
RA ROSEN A.M., GELLER D.M.;
RT "Chicken microsomal albumin: amino terminal sequence of chicken
RT albumin.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 78:1060-1066(1977).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA⁺⁺, NH⁺, K⁺, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE ALB/APP/DBE FAMILY.
CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: X60688; G63748; -;
DR EMBL: Y00381; G63039; -;
DR PIR: S15571; ABCS.
DR PROSITE: PS00212; ALBUMIN; 3.
DR PFAM: PF00273; transport_prot; 1.
DR HSSP: P02768; 100R.
KW PLASMA; METAL-BINDING; LIPID-BINDING; ALBUMIN; REPEAT; SIGNAL;
KW COPPER.
FT SIGNAL 1 18
FT PROPEP 19 23
FT CHAIN 24 615 SERUM ALBUMIN.
FT REPEAT 31 206 1.
FT REPEAT 225 398 2.
FT REPEAT 417 596 3.
FT METAL 30 30 COPPER (BY SIMILARITY).
FT DISULFID 80 89 BY SIMILARITY.
FT DISULFID 102 118 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 152 197 BY SIMILARITY.
FT DISULFID 196 205 BY SIMILARITY.
FT DISULFID 228 274 BY SIMILARITY.
FT DISULFID 273 281 BY SIMILARITY.
FT DISULFID 283 307 BY SIMILARITY.
FT DISULFID 306 317 BY SIMILARITY.
FT DISULFID 344 389 BY SIMILARITY.
FT DISULFID 388 397 BY SIMILARITY.
FT DISULFID 420 466 BY SIMILARITY.
FT DISULFID 465 476 BY SIMILARITY.

FT DISULFID 489 505 BY SIMILARITY.
 FT DISULFID 504 515 BY SIMILARITY.
 FT DISULFID 542 587 BY SIMILARITY.
 FT DISULFID 586 595 BY SIMILARITY.
 FT CARBOHYD 500 500 POTENTIAL.
 FT CONFLICT 24 F -> M (IN REF. 3).
 SQ SEQUENCE 615 AA; 69918 MW; DC56EEA CRC32.

Query Match 71.0%; Score 49; DB 1; Length 615;
 Best Local Similarity 55.6%; Pred. No. 4.25e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 249 QKYPKAPFS 257
 |||:|:|:
 QY 1 QKYNRABYT 9

RESULT 10
 FCAR_HUMAN STANDARD; PRT; 287 AA.
 P24071; Q15728; Q15727; Q13603; Q13604;
 01-MAR-1992 (REL. 21, CREATED)
 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR (IGA FC RECEPTOR) (CD89
 DE ANTIGEN).
 GN FCAR OR CD89.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATHARTINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91079769.
 RA MALISZEWSKI C.R., MARCH C.J., SCHOENBORN M.A., GIMPEL S., SHEN L.;
 RT "Expression cloning of a human Fc receptor for IGA.";
 RJ J. EXP. MED. 172:1665-1672(1990).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-BONE MARROW.
 RX MEDLINE; 95363085.
 RA DE WIT T.P.M., MORTON H.C., CAPEL P.J.A., VAN DE WINKEL J.G.J.;
 RT "Structure of the gene for the human myeloid IGA Fc receptor (CD89).";
 RJ J. IMMUNOL. 155:1203-1209(1995).
 RL [3]
 RN SEQUENCE FROM N.A. (FORMS A.2 AND A.3).
 RP TISSUE-ALVEOLAR MACROPHAGE, AND MONOCYTES;
 RX MEDLINE; 96247667.
 RA PATRY C., STIBILLE Y., LEHUEU A., MONTEIRO R.C.;
 RT "Identification of Fc alpha receptor (CD89) isoforms generated by
 alternative splicing that are differentially expressed between blood
 monocytes and alveolar macrophages.";
 RJ J. IMMUNOL. 156:4442-4448(1996).
 RL [4]
 RN SEQUENCE FROM N.A. (FORMS B AND B-DELTA-S2).
 RP VAN DIJK T.B., MORTON H.C., CALDENHOVEN E., BRACKE M.,
 RA RAUWMAKERS J.A.M., LAMERS J.W.J., KOENDEMAN L., GROOT R.P.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [5]
 RP SEQUENCE FROM N.A. (FORM A.3/RLA2).
 RX MEDLINE; 96433090.
 RA PLEAS R.J., ANDREWS P.D., KERR M.A., WOOF J.M.;
 RT "Alternative splicing of the human IGA Fc receptor CD89 in
 neutrophils and eosinophils.";
 RJ BIOCHEM. J. 318:771-777(1996).
 RL [6]
 RN SUBUNITS.
 RP MEDLINE; 94375887.
 RA PFEFFERKORN L.C., YEAMAN G.R.;
 RT "Association of IGA-Fc receptors (Fc alpha R) with Fc epsilon RI
 gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
 phosphorylation of gamma 2.";
 RJ J. IMMUNOL. 153:3228-3236(1994).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS ALPHA.
 CC MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.

CC -1- SUBUNIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
 CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
 CC (FORM B).
 CC -1- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN BLOOD AND
 CC MUCOSAL MELOID CELLS. MONOCYTES EXPRESS ISOFORMS A.1, A.2 AND A.3
 CC WHILE ALVEOLAR MACROPHAGES EXPRESS A.1 AND A.2 TRANSSCRIPTS;
 CC HOWEVER THEY EXPRESS ONLY ONE ISOFORM AT THEIR SURFACES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FIVE FORMS: A.1 (SHOWN HERE), A.2,
 CC A.3, B AND B-DELTA-S2 ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD89 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd89.htm".
 CC -----
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 CC -----
 CC EMBL; X54150; G31330; -.
 DR EMBL; X87767; G1054737; JOINED.
 DR EMBL; X87768; G1054737; JOINED.
 DR EMBL; X87769; G1054737; JOINED.
 DR EMBL; X87766; G1054737; JOINED.
 DR EMBL; X87765; G1054737; JOINED.
 DR EMBL; X43774; G1439356; -.
 DR EMBL; X43677; G1439358; -.
 DR EMBL; U56236; G1326229; -.
 DR EMBL; U56237; G1326231; -.
 DR EMBL; S82919; E302400; -.
 DR PIR; JH0332; JH0332.
 DR KIM; I47045; -.
 KW RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; IGA-BINDING PROTEIN;
 KW IMMUNOGLOBULIN FOLD; SIGNAL; ALTERNATIVE SPLICING.
 FT SIGNAL 1 21
 FT CHAIN 22 287
 FT DOMAIN 22 227
 FT TRANSMEM 228 246
 FT DOMAIN 247 287
 FT DOMAIN 42 107
 FT DOMAIN 139 200
 FT DISULFID 49 100
 FT DISULFID 146 193
 FT DISULFID 65 65
 FT CARBOHYD 79 79
 FT CARBOHYD 141 141
 FT CARBOHYD 177 177
 FT CARBOHYD 186 186
 FT CARBOHYD 198 198
 FT VARSPLIC 12 23
 FT VARSPLIC 121 216
 FT VARSPLIC 195 216
 FT VARSPLIC 217 287
 SQ SEQUENCE 287 AA; 32265 MW; 1B9B01DD CRC32;

Query Match 69.6%; Score 48; DB 1; Length 287;
 Best Local Similarity 83.3%; Pred. No. 6.94e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 197 YNRSPP 202
 |||:|:|:
 QY 3 YNRPY 8

RESULT 11
 BHMT_HUMAN STANDARD; PRT; 406 AA.

AC 093088;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE BETAINE-HOMOCYSTEINE S-METHYLTRANSFERASE (EC 2.1.1.5).
 GN BHMT.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATHARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 96394355.
 RA GARROW T.A.;
 RT "Purification, kinetic properties, and cDNA cloning of mammalian
 RT betaine-homocysteine methyltransferase.";
 RL J. BIOL. CHEM. 271:22831-22838(1996).
 CC -1- FUNCTION: INVOLVED IN THE REGULATION OF HOMOCYSTEINE METABOLISM.
 CC CONVERTS BETAINE AND HOMOCYSTEINE TO DIMETHYLGLYCINE AND
 CC METHIONINE, RESPECTIVELY. THIS REACTION IS ALSO REQUIRED FOR THE
 CC IRREVERSIBLE OXIDATION OF CHOLINE.
 CC -1- CATALYTIC ACTIVITY: TRIMETHYLAMONIACETATE + L-HOMOCYSTEINE =
 CC DIMETHYLGLYCINE + L-METHIONINE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: PRIMARILY FOUND IN LIVER AND KIDNEY.
 CC -1- DISEASE: DEFECTS IN BHMT COULD LEAD TO HYPERHOMOCYST(E)INEMIA. BUT
 CC SUCH A DEFECT HAS NOT YET BEEN OBSERVED. HYPERHOMOCYST(E)INEMIA IS
 CC AN INDEPENDENT RISK FACTOR FOR THE DEVELOPMENT OF ARTERIOSCLEROTIC
 CC VASCULAR DISEASE.
 CC -----
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 CC -----
 CC EMBL: U50929; G1522683; -
 DR MIM: 602888;
 DR HSP: P06139; IGR.
 DR TRANSFERASE; METHYLTRANSFERASE.
 KW SEQUENCE 406 AA; 44970 MW; 8DEC74F5 CRC32;
 SO

Query Match 69.68; Score 48; DB 1; Length 406;
 Best Local Similarity 62.58; Pred. No. 6.94e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 282 OKYAREAY 289
 ||| | :|
 1 OKYAREAY 8

RESULT 12
 ID BHMT_RAT STANDARD; PRT; 407 AA.
 AC 009171;
 DT 15-DEC-1998 (REL. 37, CREATED)
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE BETAINE-HOMOCYSTEINE S-METHYLTRANSFERASE (EC 2.1.1.5).
 GN BHMT.
 OS RATUUS NORVIGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCOTOGNATHI; MORIDAE; MORINAE; RATUUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
 RX MEDLINE: 96354796.
 RA FORESTIER M., REICHEN J., SOLIOZ M.;
 RT "Application of mRNA differential display to liver cirrhosis: reduced
 RT tetun expression in biliary cirrhosis in the rat.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 225:377-383(1996).
 CC [2]

RP SEQUENCE FROM N.A.
 RA SOMDEN M.P., SPARKS J.D., SPARKS C.E., SMITH H.C.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: INVOLVED IN THE REGULATION OF HOMOCYSTEINE METABOLISM.
 CC -1- CATALYTIC ACTIVITY: TRIMETHYLAMONIACETATE + L-HOMOCYSTEINE =
 CC DIMETHYLGLYCINE + L-METHIONINE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -----
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 CC -----
 CC EMBL: U96133; G2072346; -
 DR EMBL: AF038870; G2766705; -
 DR TRANSFERASE; METHYLTRANSFERASE.
 KW SEQUENCE 407 AA; 44976 MW; B245A8BF CRC32;
 SO

Query Match 69.68; Score 48; DB 1; Length 407;
 Best Local Similarity 62.58; Pred. No. 6.94e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 282 OKYAREAY 289
 ||| | :|
 1 OKYAREAY 8

RESULT 13
 ID CG2A_DROME STANDARD; PRT; 491 AA.
 AC P14785;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE G2/MITOTIC-SPECIFIC CYCLIN A.
 GN CYCA.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PTERYGOTA; DIPTERA; BRACHYCERA; MOSCOMORPHA; EPHYDROIDEA;
 OC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93077051.
 RA TAKAIISA M., YOGASHI S., UEDA R., MIKUNI M., TSURUMURA S., KONDO K.,
 RA MIYAKE T.;
 RT "Structure of the Drosophila melanogaster gene encoding cyclin A.";
 RT GENE 121:343-346(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89168447.
 RA LEHNER C.F., O'FARRELL P.H.;
 RT "Expression and function of Drosophila cyclin A during embryonic cell
 RT cycle progression.";
 RT CELL 56:957-968(1989).
 RN [3]
 RP SEQUENCE OF 235-247 AND 288-300 FROM N.A.
 RX MEDLINE: 89159430.
 RA WHITFIELD W.G.F., GONZALEZ C., SANCHEZ-HERRERO E., GLOVER D.M.;
 RT "Transcripts of one of two Drosophila cyclin genes become localized
 RT in pole cells during embryogenesis.";
 RT NATURE 338:337-340(1989).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
 CC KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
 CC AND ARE ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONGEST TO OTHER
 CC CYCLINS A.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: D10857; G407199; -
DR EMBL: D10856; G407199; JOINED.
DR EMBL: D10858; G391659; -
DR EMBL: M24841; G157157; -
DR PIR: JCI390; JCI390.
DR PIR: S03543; S03543.
DR EMBASE: FB80000404; CYCA.
DR PROSITE: PS00292; CYCLINS; 1.
DR PIR: PF00134; CYCLIN; 1.
DR HSSP: P20248; 1FIN.
DR CYCLIN; CELL CYCLE; CELL DIVISION; MITOSIS.
KM CONFLICT 147 147 M -> I (IN CDNA: G391659).
FT CONFLICT 179 179 A -> V (IN REF. 2).
CONFLICT 200 200 V -> M (IN CDNA: G391659).
CONFLICT 223 223 L -> R (IN REF. 2).
CONFLICT 474 474 H -> Q (IN CDNA: G391659).
SEQUENCE 491 AA; 56124 MW; 9F047EAD CRC32.

SO
Query Match 69.6%; Score 48; DB 1; Length 491;
Best Local Similarity 62.5%; Pred. No. 6.94e+00;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 435 EKYNRDPT 442
QY 1 OKYNRPT 8

RESULT 14
ID NPRE_BACAM STANDARD; PRT; 521 AA.
AC P06832;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE BACILLOTYSIN PRECURSOR (EC 3.4.24.28) (NEUTRAL PROTEASE).
GN NRP.
OS BACILLUS AMILOLOQUEFACIENS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-ATCC 23844;
RX MEDLINE: 85006739.
VARSANTHA N., THOMPSON L.D., RHODES C., BANNER C., MAGLE J.,
FILIPULA D.;
"Genes for alkaline protease and neutral protease from *Bacillus*
anylioliquefaciens contain a large open reading frame between the
regions coding for signal sequence and mature protein.";
J. BACTERIOL. 159:811-819(1984).
CC -1- FUNCTION: THERMO-LABILE EXTRACELLULAR ZINC METALLOPROTEASE.
CC -1- CATALYTIC ACTIVITY: SIMILAR, BUT NOT IDENTICAL, TO THAT OF
THERMOLYSIN.
CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4 (ZINC METALLOPROTEASE);
CC ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL: K02497; G143349; -
DR PIR: A25415; HYBSN.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.

DR PFAM: PF00099; zn-protease; 1.
DR HSSP: P00800; 1TRL.
KM HYDROLASE; METALLOPROTEASE; ZINC; CALCIUM; ZMOGEN; SIGNAL.
FT SIGNAL 1 27
FT PROPEP 26 221
FT CHAIN 222 521
FT METAL 364 364
FT ACT_SITE 365 365
FT METAL 368 368
FT METAL 388 388
FT ACT_SITE 449 449
SEQUENCE 521 AA; 56840 MW; BC0147D4 CRC32;

SO
Query Match 69.6%; Score 48; DB 1; Length 521;
Best Local Similarity 62.5%; Pred. No. 6.94e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 308 OKENRSTY 315
QY 1 OKYNRPT 8

RESULT 15
ID YJ51_YEAST STANDARD; PRT; 340 AA.
AC Q12524;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 39.8 KD PROTEIN IN MPT4-ACS2 INTERGENIC REGION.
GN YJ51C OR U9634.8.
OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMETES; SACHAROMYCETALES;
OC SACHAROMYCETACEAE; SACHAROMYCES.
RN [1]
RC SEQUENCE FROM N.A.
RP RIEGER M., MUELLER-AUER S., BRUECKNER M.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RP [2]
RC SEQUENCE FROM N.A.
RP STRAIN-5288C / AB972;
RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
RA FAVELLO A., FULTON L., GATUNG S., GRECO T., KIRSTEN J., KUCABA T.,
RA HALLSWORTH K., HANKINS J., HILIER L., JIER M., JOHNSON D.,
RA JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
RA MILLER N., NHAN M., PAULEY A., PELUSO D., RIKKEN L., RILES L.,
RA TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
RA WILSON R., WATSON R.;
RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: BELONGS TO THE UPF0035 FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

DR EMBL: Z73323; E245586; -
DR EMBL: U53879; G1262311; -
DR PROSITE: PS01293; UPF0035; 1.
DR PFAM: PF00293; mult; 1.
KM HYPOTHETICAL PROTEIN.
SEQUENCE 340 AA; 39755 MW; FBFD4B7 CRC32;

SO
Query Match 68.1%; Score 47; DB 1; Length 340;
Best Local Similarity 50.0%; Pred. No. 1.12e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 22 KFHRTPT 29
QY 2 KYNRPT 9

• Fri Sep 3 09:52:52 1999

US-08-599-226-16.rsp

Page 9

Search completed: Thu Sep 2 11:43:34 1999
job time : 8 secs.

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[M] [O] [S] [E] [H]
(TM)

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Mpsrch.pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:44:36 1999; MasPar time 1.35 Seconds
Module output not generated. 67.901 Million cell updates/sec

Title: >US-08-599-226-16
Description: (1-9) from US08599226.pep
Perfect Score: 69
Sequence: 1 QKXNRAPYT 9

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfile1

Statistics: Mean 15.610; Variance 46.262; scale 0.337

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	49	71.0	269	1	US-08-202-	Sequence 4, Applicatio	3.98e+01
2	48	69.6	287	4	5198342-2	Patent No. 5198342.	5.14e+01
3	48	69.6	287	1	US-07-971-	Sequence 2, Applicatio	5.14e+01
4	47	68.1	107	3	PCT-US95-0	Sequence 87, Applicati	6.62e+01
5	47	68.1	107	2	US-08-899-	Sequence 87, Applicati	6.62e+01
6	47	68.1	107	2	US-08-899-	Sequence 87, Applicati	6.62e+01
7	47	68.1	107	1	US-08-276-	Sequence 87, Applicati	6.62e+01
8	47	68.1	1708	2	US-08-508-	Sequence 2, Applicatio	6.62e+01
9	47	68.1	1708	1	US-08-493-	Sequence 2, Applicatio	6.62e+01
10	47	68.1	3056	2	US-08-508-	Sequence 8, Applicatio	6.62e+01
11	47	68.1	3056	2	US-08-629-	Sequence 3, Applicatio	6.62e+01
12	46	66.7	52	2	US-08-162-	Sequence 43, Applicati	8.52e+01
13	46	66.7	109	3	US-08-162-	Sequence 23, Applicati	8.52e+01
14	46	66.7	109	3	PCT-US93-0	Sequence 23, Applicati	8.52e+01
15	46	66.7	718	1	US-08-444-	Sequence 4, Applicatio	8.52e+01
16	46	66.7	718	1	US-08-445-	Sequence 4, Applicatio	8.52e+01
17	45	65.2	109	3	US-07-934-	Sequence 3, Applicatio	1.10e+02
18	45	65.2	109	3	PCT-US93-0	Sequence 3, Applicatio	1.10e+02
19	45	65.2	246	2	US-08-604-	Sequence 3, Applicatio	1.10e+02
20	45	65.2	466	2	US-08-604-	Sequence 4, Applicatio	1.10e+02
21	45	65.2	480	1	US-07-882-	Sequence 2, Applicatio	1.10e+02
22	45	65.2	480	3	PCT-US93-0	Sequence 2, Applicatio	1.10e+02
23	45	65.2	507	3	PCT-US95-0	Sequence 2, Applicatio	1.10e+02

24	45	65.2	507	2	US-08-604-	Sequence 5, Applicatio	1.10e+02
25	44	63.8	33	2 <td>US-08-724-<td>Sequence 12, Applicati<td>1.40e+02</td></td></td>	US-08-724- <td>Sequence 12, Applicati<td>1.40e+02</td></td>	Sequence 12, Applicati <td>1.40e+02</td>	1.40e+02
26	44	63.8	108	2 <td>US-08-899-<td>Sequence 99, Applicati<td>1.40e+02</td></td></td>	US-08-899- <td>Sequence 99, Applicati<td>1.40e+02</td></td>	Sequence 99, Applicati <td>1.40e+02</td>	1.40e+02
27	44	63.8	108	3 <td>PCT-US95-0<td>Sequence 99, Applicati<td>1.40e+02</td></td></td>	PCT-US95-0 <td>Sequence 99, Applicati<td>1.40e+02</td></td>	Sequence 99, Applicati <td>1.40e+02</td>	1.40e+02
28	44	63.8	108	2 <td>US-08-899-<td>Sequence 99, Applicati<td>1.40e+02</td></td></td>	US-08-899- <td>Sequence 99, Applicati<td>1.40e+02</td></td>	Sequence 99, Applicati <td>1.40e+02</td>	1.40e+02
29	44	63.8	108	1 <td>US-08-276-<td>Sequence 99, Applicati<td>1.40e+02</td></td></td>	US-08-276- <td>Sequence 99, Applicati<td>1.40e+02</td></td>	Sequence 99, Applicati <td>1.40e+02</td>	1.40e+02
30	44	63.8	218	2 <td>US-08-343-<td>Sequence 20, Applicati<td>1.40e+02</td></td></td>	US-08-343- <td>Sequence 20, Applicati<td>1.40e+02</td></td>	Sequence 20, Applicati <td>1.40e+02</td>	1.40e+02
31	44	63.8	1376	2 <td>US-08-420-<td>Sequence 3, Applicatio<td>1.40e+02</td></td></td>	US-08-420- <td>Sequence 3, Applicatio<td>1.40e+02</td></td>	Sequence 3, Applicatio <td>1.40e+02</td>	1.40e+02
32	44	63.8	1376	3 <td>PCT-US95-1<td>Sequence 3, Applicatio<td>1.40e+02</td></td></td>	PCT-US95-1 <td>Sequence 3, Applicatio<td>1.40e+02</td></td>	Sequence 3, Applicatio <td>1.40e+02</td>	1.40e+02
33	43	62.3	106	3 <td>PCT-US95-0<td>Sequence 85, Applicati<td>1.80e+02</td></td></td>	PCT-US95-0 <td>Sequence 85, Applicati<td>1.80e+02</td></td>	Sequence 85, Applicati <td>1.80e+02</td>	1.80e+02
34	43	62.3	106	1 <td>US-08-276-<td>Sequence 85, Applicati<td>1.80e+02</td></td></td>	US-08-276- <td>Sequence 85, Applicati<td>1.80e+02</td></td>	Sequence 85, Applicati <td>1.80e+02</td>	1.80e+02
35	43	62.3	126	2 <td>US-08-202-<td>Sequence 17, Applicati<td>1.80e+02</td></td></td>	US-08-202- <td>Sequence 17, Applicati<td>1.80e+02</td></td>	Sequence 17, Applicati <td>1.80e+02</td>	1.80e+02
36	43	62.3	126	2 <td>US-08-202-<td>Sequence 17, Applicati<td>1.80e+02</td></td></td>	US-08-202- <td>Sequence 17, Applicati<td>1.80e+02</td></td>	Sequence 17, Applicati <td>1.80e+02</td>	1.80e+02
37	43	62.3	126	2 <td>US-08-202-<td>Sequence 13, Applicati<td>1.80e+02</td></td></td>	US-08-202- <td>Sequence 13, Applicati<td>1.80e+02</td></td>	Sequence 13, Applicati <td>1.80e+02</td>	1.80e+02
38	43	62.3	131	2 <td>US-08-202-<td>Sequence 5, Applicatio<td>1.80e+02</td></td></td>	US-08-202- <td>Sequence 5, Applicatio<td>1.80e+02</td></td>	Sequence 5, Applicatio <td>1.80e+02</td>	1.80e+02
39	43	62.3	442	2 <td>US-08-363-<td>Sequence 11, Applicati<td>1.80e+02</td></td></td>	US-08-363- <td>Sequence 11, Applicati<td>1.80e+02</td></td>	Sequence 11, Applicati <td>1.80e+02</td>	1.80e+02
40	43	62.3	445	2 <td>US-08-363-<td>Sequence 12, Applicati<td>1.80e+02</td></td></td>	US-08-363- <td>Sequence 12, Applicati<td>1.80e+02</td></td>	Sequence 12, Applicati <td>1.80e+02</td>	1.80e+02
41	43	62.3	445	2 <td>US-08-363-<td>Sequence 5, Applicatio<td>1.80e+02</td></td></td>	US-08-363- <td>Sequence 5, Applicatio<td>1.80e+02</td></td>	Sequence 5, Applicatio <td>1.80e+02</td>	1.80e+02
42	43	62.3	533	1 <td>US-08-488-<td>Sequence 6, Applicatio<td>1.80e+02</td></td></td>	US-08-488- <td>Sequence 6, Applicatio<td>1.80e+02</td></td>	Sequence 6, Applicatio <td>1.80e+02</td>	1.80e+02
43	43	62.3	584	2 <td>US-08-313-<td>Sequence 17, Applicati<td>1.80e+02</td></td></td>	US-08-313- <td>Sequence 17, Applicati<td>1.80e+02</td></td>	Sequence 17, Applicati <td>1.80e+02</td>	1.80e+02
44	43	62.3	942	1 <td>US-08-141-<td>Sequence 14, Applicati<td>1.80e+02</td></td></td>	US-08-141- <td>Sequence 14, Applicati<td>1.80e+02</td></td>	Sequence 14, Applicati <td>1.80e+02</td>	1.80e+02
45	43	62.3	1358	2 <td>US-08-570-<td>Sequence 27, Applicati<td>1.80e+02</td></td></td>	US-08-570- <td>Sequence 27, Applicati<td>1.80e+02</td></td>	Sequence 27, Applicati <td>1.80e+02</td>	1.80e+02

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	269 AA.
ID	US-08-202-857-4			
XX	xxxxxx			
AC				
AC				
XX				
DE	Sequence 4, Application US/08202857			
XX				
CC	Sequence 4, Application US/08202857			
CC	Patent No. 5635345			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Scherter, Klaus			
CC	APPLICANT: Bureau, Jean-Paul			
CC	APPLICANT: Bey, Fay al			
CC	TITLE OF INVENTION: Diagnostic Method			
CC	NUMBER OF SEQUENCES: 4			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: PRO-SOMA SARL C/O AKZO PHARMA			
CC	STREET: 1330-A PICCARD DRIVE			
CC	CITY: ROCKVILLE			
CC	STATE: MARYLAND			
CC	COUNTRY: USA			
CC	ZIP: 20850-4377			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PS/2			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Microsoft word			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/202,857			
CC	FILING DATE:			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US/07/860,492			
CC	FILING DATE: 11-JUNE-1992			
CC	APPLICATION NUMBER: PCT/EP91/01945			
CC	FILING DATE: 10-OCT-1991			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: BOBROWICZ, DONNA			
CC	REGISTRATION NUMBER: 32,196			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: 301-258-5200			
CC	TELEFAX: 301-977-1403			
CC	INFORMATION FOR SEQ ID NO: 4:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 269 amino acids			

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: human
SQ SEQUENCE 269 AA; 30227 MW; 341084 CN;
Query Match 71.0%; Score 49; DB 1; Length 269;
Best Local Similarity 62.5%; Pred. No. 3.98e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 127 ORYGRPY 134
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QY 1 OKYNRAPY 8
RESULT 2
ID 5198342-2 STANDARD; PRT: 311 AA.
XX xxxxxx
DE 01-JAN-1900
XX Patent No. 5198342.
CC Patent No. 5198342
CC APPLICANT: MALIISZEMSKI, CHARLES R.
CC TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/548,059
CC FILING DATE: 05-JUL-1990
CC SEQ ID NO: 2;
CC LENGTH: 287
SQ SEQUENCE 311 AA; 34908 MW; 558002 CN;
Query Match 69.6%; Score 48; DB 4; Length 287;
Best Local Similarity 83.3%; Pred. No. 5.14e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSYPY 202
111:11
QY 3 YNRPY 8
RESULT 3
ID US-07-971-092-2 STANDARD; PRT: 287 AA.
XX xxxxxx
DE Sequence 2, Application US/07971092
XX Sequence 2, Application US/07971092
CC Patent No. 5328987
CC GENERAL INFORMATION:
CC APPLICANT: Maliszewski, Charles R.
CC TITLE OF INVENTION: Huiga Fc Receptor
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex
CC STREET: 51 University
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/971,092
CC FILING DATE: 19921104
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Perkins, Patricia A.
CC REGISTRATION NUMBER: 34693
CC REFERENCE/DOCKET NUMBER: 2603
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 287 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 287 AA; 32265 MW; 435416 CN;
Query Match 69.6%; Score 48; DB 1; Length 287;
Best Local Similarity 83.3%; Pred. No. 5.14e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSYPY 202
111:11
QY 3 YNRPY 8
RESULT 4
ID PCT-US95-08743-87 STANDARD; PRT: 107 AA.
XX xxxxxx
DE Sequence 87, Application PC/TUS9508743
XX Sequence 87, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 107 AA; 11654 MW; 62438 CN;
Query Match 68.1%; Score 47; DB 3; Length 107;
Best Local Similarity 55.6%; Pred. No. 6.62e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 88 OQYHSSPYT 96
1:1:111
QY 1 OKYNRAPYT 9
RESULT 5
ID US-08-899-575-87 STANDARD; PRT: 107 AA.
XX xxxxxx
AC
XX
DT

XX		Sequence 87, Application US/08899575	
DE			
CC		Sequence 87, Application US/08899575	
CC		Patient No. 5804440	
CC		GENERAL INFORMATION:	
CC		APPLICANT: Burton, Dennis R	
CC		APPLICANT: Barbas, Carlos F	
CC		APPLICANT: Lerner, Richard A	
CC		TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES	
CC		TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS	
CC		NUMBER OF SEQUENCES: 170	
CC		CORRESPONDENCE ADDRESS:	
CC		ADDRESSEE: The Scripps Research Institute, Office of	
CC		ADDRESSEE: Patent Counsel	
CC		STREET: 10666 NO. 5804440th Torrey Pines Road, Suite 220,	
CC		STREET: Mail Drop TPC8	
CC		CITY: La Jolla	
CC		STATE: CA	
CC		COUNTRY: USA	
CC		ZIP: 92037	
CC		COMPUTER READABLE FORM:	
CC		MEDIUM TYPE: Floppy disk	
CC		COMPUTER: IBM PC compatible	
CC		OPERATING SYSTEM: PC-DOS/MS-DOS	
CC		SOFTWARE: PatentIn Release #1.0, Version #1.25	
CC		CURRENT APPLICATION DATA:	
CC		APPLICATION NUMBER: US/08/899,575	
CC		FILING DATE: 24-JUL-1997	
CC		CLASSIFICATION:	
CC		PRIOR APPLICATION DATA:	
CC		APPLICATION NUMBER: US 08/276,852	
CC		FILING DATE: 18-JUL-1994	
CC		APPLICATION NUMBER: US 08/178,302	
CC		FILING DATE: 30-SEP-1993	
CC		PRIOR APPLICATION DATA:	
CC		APPLICATION NUMBER: US 07/954,148	
CC		FILING DATE: 30-SEP-1992	
CC		ATTORNEY/AGENT INFORMATION:	
CC		NAME: Fitting, Thomas	
CC		REGISTRATION NUMBER: 34,163	
CC		REFERENCE/DOCKET NUMBER: SCRI452P	
CC		TELECOMMUNICATION INFORMATION:	
CC		TELEPHONE: 619-554-2937	
CC		TELEFAX: 619-554-6312	
CC		INFORMATION FOR SEQ ID NO: 87:	
CC		SEQUENCE CHARACTERISTICS:	
CC		LENGTH: 107 amino acids	
CC		TYPE: amino acid	
CC		TOPOLOGY: linear	
CC		MOLECULE TYPE: protein	
CC		SEQUENCE 107 AA; 11654 MW; 62438 CN;	
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DB	88 QGYHSSPT 96		
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XX	xxxxxx		
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XX			
DE	Sequence 87, Application US/08899575		
CC	Sequence 87, Application US/08899575		
CC	Patient No. 5770440		
CC			

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CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
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CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
CC SQ
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CC Query Match 68.1%; Score 47; DB 2; Length 107;
CC Best Local Similarity 55.6%; Pred. No. 6.62e+01;
CC Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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CC Db 88 QOYHSSPYT 96
CC | : : | | |
CC Oy 1 QOYRAPYT 9
CC
CC RESULT 7
CC ID US-08-276-852-87 STANDARD; PRT; 107 AA.
CC XX xxxxxx
CC XX
CC
CC Sequence 87, Application US/08276852
CC DE Patent No. 5652138
CC CC GENERAL INFORMATION:
CC CC APPLICANT: Burton, Dennis R
CC CC APPLICANT: Barbas, Carlos F
CC CC APPLICANT: Lerner, Richard A
CC CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

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CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ
Query Match 68.1%; Score 47; DB 1; Length 107;
Best Local Similarity 55.6%; Pred. No. 6.62e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYHSSPYT 96
1 QKYNRPYT 9

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CC AC xxxxxx
CC DT
CC XX
CC DE
CC XX
CC Sequence 2, Application US/08508836A
CC Patent No. 5777093
CC GENERAL INFORMATION:
CC APPLICANT: Shiloh, Yosef
CC APPLICANT: Tagle, Danilo A.
CC APPLICANT: Collins, Francis S.
CC TITLE OF INVENTION: Ataxia-telangiectasia Gene
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Relisng, Ethlington, Barnard & Perry
CC STREET: P.O. Box 4390
CC CITY: Troy
CC STATE: Michigan
CC COUNTRY: US

CC ZIP: 48099
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/508,836A
CC FILING DATE:
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kohn, Kenneth I.
CC REGISTRATION NUMBER: 30,955
CC REFERENCE/DOCKET NUMBER: P-313 (TAV)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (810) 689-3500
CC TELEFAX: (810) 689-4071
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1708 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC CC SEQUENCE 1708 AA; 195977 MW; 14824289 CN;
SQ
Query Match 68.1%; Score 47; DB 2; Length 1708;
Best Local Similarity 50.0%; Pred. No. 6.62e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 234 KYSRGPS 241
2 KYNRPYT 9

CC RESULT 9
CC ID US-08-493-092-2 STANDARD; PRT; 1708 AA.
CC AC xxxxxx
CC DT
CC XX
CC DE
CC Sequence 2, Application US/08493092
CC Patent No. 5728807
CC GENERAL INFORMATION:
CC APPLICANT: Shiloh, Yosef
CC APPLICANT: Tagle, Danilo A.
CC APPLICANT: Collins, Francis S.
CC TITLE OF INVENTION: Ataxia-telangiectasia Gene
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Relisng, Ethlington, Barnard & Perry
CC STREET: P.O. Box 4390
CC CITY: Troy
CC STATE: Michigan
CC COUNTRY: US
CC ZIP: 48099
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/493,092
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kohn, Kenneth I.
CC REGISTRATION NUMBER: 30,955
CC REFERENCE/DOCKET NUMBER: P-310 (TAV)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (810) 689-3500

CC TELEFAX: (810) 689-4071
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1708 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC SEQUENCE 1708 AA; 19597 MW; 14824289 CN;
SQ
DB 234 KXSRGPF 241
OY 2 KYNRAPYT 9
Query Match 68.1%; Score 47; DB 1; Length 1708;
Best Local Similarity 50.0%; Pred. No. 6.62e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
RESULT 10
US-08-508-836A-8 STANDARD; PRT; 3056 AA.
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Sequence 8, Application US/08508836A
Sequence 8, Application US/08508836A
Patent No. 5777093
GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: Ataxia-Telangiectasia Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethlington, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: US
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,836A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-313 (TAU)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 689-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3056 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE 3056 AA; 350651 MW; 47948122 CN;
SQ
Query Match 68.1%; Score 47; DB 2; Length 3056;
Best Local Similarity 50.0%; Pred. No. 6.62e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 1582 KXSRGPF 1589
OY 2 KYNRAPYT 9

RESULT 11
ID US-08-629-001A-3 STANDARD; PRT; 3056 AA.
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Sequence 3, Application US/08629001A
Sequence 3, Application US/08629001A
Patent No. 5858661
GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE AND ITS
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5858661Western Hwy.
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,001A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2290,00032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3056 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE 3056 AA; 350651 MW; 47948122 CN;
SQ
Query Match 68.1%; Score 47; DB 2; Length 3056;
Best Local Similarity 50.0%; Pred. No. 6.62e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 1582 KXSRGPF 1589
OY 2 KYNRAPYT 9
RESULT 12
ID US-08-162-102C-43 STANDARD; PRT; 52 AA.
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Sequence 43, Application US/08162102C
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Patent No. 5762905
GENERAL INFORMATION:

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08786
CC FILING DATE: 16-SEP-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Welnerell, Jr., Ph.D., John R.
CC REGISTRATION NUMBER: 31,678
CC REFERENCE/DOCKET NUMBER: FD-2791
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
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CC CLONE: rsv 6L; 11L; 21L; and 22L
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..109
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Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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AC xxxxxx
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DE Sequence 4, Application US/08444792
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CC Sequence 4, Application US/08444792
CC Patent No. 5726037
CC GENERAL INFORMATION:
CC APPLICANT: Bodary, Sarah C.
CC APPLICANT: Gorman, Cornelia M.
CC APPLICANT: McLean, John W.
CC APPLICANT: Napier, Mary A.
CC TITLE OF INVENTION: METHOD FOR PREPARING WATER SOLUBLE
CC TITLE OF INVENTION: POLYPEPTIDES
CC NUMBER OF SEQUENCES: 18
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WinPatIn (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/444,792
CC FILING DATE: 19-May-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/380227
CC FILING DATE: 30-JAN-1995
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/218878
CC FILING DATE: 28-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/821337
CC FILING DATE: 13-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/444490
CC FILING DATE: 01-DEC-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/290224
CC FILING DATE: 22-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lee, Wendy M.
CC REGISTRATION NUMBER: 00,000
CC REFERENCE/DOCKET NUMBER: P0552P1C3D4
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-1994
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 718 amino acids
CC TYPE: Amino Acid
CC TOPOLOGY: linear
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Best Local Similarity 57.1%; Pred. No. 8.52e+01;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
DB 645 KFDREPY 651
QY 2 KYNRAPY 8

Search completed: Thu Sep 2 11:44:43 1999
Job time : 7 secs.

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 W2583 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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 Distribution rights by Oxford Molecular Ltd

MSRch_gp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:42:17 1999; Maspar time 3.67 Seconds
 52.143 Million cell updates/sec

 Molecular output not generated.

Title: >US-08-599-226-16
 Description: (1-9) from US08599226.pep
 Perfect Score: 69
 Sequence: 1 OKYNRAPYT 9

Scoring table: PAM 150
 Gap 15

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseqs
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 16.601; Variance 48.209; scale 0.344

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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3	66	95.7	9	27	W27571	Anti-TNF-alpha antibo	9.62e-01
4	66	95.7	107	27	W27568	Anti-TNF-alpha antibo	1.67e+00
5	64	92.8	9	27	W27572	Anti-TNF-alpha antibo	1.67e+00
6	64	92.8	9	27	W27579	Anti-TNF-alpha antibo	1.67e+00
7	63	91.3	9	27	W27585	Anti-TNF-alpha antibo	2.19e+00
8	61	88.4	9	27	W27562	Anti-TNF-alpha antibo	3.78e+00
9	59	85.5	9	27	W27574	Anti-TNF-alpha antibo	6.49e+00
10	56	81.2	9	27	W27570	Anti-TNF-alpha antibo	1.45e+01
11	55	79.7	9	27	W27573	Anti-TNF-alpha antibo	1.88e+01
12	55	79.7	9	27	W27582	Anti-TNF-alpha antibo	1.88e+01
13	54	78.3	9	27	W27577	Anti-TNF-alpha antibo	2.45e+01
14	54	78.3	9	27	W27576	Anti-TNF-alpha antibo	2.45e+01
15	54	78.3	9	27	W27578	Anti-TNF-alpha antibo	2.45e+01
16	52	75.4	360	13	R75006	Tomato S-adenosyl-met	4.13e+01

17	51	73.9	9	27	W27583	Anti-TNF-alpha antibo	5.35e+01
18	49	71.0	9	27	W27580	Anti-TNF-alpha antibo	8.93e+01
19	49	71.0	263	4	R22957	Human proteasome comp	8.93e+01
20	49	71.0	269	1	R22666	Protein used to raise	8.93e+01
21	48	69.6	107	39	W86127	Murine 708 VI amino a	1.15e+02
22	48	69.6	107	39	W86129	Protein sequence of d	1.15e+02
23	48	69.6	287	11	R59920	Human Fc-alpha-R.	1.15e+02
24	48	69.6	287	7	R34030	Fc-alpha-R.	1.15e+02
25	48	69.6	520	1	P94617	Neutral protease enco	1.15e+02
26	48	69.6	521	3	P51009	Sequence of neutral p	1.15e+02
27	47	68.1	107	10	R54308	Anti-HIV gp120 immuno	1.48e+02
28	47	68.1	107	19	W01266	VL region of HIV neut	1.48e+02
29	47	68.1	1625	22	W19689	ATM mutant 4777del1830	1.48e+02
30	47	68.1	1727	22	W19669	ATM mutant 5178del1142	1.48e+02
31	47	68.1	1651	22	W19666	ATM mutant 5539del111.	1.48e+02
32	47	68.1	2014	22	W19663	ATM mutant 5978del15.	1.48e+02
33	47	68.1	2598	22	W19656	ATM mutant 7789del1139	1.48e+02
34	47	68.1	2652	22	W19655	ATM mutant 7883del15.	1.48e+02
35	47	68.1	2759	22	W19652	ATM mutant 8269del1403	1.48e+02
36	47	68.1	2766	22	W19651	ATM mutant 8283del17C.	1.48e+02
37	47	68.1	2768	22	W19650	ATM mutant G8307A..	1.48e+02
38	47	68.1	2998	22	W19691	ATM mutant 3403del1174	1.48e+02
39	47	68.1	3005	22	W19648	ATM mutant 9001del1AG.	1.48e+02
40	47	68.1	3005	22	W19653	ATM mutant 8269del1153	1.48e+02
41	47	68.1	3026	22	W19676	ATM mutant 2377del190.	1.48e+02
42	47	68.1	3055	22	W19693	ATM mutant 8578del13.	1.48e+02
43	47	68.1	3055	22	W19697	ATM mutant 5435del11.	1.48e+02
44	47	68.1	3056	32	W37133	Ataxia-telangiectasia	1.48e+02
45	47	68.1	3085	22	W19701	ATM mutant G9170C.	1.48e+02

ALIGNMENTS

RESULT 1
 ID W27575 standard; peptide: 9 AA.
 AC W27575;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumor necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226. *new*
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manukovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 PI Sallied JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumor necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerostis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 100.0%; Score 69; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.18e-01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gkyrnppt 9
 1 OKXNRAPPT 9

AC W27584: W27584 standard; peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
 AC W27584:
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-A1.

PD 14-AUG-1997; U02219.

PF 10-FEB-1997; US-031476.

PR 25-NOV-1996; US-031476.

PA 09-FEB-1996; US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Milton AJ;
 PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 72; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 95.7%; Score 66; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 9.62e-01;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 gkyrnppt 9
 1 OKXNRAPPT 9

AC W27571: W27571 standard; peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
 AC W27571:
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.
 PN W09729131-A1.

PD 14-AUG-1997; U02219.

PF 10-FEB-1997; US-031476.

PR 25-NOV-1996; US-031476.

PA 09-FEB-1996; US-599226.

PI (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorats P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Milton AJ;
 PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 68; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 95.7%; Score 66; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 9.62e-01;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 gkyrnppt 9
 1 OKXNRAPPT 9

AC W27568: W27568 standard; Protein; 107 AA.

DE Anti-TNF-alpha antibody light chain variable region.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody;

KM light chain: variable region; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 N-PSDB: T88403.
 High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 15; Page 75; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 107 AA:
 SQ

Query Match 95.7%; Score 66; DB 27; Length 107;
 Best Local Similarity 88.9%; Pred. No. 9.62e-01;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 89 grynrapyt 97
 1-1111111111
 1 OKINRAPYT 9

RESULT 5
 ID W2572 standard; peptide: 9 AA.
 AC W2572:
 DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.

PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 DR High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 66; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 92.8%; Score 64; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.67e-00;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 gkyrapyt 9
 1-1111111111
 1 OKINRAPYT 9

RESULT 6
 ID W2579 standard; peptide: 9 AA.
 AC W2579:
 DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 DR High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 92.8%; Score 64; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.67e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynraby 8
 QY 1 QKYNRABY 8

RESULT 7
 ID W27585 standard; peptide: 9 AA.

AC W27585;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha: TNF-alpha; antibody: CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-AI.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manokovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 72; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, allergy, multiple
 CC spondylitis, osteoarthritis, gouty arthritis, rheumatoid
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 91.3%; Score 63; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.19e+00;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynraby 9
 QY 1 QKYNRABYT 9

RESULT 8
 ID W27562 standard; peptide: 9 AA.

AC W27562;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human: tumour necrosis factor-alpha: TNF-alpha; antibody: CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-AI.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manokovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9; Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, allergy, multiple
 CC spondylitis, osteoarthritis, gouty arthritis, rheumatoid
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 88.4%; Score 61; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 3.78e+00;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qrynary 8
|:|||||
QY 1 OKYNAPY 8

RESULT 9
ID W27574 standard: peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain: complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

PD W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PR 25-NOV-1996: US-031476.
PR 09-FEB-1996: US-599226.

PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Markovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 69; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
CC Sequence 9 AA;

Query Match 85.5%; Score 59; DB 27; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.49e+00;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynaspyt 9
|:|||||
QY 1 OKYNAPY 9

RESULT 10
ID W27570 standard: peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain: complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PR 25-NOV-1996: US-031476.
PR 09-FEB-1996: US-599226.

PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Markovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 67; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
CC Sequence 9 AA;

Query Match 81.2%; Score 56; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.45e+01;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynaspya 9
|:|||||
QY 1 OKYNAPY 9

RESULT 11
ID W27573 standard: peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain: complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.

OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997: U02219.
PR 25-NOV-1996: US-031476.
PR 09-FEB-1996: US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumor necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 79.7%; Score 55; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.88e+01;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||: |||
 QY 1 QKXNRAPT 9

RESULT 12
 ID W27582 standard; peptide: 9 AA.

AC W27582:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumor necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW keloid formation; scar tissue formation; pyrexia; burn; ELAM-1;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumor necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA;

Query Match 79.7%; Score 55; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.88e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||: |||
 QY 1 QKXNRAPT 9

RESULT 13
 ID W27577 standard; peptide: 9 AA.

AC W27577:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumor necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 70; 102pp; English.
 CC The present sequence is a novel anti-human tumor necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 78.3%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.45e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkyrsapy 8
 |||||
 QY 1 QKYNRAPY 8

RESULT 14
 ID W2576 standard; peptide: 9 AA.

AC W2576:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Mankovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 78.3%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.45e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkyrsapy 8
 |||||
 QY 1 QKYNRAPY 8

RESULT 15
 ID W2578 standard; peptide: 9 AA.

AC W2578:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.

not

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRM, Kaymakalan Z, Labkovsky B,
 PI Mankovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 70; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Kof rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA;

Query Match 78.3%; Score 54; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.45e+01;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 gkyrsapyt 9
 |||||
 QY 1 QKYNRAPYT 9

Search completed: Thu Sep 2 11:42:36 1999
 Job time : 19 secs.

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Best Local Similarity 66.7%; Pred. No. 5.32e-01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 81 OKKRAPY 89
||:||||
QY 1 OKNSAPY 9

RESULT 2
ID 087136 PRELIMINARY; PRT; 337 AA.
AC 087136;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ORE139-17 PROTEIN.
OS VIBRIO CHOLERAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
RN [1]
RP SEQUENCE FROM N.A.
PP STRAIN-MO45;
NA YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,
TAKEDA Y.;
RT "The genes responsible for O-antigen synthesis of Vibrio cholerae
O139 are closely related to those of Vibrio cholerae O22.";
RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AB012956; D1034567;
SQ SEQUENCE 337 AA; 40147 MW; 176BA6EB CRC32;

Query Match 78.9%; Score 56; DB 2; Length 337;
Best Local Similarity 87.5%; Pred. No. 8.58e-01;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 147 OKNSAPY 154
||:||||
QY 1 OKNSAPY 8

RESULT 3
ID 034232 PRELIMINARY; PRT; 337 AA.
AC 034232;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ORE40X1 PROTEIN.
OS VIBRIO CHOLERAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
RN [1]
RP SEQUENCE FROM N.A.
PP STRAIN-A1-1837;
NA MEDLINE; 97252505.
RT "Novel Vibrio cholerae O139 genes involved in lipopolysaccharide
biosynthesis.";
RL J. BACTERIOL. 179:2740-2747(1997).
DR EMBL; Y07786; E274690;
SQ SEQUENCE 337 AA; 40132 MW; 2D4A7939 CRC32;

Query Match 78.9%; Score 56; DB 2; Length 337;
Best Local Similarity 87.5%; Pred. No. 8.58e-01;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 147 OKNSAPY 154
||:||||
QY 1 OKNSAPY 8

RESULT 4
ID 020227 PRELIMINARY; PRT; 879 AA.
AC 020227;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE F40F8.5 PROTEIN.

GN F40F8.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
PP MACDOUGALL R.;
NA SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
PP MEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAWFORD M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAKINS T., HILLER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISNER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL NATURE 368:32-38(1994).
DR EMBL; Z69302; E1351710;
SQ SEQUENCE 879 AA; 99694 MW; 1DA3D603 CRC32;

Query Match 77.5%; Score 55; DB 5; Length 879;
Best Local Similarity 66.7%; Pred. No. 1.38e+00;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 461 QAYEAPY 469
||:||||
QY 1 OKNSAPY 9

RESULT 5
ID 059462 PRELIMINARY; PRT; 1179 AA.
AC 059462;

DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE 1179AA LONG HYPOTHETICAL CHROMOSOME ASSEMBLY PROTEIN.
GN PH1798.
OS PYROCOCUS HORIKOSHII.
OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
PP STRAIN-OT3;
NA MEDLINE; 98344137.
RA KAWARABAYASHI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEXINE M., BABA S., KOSUGI H., HOSOGAWA A., NGAI Y.,
RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMURA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
RA KIRUCHI H.;
RT "Complete Sequence and Gene Organization of the Genome of a
Hyper-thermophilic Archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA RES. 5:55-76(1998).
DR EMBL; AP000007; D1031860;
SQ SEQUENCE 1179 AA; 135656 MW; 38A49B18 CRC32;

Query Match 76.1%; Score 54; DB 1; Length 1179;
Best Local Similarity 55.6%; Pred. No. 2.20e+00;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1086 OKKRAPY 1094
||:||||
QY 1 OKNSAPY 9

RESULT 6
ID 028714 PRELIMINARY; PRT; 1156 AA.

AC 028714;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-ANG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE CHROMOSOME SEGREGATION PROTEIN (SMC1).
 GN AF1558.
 OS ARCHAEOGLOBUS FULGIDUS.
 OC ARCHAEEA: EURYARCHAEOTA: ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
 OC ARCHAEOGLOBUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE: 98049343.
 RA KLEIN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
 RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
 RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
 RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
 RA PETERSON S., REICH C.I., MCNEIL L.R., BADGER J.B., GLODER A., ZHOU L.,
 RA OVERBERG R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
 RA COTTON M.D., SPRIGGS T., ARTACH P., RAINE B.P., STRES S.M.,
 RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
 RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOJSE C.R.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the hyperthermophilic,
 RT sulphate-reducing archaeon Archaeoglobus fulgidus.";
 RL NATURE 390:364-370(1997).
 DR EMBL: AF000995; G2649004; -.
 DR TIGR: AF1558; -.
 KW HYPOTHEICAL PROTEIN.
 SQ SEQUENCE 1156 AA; 134244 MW; 1B5C7DDA CRC32;

Query Match 74.6%; Score 53; DB 1; Length 1156;
 Best Local Similarity 55.6%; Pred. NO. 3.50e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Db 1082 QMXPAPY 1090
 Oy 1 OKYNSAPY 9

RESULT 7
 ID 052187; PRELIMINARY; PRT; 436 AA.
 AC 052187;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE 1GG-BINDING PROTEIN SBI.
 GN SBI.
 OS STAPHYLOCOCCUS AUREUS.
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC STAPHYLOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-8325-4;
 RX MEDLINE: 98240235.
 RA ZHANG L., JACOBSON K., VASI J., LINDBERG M., FRYKBERG L.;
 RT "A second 1GG-binding protein in Staphylococcus aureus.";
 RL MICROBIOLOGI 144:985-991(1998).
 DR EMBL: AF027155; G2827912; -.
 SQ SEQUENCE 436 AA; 50070 MW; 47COE238 CRC32;

Query Match 73.2%; Score 52; DB 2; Length 436;
 Best Local Similarity 55.6%; Pred. NO. 5.52e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 333 EKYDTAKY 341
 Oy 1 OKYNSAPY 9
 RESULT 8
 ID Q41707; PRELIMINARY; PRT; 489 AA.

AC Q41707; Q43689;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE EXTENSIN CLASS I PROTEIN PRECURSOR (EXTENSIN-LIKE PROTEIN).
 GN EXT26G.
 OS VIGNA UNGUICULATA (COMPEA).
 OC EUKARYOTA: VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ARSENIJEVIC-MARKSIMOVIC I., BROUGHTON W.J., KRAUSE A.;
 RL MOL. PLANT MICROBE INTERACT. 10:95-101(1997).
 DR EMBL: X91836; G1015937; -.
 DR EMBL: X86030; G791150; -.
 DR MENDEL; 16557; VIGUN:2930;mm16557.
 DR MENDEL; 16560; VIGUN:2930;mm16560.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 489 AA; 53896 MW; 5B67DECT CRC32;

Query Match 73.2%; Score 52; DB 10; Length 489;
 Best Local Similarity 71.4%; Pred. NO. 5.52e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 47 YNAPY 53
 Oy 3 YNSAPY 9

RESULT 9
 ID Q47786; PRELIMINARY; PRT; 509 AA.
 AC Q47786;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE GELATINASE.
 GN GEL.
 OS ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS).
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; ENTEROCOCCACEAE;
 OC ENTEROCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IF03889;
 RA KIRIMURA K., EBIHARA T., KAMIGAKI K., USAMI S.;
 RT "Development of host-vector system for Enterococcus faecalis and
 RT Escherichia coli, and expression of neopulvinase gene from Bacillus
 RT stearothermophilus in E. faecalis.";
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: D85393; D1013484; -.
 DR PFAM: PF00099; zn-Protease; 1.
 SQ SEQUENCE 509 AA; 55389 MW; 1E5FE7A5 CRC32;

Query Match 73.2%; Score 52; DB 2; Length 509;
 Best Local Similarity 50.0%; Pred. NO. 5.52e+00;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Db 405 RYKGTPTY 412
 Oy 2 KYNAPY 9

RESULT 10
 ID P73340; PRELIMINARY; PRT; 1200 AA.
 AC P73340;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE CHROMOSOME SEGREGATION PROTEIN SMC1.
 OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
 OC BACTERIA: CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RA TABATA S.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RA MEDLINE: 97061201.
 RX KANEKO T., SATO S., KOTANI H., TANAKA A., ASANIZU E., NAKAMURA Y.,
 MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAKOTO S., KIMURA T.,
 HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARAO K., OKUMURA S.,
 SHIMO S., TAKEUCHI C., WADA T., MATSUMBE A., YAMADA M., YASUDA M.,
 TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. PCC6803. II. Sequence determination of the entire
 RT genome and assignment of potential protein-coding regions.";
 RL DNA RES. 3:109-136(1996).
 DR EMBL: D90905; D1018104;
 SO SEQUENCE 1200 AA; 136135 MW; 6A49E967 CRC32;
 Query Match 73.2%; Score 52; DB 2; Length 1200;
 Best Local Similarity 44.4%; Pred. No. 5.52e+00;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 1128 ORFSPSPY 1136
 Oy 1 OKNSAPY 9

RESULT 11
 ID 017664 PRELIMINARY; PRT; 215 AA.
 AC 017664;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE C41G6.12 PROTEIN.
 GN C41G6.12.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC CUMMINGS P.;
 RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAUREILLE P.,
 LIGHNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 THIERRY-WIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL NATURE 368:32-38(1994).
 DR EMBL: Z81047; E1344616;
 SO SEQUENCE 215 AA; 24549 MW; 8ABD249E CRC32;
 Query Match 70.4%; Score 50; DB 5; Length 215;
 Best Local Similarity 62.5%; Pred. No. 1.36e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 89 KENTIPY 96
 Oy 2 KYNAPY 9

RESULT 12

ID 091905 PRELIMINARY; PRT; 367 AA.
 AC 091905;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE FORK HEAD PROTEIN.
 GN XFD2.
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 OC MESOBATRACHIA; PIPOIDEA; PIPIIDAE; XENOPODINAE; XENOPUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94257528.
 RA LEF J., CLEMENT J.H., OSCHWALD R., KOESTER M., KNOECHEL M.;
 RT "Spatial and temporal transcription patterns of the forkhead related
 RT xfd-2/xfd-2' genes in Xenopus laevis embryos.";
 RL MECH. DEV. 45:117-126(1994).
 DR EMBL: X74316; G511162;
 DR PROSITE: PS00657; FORK_HEAD_1; 1.
 DR PROSITE: PS00658; FORK_HEAD_2; 1.
 DR PFM: PF00250; Fork_head; 1.
 SO SEQUENCE 367 AA; 40971 MW; 00A22C07 CRC32;
 Query Match 70.4%; Score 50; DB 13; Length 367;
 Best Local Similarity 71.4%; Pred. No. 1.36e+01;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 337 YNSPY 343
 Oy 3 YNSAPY 9

RESULT 13
 ID 009085 PRELIMINARY; PRT; 368 AA.
 AC 009085;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE EXTENSIN CLASS II PRECURSOR
 DE (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) (HNGP) (HY2.13)
 DE (FRAGMENT).
 OS PHASEOLUS VULGARIS (FRENCH BEAN).
 OC EUKARYOTA; VIRIDIPHYTES; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC FABACEAE; PAPILIONOIDEAE; PHASEOLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LEAF AND STEM;
 RX MEDLINE: 88142825.
 RA CORBIN D.R., SAUER N., LAMB C.J.;
 RT "Differential regulation of a hydroxyproline-rich glycoprotein gene
 RT family in wounded and infected plants.";
 RL MOL. CELL. BIOL. 7:4337-4344(1987).
 CC -1- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY IN THE
 CC MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF THE MAIN
 CC ROOT. INVOLVED IN PLANT DEFENSE AGAINST INFECTION.
 CC -1- PFM: EXTENSIN CONTAIN A CHARACTERISTIC REPEAT OF THE
 CC PENTAPEPTIDE SER-PRO(4)
 CC THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
 CC -1- INDUCTION: BY WOUNDING AND PATHOGEN INFECTION.
 DR EMBL: M18095; G169349;
 DR MENDEL: 16550; PHAVU:2930; m16550.
 KW REPEAT: CELL WALL; GLYCOPROTEIN; STRUCTURAL PROTEIN; HYDROXYLATION;
 KW MULTIGENE FAMILY.
 FT NON-TER 1
 FT DOMAIN 110 355
 FT REPEAT 110 118 17 x 16 AA APPROXIMATE TANDEM REPEATS OF
 FT REPEAT 119 125 Y-Y-X-K-S-P-P-P-S-P-S-P-P-P.
 FT REPEAT 126 140 1 (INCOMPLETE).
 FT REPEAT 141 153 2 (INCOMPLETE).
 FT REPEAT 158 173 3 (INCOMPLETE).
 FT REPEAT 173 5. 4 (INCOMPLETE).

FT REPEAT 174 189 6.
 FT REPEAT 190 205 7.
 FT REPEAT 206 221 8.
 FT REPEAT 222 237 9.
 FT REPEAT 238 252 10.
 FT REPEAT 253 259 11 (INCOMPLETE).
 FT REPEAT 260 275 12.
 FT REPEAT 276 291 13.
 FT REPEAT 292 307 14.
 FT REPEAT 308 323 15.
 FT REPEAT 324 339 16.
 FT REPEAT 340 355 17.
 SQ SEQUENCE 368 AA; 40714 MW; ED457D1B CRC32;

Query Match 70.48; Score 50; DB 13; Length 368;
 Best Local Similarity 71.48; Pred. No. 1.36e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 121 YNSPPY 127
 1:1:111
 3 YNSAPY 9

RESULT 14
 ID 091904 PRELIMINARY; PRT; 370 AA.
 AC 091904;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE FORK HEAD PROTEIN.
 GN XFD2.
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA.
 OC MESOBRANCHIA; PIPOIDA; PIPIIDAE; XENOPODINAE; XENOPUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94257528.
 RA LEE J., CLEMENT J.H., OSCHWALD R., KOESTER M., KNOCHEL W.;
 RT "Spatial and temporal transcription patterns of the forkhead related
 MECH. DEV. 45:117-126(1994).
 DR EMBL: X74315; G511160; -.
 DR TRANSFAC: T02294; -.
 DR PFAM: PF00250; Fork head; 1.
 SQ SEQUENCE 370 AA; 41388 MW; 0076CBA6 CRC32;

Query Match 70.48; Score 50; DB 13; Length 370;
 Best Local Similarity 71.48; Pred. No. 1.36e+01;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 335 YNSPPY 341
 1:1:111
 3 YNSAPY 9

RESULT 15
 ID 008932 PRELIMINARY; PRT; 381 AA.
 AC 008932;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE CHROMOSOME XVI READING FRAME ORF YPL193W.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCAROMYCETALES;
 OC SACCAROMYCETACEAE; SACCAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RIEGER M., MUELLER-AUER S., SCHAEFER M.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: 273549; E246919; -;
 SQ SEQUENCE 381 AA; 43997 MW; E0438908 CRC32;

Query Match 70.48; Score 50; DB 3; Length 381;
 Best Local Similarity 44.48; Pred. No. 1.36e+01;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 51 HMTNSPY 59
 1:1:111
 1 QYNSAPY 9

Search completed: Thu Sep 2 11:47:55 1999
 Job time : 26 secs.

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Query Match 73.2%; Score 52; DB 1; Length 438;
 Best Local Similarity 66.7%; Pred. No. 3.65e+00;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 246 QIYDAPY 254
 1 OKNSAPY 9

RESULT 2
 ID CDAS THEET STANDARD; PRT; 574 AA.
 AC P29964;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 DE CYCLOMALTODEXTRINASE (EC 3.2.1.54) (CDASE) (CYCLOMALTODEXTRIN
 DE HYDROLASE, DECYCLING)
 OS THERMOANEROBACTER ETHANOLICUS (CLOSTRIDIUM THERMOHYDROSULFURICUM).
 CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
 CC THERMOANEROBACTER GROUP; THERMOANEROBACTER.
 [1]
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
 RC STRAIN-39E;
 RX MEDLINE; 92355516.
 RA PODKOYROV S.M., ZEIKUS J.G.;
 RT "Structure of the gene encoding cyclomaltoextrinase from Clostridium
 RT thermohydrosulfuricum 39E and characterization of the enzyme purified
 RT from Escherichia coli.";
 RT J. BACTERIOL. 174:5400-5405(1992).
 RL [2]
 RN ACTIVE SITES.
 RP MEDLINE; 93146171.
 RA PODKOYROV S.M., BURDETTE D., ZEIKUS J.G.;
 RT "Analysis of the catalytic center of cyclomaltoextrinase from
 RT Thermohydrosulfuricum 39E.";
 RL FEBS LETT. 317:259-262(1993).
 CC -1- FUNCTION: HYDROLYZES CYCLODEXTRINS. CAN ALSO ACT ON LINEAR
 CC MALTODEXTRINS, WITH THE EXCEPTION OF MALTOSE.
 CC -1- CATALYTIC ACTIVITY: CYCLOMALTODEXTRIN + H(2)O = LINEAR
 CC MALTODEXTRIN.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES. ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY. CDASE MOST CLOSELY RESEMBLES
 CC NEOPOLYLAMINASE FROM B. STEROTHERMOPHILUS AND ALPHA-AMYLASE-
 CC POLYLAMINASE FROM C. THERMOHYDROSULFURICUM.
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 CC
 CC EMBL; M88602; G144751; -.
 DR PIR; A42950; A42950.
 KW HYDROLASE; GLYCOSIDASE.
 KM ACT_SITE 325 325
 FT ACT_SITE 354 354
 FT ACT_SITE 421 421
 FT ACT_SITE 421 421
 FT MOTAGN 325 325 D->N: LOSS OF ACTIVITY.
 FT MOTAGN 354 354 E->Q: LOSS OF ACTIVITY.
 FT MOTAGN 421 421 D->N: LOSS OF ACTIVITY.
 FT CONFLICT 4 4 E->G (IN AA SEQUENCE).
 SO SEQUENCE 574 AA; 68026 MM; 9DC2C2B4 CRC32;
 Query Match 73.2%; Score 52; DB 1; Length 574;
 Best Local Similarity 44.4%; Pred. No. 3.65e+00;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 DB 201 HKYDTTOY 209
 :11:::11

QY 1 OKNSAPY 9
 3
 ID CG24_YEAST STANDARD; PRT; 460 AA.
 AC P24871;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE G2/MITOTIC-SPECIFIC CYCLIN 4.
 GN CLB4 OR YLR210W OR L8167.3.
 OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACHAROMYCETALES;
 CC SACHAROMYCETACEAE; SACHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE; 93051323.
 RA RICHARDSON H., LEW D.J., HENZE M., SUGIMOTO K., REED S.I.;
 RT "Cyclin-B homologs in Saccharomyces cerevisiae function in S phase
 RT and in G2.";
 RL GENES DEV. 6:2021-2034(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92385891.
 RA FITCH I., DAHMANN C., SUPANA U., AMON A., NASMYTH K., GOETSCH L.,
 RA BYERS B., FUTCHER B.;
 RT "Characterization of four B-type cyclin genes of the budding yeast
 RT Saccharomyces cerevisiae.";
 RL MOL. BIOL. CELL 3:805-818(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
 RA FAYELLO A., FULTON L., GATTUNG S., GREGO T., KIRSTEN J., KUCABA T.,
 RA HALSWORTH K., HARKINS J., HILLER L., JIR M., JOHNSON D.,
 RA JOHNSTON L., LANGSTON Y., LATREILLE P., NARDS E., MENZES S.,
 RA MILLER N., NEAM M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
 RA TAICH S., TREVASKIS E., VAUDIN M., VIGNATI D., WILCOX L., WILSON R.,
 RA WOLDMAN P., WATERSTON R.;
 RL SUBMITTED (SEP-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE OF 233-422 FROM N.A.
 RX MEDLINE; 91191554.
 RA SPRANA U., ROBERSCH H., PRICE C., SCHUSTER T., FITCH I., FUTCHER A.B.,
 RA NASMYTH K.;
 RT "The role of Cdc28 and cyclins during mitosis in the budding yeast S.
 RT cerevisiae.";
 RL CELL 65:145-161(1991).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 PROTEIN KINASE TO
 CC FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE
 CC ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONGEST TO OTHER
 CC CYCLINS B.
 CC
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 CC EMBL; X69426; G5527; -.
 DR EMBL; M80303; G171914; -.
 DR EMBL; U14913; G544500; -.
 DR PIR; S14168; S14168.
 DR PIR; B46228; B46228.
 DR PIR; B60048; B60048.
 DR PIR; S48561; S48561.
 DR SGD; L0000352; CLB4.
 DR PROSITE; PS00292; CYCLINS; 1.

DR PFAM: PF00134; CYCLIN: 1.
 DR HSSP: P30274; 1VIN.
 RM CYCLIN: CELL CYCLE; CELL DIVISION; MITOSIS; MULTIGENE FAMILY.
 FT CONFLICT 255 255 Q -> R (IN REF. 4).
 FT CONFLICT 318 318 D -> S (IN REF. 4).
 FT CONFLICT 328 328 I -> T (IN REF. 4).
 SQ SEQUENCE 460 AA; 53852 MW; 8582564A CRC32;
 Query Match 71.8%; Score 51; DB 1; Length 460;
 Best Local Similarity 62.5%; Pred. No. 5.71e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 DB 221 KYRNPY 228
 QY 2 KYNSAPY 9
 RESULT 4
 ID TYR2_MOUSE STANDARD; PRT; 517 AA.
 P29812:
 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE DOPACHROME TAUTOMERASE PRECURSOR (EC 5.3.3.12) (DT) (DCT) (DOPACHROME
 DELTA-ISOMERASE) (TYROSINASE-RELATED PROTEIN 2) (TRP-2) (SLATY
 LOCUS PROTEIN).
 GN DCT OR TRP2 OR TYRP-2.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92164640.
 RA JACKSON I.J., CHAMBERS D.M., TSUKAMOTO K., COPELAND N.G.,
 RA GILBERT D.J., JENKINS N.A., HEARING V.J.;
 RT "A second tyrosinase-related protein, TRP-2, maps to and is mutated
 RT at the mouse slaty locus.";
 RL EMBO J. 11:527-536(1992).
 RN [2]
 RP SEQUENCE OF 1-98 FROM N.A., AND VARIANTS SLATY-2J AND SLATY-LT.
 RC STRAIN-129/SV;
 RX MEDLINE: 96079089.
 RA BUDD P.S., JACKSON I.J.;
 RT "Structure of the mouse tyrosinase-related protein-2/dopachrome
 RT tautomerase (tyrp2/dct) gene and sequence of two novel slaty
 RT alleles.";
 RL GENOMICS 29:35-43(1995).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE: 92164639.
 RA TSUKAMOTO K., JACKSON I.J., URABE K., MONTAGUE P.M., HEARING V.J.;
 RT "A second tyrosinase-related protein, TRP-2, is a melanogenic enzyme
 RT termed DOPACHROME TAUTOMERASE.";
 RL EMBO J. 11:519-526(1992).
 RN [4]
 RP ZINC-BINDING.
 RX MEDLINE: 95071460.
 RA SOLANO F., MARTINEZ-LIARTE J.H., JIMENEZ-CERVANTES C.,
 RA GARCIA-BORRON J.C., LOZANO J.A.;
 RT "Dopachrome tautomerase is a zinc-containing enzyme.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 204:1243-1250(1994).
 RN [5]
 RP ZINC-BINDING.
 RX MEDLINE: 96152526.
 RA SOLANO F., JIMENEZ-CERVANTES C., MARTINEZ-LIARTE J.H.,
 RA GARCIA-BORRON J.C., JARA J.R., LOZANO J.A.;
 RT "Molecular mechanism for catalysis by a new zinc-enzyme, dopachrome
 RT tautomerase.";
 RL BIOCHEM. J. 313:447-453(1996).
 CC -1- CATALYTIC ACTIVITY: L-DOPACHROME -> 5,6-DIHYDROXYINDOLE-2-
 CC CARBOXYLATE.
 CC -1- COFACTOR: CONTAINS TWO ZINC ATOMS.
 CC -1- PATHWAY: MELANIN BIOSYNTHESIS.

CC -1- SUBUNIT: TYROSINASE, TRP-1 AND TRP-2 MAY FORM A MULTIZENZYME
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, MELANOSOMAL.
 CC -1- TISSUE SPECIFICITY: MELANOCYTES AND RETINAL PIGMENTED EPITHELIUM.
 CC -1- DISEASE: THE SLATY MUTATION IN TYRP2 LEADS TO A DECREASE OF DT
 CC ACTIVITY AND A CONSEQUENT CHANGE IN THE PIGMENTATION OF THE MICE
 CC TO A DARK GRAY/BROWN EMBELANIN. THE SLATY-2J MUTATION HAS A
 CC SIMILAR PHENOTYPE. THE SLATY-LT (LIGHT) MUTATION HAS A MORE SEVERE
 CC EFFECT AND IS SEMIDOMINANT. ITS PHENOTYPE MAY BE A RESULT OF THE
 CC FAILURE OF THE ENZYME TO BE CORRECTLY TARGETED TO ITS NORMAL
 CC LOCATION ON THE INNER FACE OF THE MELANOSOMAL MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
 CC -----
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 CC DR EMBL: X63349; G55066; -;
 CC DR EMBL: X85126; G854335; -;
 CC DR PIR: S19243; S19243.
 CC DR MGD: MGI:102563; DCT.
 CC DR PROSITE: PS00497; TYROSINASE_1; 1.
 CC DR PROSITE: PS00498; TYROSINASE_2; 1.
 CC DR PFAM: PF00264; Tyrosinase; 1.
 CC DR ISOMERASE; ZINC; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE;
 CC KW MELANIN BIOSYNTHESIS; DISEASE MUTATION.
 CC FT SIGNAL 1 23
 CC FT CHAIN 24 517
 CC FT DOMAIN 24 472
 CC FT TRANSMEM 473 491
 CC FT DOMAIN 492 517
 CC FT METAL 189 189
 CC FT METAL 211 211
 CC FT METAL 220 220
 CC FT METAL 369 369
 CC FT METAL 373 373
 CC FT METAL 396 396
 CC FT CARBOHYD 92 92
 CC FT CARBOHYD 170 170
 CC FT CARBOHYD 178 178
 CC FT CARBOHYD 237 237
 CC FT CARBOHYD 300 300
 CC FT CARBOHYD 342 342
 CC FT CARBOHYD 377 377
 CC FT CARBOHYD 377 377
 CC FT VARIANT 194 194
 CC FT VARIANT 434 434
 CC FT VARIANT 486 486
 CC SQ SEQUENCE 517 AA; 58569 MW; 8EBA0B41 CRC32;
 Query Match 71.8%; Score 51; DB 1; Length 517;
 Best Local Similarity 44.4%; Pred. No. 5.71e+00;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 DB 332 ORFDSPPF 340
 QY 1 ORXNSAPY 9
 RESULT 5
 ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (MPC 11).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 81053741.
 RA ZAKUT R., COHEN J., GIVOL D.;
 RT "Cloning and sequencing of the cDNA corresponding to the variable
 region of immunoglobulin heavy chain MPC11.";
 RL NUCLEIC ACIDS RES. 8:3591-3601(1980).
 RN (2)
 RP REVISIONS.
 RA ZAKUT R., COHEN J., GIVOL D.;
 RL NUCLEIC ACIDS RES. 8:4839-4840(1980).
 CC -1- THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED FROM A
 CC MYELOMA THAT SECRETES IGG2B.
 DR PIR: A02027; GYMS11.
 KW IMMUNOGLOBULIN V REGION.
 FT NON_TER 121 121
 SO SEQUENCE 121 AA; 13135 MW; 2A8FC8CC CRC32;

Query Match 70.4%; Score 50; DB 1; Length 121;
 Best Local Similarity 71.4%; Pred. No. 8.88e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 102 YNSPPY 108
 ||:|:
 QY 3 YNSAPY 9

RESULT 6 STANDARD: PRT; 323 AA.
 AC P29655;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE ANTIHEMORRAGIC FACTOR HSF (METALLOPROTEINASE INHIBITOR).
 OS TRIMERESURUS FLAVOVIDRIS (HABU).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPTODONTIA; SQUAMATA;
 OC SCLEROGLOSSA; SERPENTES; COLUBROIDA; VIPERIDAE; CROTALINAE;
 OC TRIMERESURUS.
 RN (1)
 RP SEQUENCE.
 RC TISSUE-SERUM;
 RX MEDLINE; 93123185.
 RA YAMAKAWA Y., OMORI-SATO T.;
 RT Primary structure of the antihemorrhagic factor in serum of the
 Japanese Habu: a snake venom metalloproteinase inhibitor with a
 double-headed cystatin domain.";
 RL J. BIOCHEM. 112:583-589(1992).
 CC -1- FUNCTION: INHIBITS NOT ONLY HEMORRHAGIC BUT ALSO PROTEOLYTIC
 CC ACTIVITIES OF THE VENOM OF THE SNAKE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- PTM: CYS-44 MAY EXIST IN A MIXED DISULFIDE FORM WITH A THIOL
 CC COMPOUND SUCH AS GLUTATHIONE.
 CC -1- SIMILARITY: BELONGS TO THE FETUIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE REPEATS.
 DR PIR: JX0240; JX0240.
 DR PROSITE: PS01254; FETUIN_1; 1.
 DR DR PROSITE: PS01255; FETUIN_2; 1.
 DR PFAM: PF00031; cystatin; 2.
 KW METALLOPROTEINASE INHIBITOR; GLYCOPROTEIN; REPEAT.
 FT REPEAT 4 122
 FT SITE 4 247
 FT SITE 4 6
 FT DISULFID 9 122
 FT DISULFID 66 77
 FT DISULFID 91 110
 FT DISULFID 124 127
 FT DISULFID 186 198
 FT DISULFID 211 234
 FT CARBOHYD 123 123
 FT CARBOHYD 185 185
 FT CARBOHYD 263 263
 SO SEQUENCE 323 AA; 37075 MW; 46A4096C CRC32;

Query Match 70.4%; Score 50; DB 1; Length 323;
 Best Local Similarity 44.4%; Pred. No. 8.88e+00;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 168 HKPEAPY 176
 ||:|:
 QY 1 OKYNSAPY 9

RESULT 7 STANDARD: PRT; 251 AA.
 AC YG64; HAEIN
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL PROTEIN H11664.
 GN H11664.
 OS HAEMOPHILUS INFLUENZAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURILLACEAE;
 OC HAEMOPHILUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BOLT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIO L.-I., GLODER A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLON E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SADER D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GENEH C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RL SCIENCE 269:496-512(1995).
 CC -1- SIMILARITY: BELONGS TO THE UPF0006 FAMILY.

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CC EMBL: U32839; G1574514; ALT_INIT.
 DR TIGR: H11664;
 DR PROSITE: PS01137; UPF0006_1; 1.
 DR PROSITE: PS01090; UPF0006_2; FALSE_NEG.
 DR PROSITE: PS01091; UPF0006_3; 1.
 DR PFAM: PF01026; UPF0006; 1.
 KW HYPOTHETICAL PROTEIN.
 SO SEQUENCE 251 AA; 29334 MW; B07778CC CRC32;

Query Match 69.0%; Score 49; DB 1; Length 251;
 Best Local Similarity 55.6%; Pred. No. 1.37e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 164 QKFSPPY 172
 ||:|:
 QY 1 OKYNSAPY 9

RESULT 8 STANDARD: PRT; 430 AA.
 AC P05049;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 15-UTL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE SERINE PROTEASE SNAKE PRECURSOR (BC 3.4.21.-).
 GN SNK.


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DR FLIBASE; E89H0003430; SNK.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PFAM; PF00089; trypsin; 1.
DR HSP; P00757; 1SGF.
KM DEVELOPMENTAL PROTEIN; SERINE PROTEASE; HYDROLASE; SIGNAL.
FT SIGNAL. 1 ? POTENTIAL.
FT CHAIN ? 430 SERINE PROTEASE SNAKE.
FT DOMAIN 184 430 CATALYTIC.
FT ACT_SITE 233 233 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 280 280 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 376 376 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 177 300 BY SIMILARITY.
FT DISULFID 218 234 BY SIMILARITY.
FT DISULFID 342 362 BY SIMILARITY.
FT DISULFID 372 403 BY SIMILARITY.
SQ SEQUENCE 430 AA; 47782 MW; 182E3F87 CRC32;

Query Match 69.0%; Score 49; DB 1; Length 430;
Best Local Similarity 62.5%; Pred. No. 1.37e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

271 KYRSSAYY 278
11111111
2 KYNSAPYY 9

RESULT 9
ID XP25 CAEEL STANDARD; PRT; 497 AA.
AC 009436;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 56.2 KD PROTEIN AH6.5 IN CHROMOSOME II.
GN AH6.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERMAE; CAENORHABDITIS.
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN-BRISTOL NZ;
RA JASAL B.;
RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RN REVISIONS.
RC STRAIN-BRISTOL NZ;
RA JONES S.J.M.;
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

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CC      -1- SUBCELLULAR LOCATION: NUCLEAR(POTENTIAL).
CC      -1- SIMILARITY: CONTAINS 2 CX(8)CX(3)CX(3)H-TYPE ZINC FINGERS.
CC      -----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      CC      or send an email to license@isb-sib.ch).
CC      -----
CC      DR      EMBL: Z48009; E1297480; -
CC      DR      WORMPEP; AH6.5; CE15550.
CC      DR      PFMAM; PF00128; alpha-amylase; 1.
CC      RW      HYPOTHETICAL PROTEIN; ZINC-FINGER; METAL-BINDING; DNA-BINDING;
CC      RW      NUCLEAR PROTEIN; REPEAT.
CC      FT      2N.FING 309 329      CX(9)CX(5)CX(3)H (POTENTIAL).
CC      FT      3N.FING 353 374      CX(10)CX(5)CX(3)H (POTENTIAL).
CC      SO      SEQUENCE 497 AA; 56151 MW; A5F46D99 CRC32;
CC
CC      Query Match      69.0%; Score 49; DB 1; Length 497;
CC      Best Local Similarity 44.4%; Pred. NO. 1.376+01;
CC      Matches      4; Conservative      3; Mismatches      2; Indels      0; Gaps      0;
CC
CC      Db      98 Q0FGTPEPT 106
CC      QY      1 QKNSAPY 9
CC      1 : : : : :
CC
CC      RESULT      10      STANDARD;      PRT;      588 AA.
CC      ID      NEPU_BACST
CC      AC      P38940;
CC      DT      01-FEB-1995 (REL. 31, CREATED)
CC      DT      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
CC      DT      15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
CC      DE      NEOPUTULANASE (EC 3.2.1.135).
CC      GN      NPLT.
CC      OS      BACILLUS STEAROTHERMOPHILUS.
CC      OC      BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
CC      OC      BACILLUS.
CC      RN      [1]
CC      RP      SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
CC      RC      STAIN-TRN540;
CC      RX      MEDLINE; 90132572.
CC      RA      KURIKI T., IMANAKA T.;
CC      RT      *Nucleotide sequence of the neopullulanase gene from Bacillus
CC      RT      stearothermophilus.*;
CC      RL      J. GEN. MICROBIOL. 135:1521-1528(1989).
CC      CC      -1- FUNCTION: HYDROLYSES PULULAN EFFICIENTLY BUT ONLY A SMALL AMOUNT
CC      CC      OF STARCH. ENDHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN
CC      CC      PULULAN TO FORM PANOSE. CLEAVES ALSO (1-6)-ALPHA-GLUCOSIDIC
CC      CC      LINKAGES TO FORM MALTOSE.
CC      CC      -1- CATALYTIC ACTIVITY: HYDROLYSIS OF PULULAN TO PANOSE (6-ALPHA-D-
CC      CC      GLUCOSYLALDOSE).
CC      CC      -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC      CC      KNOWN AS THE ALPHA-AMYLASE FAMILY. RESEMBLES T.ETHANOLICUS CDASE.
CC      CC      -----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
CC      DR      EMBL: M28138; G541633; -
CC      DR      PIR; A37008; A37008.
CC      DR      PFMAM; PF00128; alpha-amylase; 1.
CC      RW      HYDROLASE; GLYCOSIDASE.
CC      FT      ACT_SITE 328 328      BY SIMILARITY.
CC      FT      ACT_SITE 357 357      BY SIMILARITY.
CC      FT      ACT_SITE 424 424      BY SIMILARITY.
CC      SO      SEQUENCE 588 AA; 69145 MW; 85DB267B CRC32;

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RA OGLE K.F., LEE K.K., KRAUSE D.C.;
 RT Nucleotide sequence analysis reveals novel features of the phase-
 RT variable cytochrome oxidase accessory protein Hmw3 of Mycoplasma
 RT pneumoniae.";
 RL INFECT. IMMUN. 60:1633-1641(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE: 97105885.
 RA HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
 RA HERRMANN R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL NUCLEIC ACIDS RES. 24:4420-4449(1996).
 CC -1- FUNCTION: COMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH
 CC STABILIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS
 CC CYTOSKELETON-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING Hmw
 CC PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTOCHROME PROTEINS
 CC IN THE MYCOPLASMA MEMBRANE AT THE ATTACHMENT ORGANELLAE.
 CC ESSENTIAL FOR SUCCESSFUL SURFACE PARASITISM.
 CC -1- SUBCELLULAR LOCATION: LOCALIZES SPECIFICALLY TO THE ATTACHMENT
 CC MEMBRANE.
 CC -----
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 CC -----
 CC EMBL: L38997; G639785; -
 CC EMBL: AEO00037; G1674070; -
 CC CYTADHERENCE; STRUCTURAL PROTEIN; REPEAT.
 CC KMW
 CC DOMAIN 98 251 9 X 3 AA REPEAT OF Y-D-Q.
 CC FT REPEAT 98 100 1-1.
 CC FT REPEAT 106 108 1-2.
 CC FT REPEAT 197 199 1-3.
 CC FT REPEAT 206 208 1-4.
 CC FT REPEAT 211 213 1-5.
 CC FT REPEAT 221 223 1-6.
 CC FT REPEAT 226 228 1-7.
 CC FT REPEAT 235 237 1-8.
 CC FT REPEAT 249 251 1-9.
 CC FT DOMAIN 160 456 8 X 3 AA REPEAT OF P-V-V.
 CC FT REPEAT 160 162 2-1.
 CC FT REPEAT 288 290 2-2.
 CC FT REPEAT 316 318 2-3.
 CC FT REPEAT 322 324 2-4.
 CC FT REPEAT 336 338 2-5.
 CC FT REPEAT 402 404 2-6.
 CC FT REPEAT 413 415 2-7.
 CC FT REPEAT 454 456 2-8.
 CC FT DOMAIN 310 339 2 X 10 AA REPEAT OF V-E-P-T-P-T-D-V-E.
 CC FT REPEAT 310 319 3-1.
 CC FT REPEAT 330 339 3-2.
 CC FT DOMAIN 312 428 7 X 5 AA REPEAT OF P-X-P-X-P.
 CC FT REPEAT 312 316 4-1.
 CC FT REPEAT 332 336 4-2.
 CC FT REPEAT 354 358 4-3.
 CC FT REPEAT 385 389 4-4.
 CC FT REPEAT 396 400 4-5.
 CC FT REPEAT 424 428 4-6.
 CC FT REPEAT 424 428 4-7.
 CC FT CONFLICT 288 288 P -> R (IN AA SEQUENCE).
 CC SQ SEQUENCE 672 AA; 73721 MW; 3FB64A30 CRC32;
 CC -----
 CC Query Match 69.0%; Score 49; DB 1; Length 672;
 CC Best Local Similarity 44.4%; Pred. No. 1.37e+01;
 CC Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 CC DB 213 ONYDPAVY 221
 CC |:|:|:|

QY 1 OKYNSAPY 9
 RESULT 14
 ID ANPMJMANSE STANDARD; PRT; 990 AA.
 AC 011001;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MEMBRANE ALANYL AMINOPEPTIDASE PRECURSOR (EC 3.4.11.-)
 DE (AMINOPEPTIDASE N-LIKE PROTEIN) (CRYIA(C) RECEPTOR) (FRAGMENT).
 OS MANDUCA SEXTA (TOBACCO HAWKMOOTH) (TOBACCO HORNWORM).
 OS EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PTERYGOTA; LEPIDOPTERA; SPHINGIDAE; SPHINGINAE; MANDUCA.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=MIDGUT;
 RX MEDLINE: 9535365.
 RA KNIGHT P.J.K., KNOWLES B.H., ELLAR D.J.;
 RT "Molecular cloning of an insect aminopeptidase N that serves as a
 RT receptor for Bacillus thuringiensis CryIA(c) toxin.";
 RL J. BIOL. CHEM. 270:17765-17770(1995).
 CC -1- FUNCTION: BINDS TO THE B. THURINGIENSIS TOXIN, CRYIA(C).
 CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
 CC PROTEOLYTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1 (ZINC METALLOPROTEASES);
 CC ALSO KNOWN AS THE PEPTIN SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: X89081; G953186; -
 CC DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC DR PFAM; PF000099; zn-protease; 1.
 CC KM HYDROLASE; METALLOPROTEASE; AMINOPEPTIDASE; ZINC; GLYCOPROTEIN;
 CC FT GPI-ANCHOR; SIGNAL.
 CC FT NON_TER 1 1
 CC FT SIGNAL. <1 15
 CC FT PROPEP 16 35
 CC FT CHAIN 36 968
 CC FT PROPEP 969 990
 CC FT METAL 357 357
 CC FT ACT_SITE 358 358
 CC FT METAL 361 361
 CC FT METAL 380 380
 CC FT ACT_SITE 460 460
 CC FT LIPID 968 968
 CC FT CARBOHYD 295 295
 CC FT CARBOHYD 609 609
 CC FT CARBOHYD 623 623
 CC FT CARBOHYD 752 752
 CC SQ SEQUENCE 990 AA; 111293 MW; 0EA90F91 CRC32;
 CC -----
 CC Query Match 69.0%; Score 49; DB 1; Length 990;
 CC Best Local Similarity 44.4%; Pred. No. 1.37e+01;
 CC Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC DB 294 ENTALPY 302
 CC QY 1 OKYNSAPY 9
 RESULT 15
 ID HK31_HUMAN STANDARD; PRT; 234 AA.
 AC G99801; O15465;
 DT 15-JUL-1998 (REL. 36, CREATED)

DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE HOMEBOX PROTEIN NKX-3.1.
 GN NKX3A OR NKX3.1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; MEIZOON; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PROSTATE:
 RX MEDLINE: 97369933.
 RA HE W.-W., SCIANVOLINO P.J., WING J., AUGUSTUS M., HUDSON P.,
 RA WEISSNER P.S., CURTIS R.T., SHELL B.K., BOSTWICK D.G., TINDALL D.J.,
 RA GELMANN E.P., ABATE-SHEN C., CARTER K.C.;
 RT "A novel human prostate-specific, androgen-regulated homeobox gene
 RT (NKX3.1) that maps to 8p21, a region frequently deleted in prostate
 RT cancer";
 RL GENOMICS 43:69-77(1997).
 CC -1- FUNCTION: MAY PARTICIPATE IN EARLY UROGENITAL DEVELOPMENT AND MAY
 CC PLAY A ROLE IN THE ANDROGEN-DRIVEN MAINTENANCE OF THE
 CC DIFFERENTIATED STATE IN ADULT PROSTATIC TISSUE.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE PROSTATE. PRESENT AT A LOWER
 CC LEVEL IN THE TESTIS, AND ABSENT FROM ALL OTHER TISSUES TESTED.
 CC -1- INDUCTION: STIMULATED BY ANDROGEN.
 CC -1- SIMILARITY: BELONGS TO THE NK-3 FAMILY OF HOMEBOX PROTEINS.
 CC -----
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 CC -----
 DR EMBL: U80669; G1733378; -
 DR EMBL: U91540; G2351792; -
 DR MIM: 602041; -
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 DR PFAM: PF00046; homeobox; 1.
 DR HSSP: P23441; 1FTT
 KW HOMEBOX; DNA-BINDING; NUCLEAR PROTEIN.
 FT DNA_BIND 124 183 HOMEBOX.
 FT CONFLICT 85 85 D -> E (IN G2351792).
 FT CONFLICT 196 196 F -> S (IN G2351792).
 FT CONFLICT 224 224 H -> Y (IN G2351792).
 FT CONFLICT 234 234 W -> G (IN G2351792).
 FT SEQUENCE 234 AA; 26370 MW; A0D7D353 CRC32;
 Query Match 67.6%; Score 48; DB 1; Length 234;
 Best local Similarity 85.7%; Pred. No. 2,11e+01;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 214 YNSAPY 220
 Y 111111
 QY 3 YNSAPY 9

Search completed: Thu Sep 2 11:47:11 1999
 Job time : 8 secs.

 W O R L D
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MPSEARCH protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:46:30 1999; Maspar time 3.04 Seconds
 Modular output not generated. 118.709 Million cell updates/sec

Title: >US-08-599-226-17
 Description: (1-9) from US08599226.pep
 Perfect Score: 71
 Sequence: 1 OKXNSAPY 9

Scoring table: PAM 150
 Gap 15
 Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r60
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 23.489; Variance 34.859; scale 0.674

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	54	76.1	1179	2	F71190	probable chromosome a
2	53	74.6	1156	2	E69444	chromosome segregatio
3	52	73.2	438	2	C64148	hypothetical protein
4	52	73.2	509	2	A43580	coccolysin (EC 3.4.24
5	52	73.2	574	1	A42950	cyclomaltoextrinase
6	52	73.2	1200	2	S7524	chromosome segregatio
7	51	71.8	332	2	B71605	probable integral mem
8	51	71.8	460	2	B60048	cyclin B4 - yeast (Sa
9	51	71.8	517	2	S19243	tyrosinase-related pr
10	50	70.4	121	1	GVMS1	ig heavy chain V reg1
11	50	70.4	333	2	JX0240	antihemorrhagic facto
12	50	70.4	367	2	S49009	fork head protein 2 -
13	50	70.4	368	2	C29356	hydroxyproline-rich g
14	50	70.4	370	2	S49008	fork head protein - A
15	50	70.4	381	2	S65212	hypothetical protein
16	49	69.0	110	2	G70305	ribosomal protein S06
17	49	69.0	259	2	E64174	hypothetical protein
18	49	69.0	384	2	B70675	hypothetical protein
19	49	69.0	430	2	A24702	serine proteinase sna
20	49	69.0	588	1	A37008	neophilinase (EC 3.
21	49	69.0	600	2	E53290	oligopeptide transpor
22	49	69.0	672	2	S73715	cytadherence accessor
23	49	69.0	853	2	H70470	hypothetical protein

24	49	69.0	1156	2	B70356	chromosome assembly p
25	49	69.0	1301	2	S18118	alpha-amyase - Alicy
26	48	67.6	73	2	A24862	hypothetical protein
27	48	67.6	119	2	B34353	anti-peptide Fab' B13
28	48	67.6	266	2	S77446	nitrate transport pro
29	48	67.6	267	2	S30277	ISC10 protein - yeast
30	48	67.6	500	2	S64220	hypothetical protein
31	48	67.6	519	1	YRHUR2	dopachrome Delta-1som
32	48	67.6	520	2	S01031	alpha-amyase (EC 3.2
33	48	67.6	590	2	A44068	cell pattern formatio
34	48	67.6	741	2	A47063	cellulase S5 (EC 3.2.
35	48	67.6	757	2	S71206	DNA repair protein ho
36	48	67.6	760	2	A45174	eye cell development
37	48	67.6	1054	2	D70425	conserved hypothetical
38	48	67.6	1075	2	S54067	probable membrane pro
39	48	67.6	1202	2	S05362	probable DNA-directed
40	48	67.6	1231	2	S70553	chromosome-associated
41	48	67.6	4930	2	E69679	polyketide synthase p
42	47	66.2	107	2	B71010	hypothetical protein
43	47	66.2	189	2	S61210	probable GTP binding
44	47	66.2	513	2	H69735	endo-1,4-beta-xylanas
45	47	66.2	681	2	I78558	hypothetical Brachyur

ALIGNMENTS

RESULT 1
 ENTRY F71190 #type complete
 TITLE probable chromosome assembly protein - Pyrococcus horikoshii
 ORGANISM #formal_name Pyrococcus horikoshii
 DATE 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998

ACCESSIONS
 REFERENCE #authors
 F71190 Kawarabayashi, Y.; Sawada, M.; Horikawa, R.; Halkawa, Y.;
 A71000 Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
 Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
 Nakazawa, H.; Takamiya, M.; Ofuku, Y.; Funahashi, T.;
 Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kuchida, N.; Oguchi,
 A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
 Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.

#journal
 #title DNA Res. (1998) 5:55-76
 Complete sequence and gene organization of the genome of a
 hyper-thermophilic archaeobacterium, Pyrococcus horikoshii
 OT3

#cross-references NCBI:98344137
 #accession F71190
 #status preliminary; nucleic acid sequence not shown;
 translation not shown

#molecule_type DNA
 ##residues 1-1179 ##label RAW
 ##cross-references GB:AP000007; NID:93236134; PID:di031860; PID:93258234
 ##experimental_source strain OT3
 ##note this accession replaces an interim accession for a
 sequence replaced by Genbank

GENETICS
 #gene PH1798
 SUMMARY #length 1179 #molecular_weight 135656 #checksum 6390

Query Match
 Best local similarity 76.1%; Score 54; DB 2; Length 1179;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 1086 OKXNSAPY 1094
 11::11:1
 1 OKXNSAPY 9
 RESULT 2
 ENTRY E69444 #type complete
 TITLE chromosome segregation protein (smc1) homolog - Archaeoglobus
 fulgidus
 ORGANISM #formal_name Archaeoglobus fulgidus

DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
04-Sep-1998
ACCESSIONS E69444
REFERENCE A69250
#authors
Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kierlavage, A.R.; Graham, D.E.; Kyriakides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
#journal Nature (1997) 390:364-370
#title The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.
#cross-references MVID:98049343
#accession E69444
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1-1156 #label KLE
#cross-references GB:AE000995; GB:AE000782; NID:g2689318; PID:g2649004; TIGR:AF1558
CLASSIFICATION #superfamily conserved hypothetical P115 protein
SUMMARY #length 1156 #molecular_weight 134244 #checksum 9949

Query Match 74.6%; Score 53; DB 2; Length 1156;
Best Local Similarity 55.6%; Pred. No. 8.18e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 1082 QMKRPAPY 1090
1-1156
1 QKNSAPY 9

RESULT 3
ENTRY C64148 #type complete
TITLE hypothetical protein HI0333 - Haemophilus influenzae (strain Rd KW20)
ORGANISM #formal_name Haemophilus influenzae
DATE 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998
ACCESSIONS C64148
REFERENCE A64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirnesh, E.F.; Kierlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal Science (1995) 269:496-512
#title Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
#cross-references MVID:95350630
#accession C64148
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-438 #label TIGR
#cross-references GB:U32718; GB:L42023; NID:g1573399; PID:g1573302; TIGR:HI0333
CLASSIFICATION #best homolog was a hypothetical protein from Vibrio
SUMMARY #length 438 #molecular_weight 49869 #checksum 1905

Query Match 73.2%; Score 52; DB 2; Length 438;
Best Local Similarity 66.7%; Pred. No. 1.22e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DB 246 QITGDAPY 254
1-438
1 QKNSAPY 9

RESULT 4
ENTRY A43580 #type complete
TITLE coccolysin (EC 3.4.24.30) precursor - Enterococcus faecalis
ALTERNATE_NAMES gelatinase; metalloendopeptidase II; microbial metalloproteinase (EC 3.4.24.4)
ORGANISM #formal_name Enterococcus faecalis
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Sep-1997
ACCESSIONS A43580
REFERENCE A43580
#authors Su, Y.A.; Sulavik, M.C.; He, P.; Makinen, K.K.; Makinen, P.L.; Fiedler, S.; Wirth, R.; Clewell, D.B.
#journal Infect. Immun. (1991) 59:415-420
#title Nucleotide sequence of the gelatinase gene (gelE) from Enterococcus faecalis subsp. liquefaciens.
#cross-references MVID:91099994
#accession A43580
#molecule_type DNA
#residues 1-509 #label SUA
#cross-references GB:M37185; NID:g148310; PID:g148311
GENETICS
#gene gelE
#KEYWORDS hydrolase; metalloproteinase; zinc
FEATURE
1-29 #domain signal sequence #status predicted #label SIG
30-191 #domain propeptide #status predicted #label PRO
192-509 #product coccolysin #status experimental #label MAP
SUMMARY #length 509 #molecular_weight 55376 #checksum 5494

Query Match 73.2%; Score 52; DB 2; Length 509;
Best Local Similarity 50.0%; Pred. No. 1.22e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 405 RYKGPY 412
1-509
2 KNSAPY 9

RESULT 5
ENTRY A42950 #type complete
TITLE cyclomaltoodextrinase (EC 3.2.1.54) - Thermoanaerobacter thermoautotrophicus
ALTERNATE_NAMES cyclodextrin-degrading enzyme; cyclodextrinase
ORGANISM #formal_name Thermoanaerobacter thermoautotrophicus
DATE 17-Feb-1994 #sequence_revision 18-Aug-1995 #text_change 05-Sep-1997
ACCESSIONS A42950
REFERENCE A42950
#authors Podkovyrov, S.M.; Zelkus, J.G.
#journal J. Bacteriol. (1992) 174:5400-5405
#title Structure of the gene encoding cyclomaltoodextrinase from *Clostridium thermoautotrophicum* 39E and characterization of the enzyme purified from *Escherichia coli*.
#cross-references MVID:92355516
#accession A42950
#molecule_type DNA
#residues 1-574 #label POD
#cross-references GB:M88602; NID:g144750; PID:g144751
#experimental_source Clostridium thermoautotrophicum 39E
#note sequence extracted from NCBI backbone (NCBI:110537)
FUNCTION amino end of mature protein is Met-Ile-Lys-Gly-Ala
#description hydrolyzes cyclomaltoodextrin to linear maltodextrins; also hydrolyzed linear maltodextrin

CLASSIFICATION #superfamily neopullulanase: alpha-amylase core homology
KEYWORDS glycosidase; heat-stable protein; hydrolase; monomer
FEATURE
1-574 #product neopullulanase #status experimental #label MARY
292-424 #domain alpha-amylase core homology #label AMY
329,354,421 #active-site glu, glu, asp #status predicted
SUMMARY #length 574 #molecular-weight 68025 #checksum 3953

Query Match 73.2%; Score 52; DB 1; Length 574;
Best Local Similarity 44.4%; Pred. No. 1.22e+01;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 201 HKYDTDY 209
QY 1 QKNSAPY 9

RESULT 6
ENTRY S77524 #type complete
TITLE chromosome segregation protein smc1 - *Synechocystis* sp.
(strain PCC 6803)
protein s11120
ALTERNATE_NAMES #formal_name *Synechocystis* sp.
ORGANISM PCC 6803
#variety 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
DATE 04-Sep-1998
ACCESSIONS S77524
REFERENCE S74322
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; Hikosawa, M.; Sugiyama, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MIMD:97061201
#accession S77524
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-1200 #label KAN
#cross-references EMBL:D90905; GB:AB001339; NID:g1652360; PID:d1018104; PID:g1652449
#note the nucleotide sequence was submitted to the EMBL Data Library, June 1996

CLASSIFICATION #superfamily conserved hypothetical P115 protein
SUMMARY #length 1200 #molecular-weight 136135 #checksum 484

Query Match 73.2%; Score 52; DB 2; Length 1200;
Best Local Similarity 44.4%; Pred. No. 1.22e+01;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1128 ORYRSPFY 1136
QY 1 QKNSAPY 9

RESULT 7
ENTRY B71606 #type complete
TITLE probable integral membrane protein PRB0790C - malaria
ORGANISM Parasite (*Plasmodium falciparum*)
#formal_name *Plasmodium falciparum*
DATE 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change
ACCESSIONS B71606
REFERENCE A71600
#authors Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Shallow, S.; Mason, T.; Yu, K.; Fujii, C.; Pederson, J.; Shen, K.; Jing, J.; Aston, C.; Lai, Z.; Schwartz, D.C.; Pertea, M.; Salzberg, S.; Zhou,

L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Fraser, C.M.; Adams, M.D.; Venter, J.C.; Hoffman, S.L.
Science (1998) 282:1126-1132
#journal Chromosome 2 sequence of the human malaria parasite
#title *Plasmodium falciparum*.
#accession B71606
#status preliminary; nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-1332 #label GAR
#cross-references GB:AE001418; GB:AE001362; NID:g3845275; PID:g3845278; TIGR:PRB0790C
#experimental_source clone 3D7

GENETICS
#gene PRB0790C
SUMMARY #length 332 #molecular-weight 39208 #checksum 3654

Query Match 71.8%; Score 51; DB 2; Length 332;
Best Local Similarity 62.5%; Pred. No. 1.82e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 257 KYNSPY 264
QY 2 KYNSAPY 9

RESULT 8
ENTRY B60048 #type complete
TITLE cyclin B4 - yeast (*Saccharomyces cerevisiae*)
protein B6167.3; protein YLR210W
ALTERNATE_NAMES #formal_name *Saccharomyces cerevisiae*
ORGANISM 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
DATE 06-Feb-1998
ACCESSIONS B60048; B46228; S48561; S14168; S31292
REFERENCE A60048
#authors Fitch, I.; Dahmann, C.; Surana, U.; Amon, A.; Nasmyth, K.; Goetsch, L.; Byers, B.; Futcher, B.
#journal Mol. Biol. Cell (1992) 3:805-818
#title Characterization of four B-type cyclin genes of the budding yeast *Saccharomyces cerevisiae*.
#cross-references MIMD:92385891
#accession B60048
#molecule_type DNA
#residues 1-460 #label FIT
#cross-references GB:M60303; NID:g171913; PID:g171914
REFERENCE A46228
#authors Richardson, H.; Lew, D.J.; Henze, M.; Sugimoto, K.; Reed, S.I.
#journal Genes Dev. (1992) 6:2021-2034
#title Cyclin-B homologs in *Saccharomyces cerevisiae* function in S phase and in G2.
#cross-references MIMD:93051323
#accession B46228
#molecule_type DNA
#residues 1-460 #label RIC
#cross-references EMBL:X69426; NID:g55526; PID:g55527
#note sequence extracted from NCBI backbone (NCBIN:117854, NCBI:P:117855)

REFERENCE S48545
#authors Pauley, A.
#submission submitted to the EMBL Data Library, September 1994
#description The sequence of *S. cerevisiae* cosmid 8167.
#accession S48561
#molecule_type DNA
#residues 1-460 #label PAU
#cross-references EMBL:U14913; NID:g544497; PID:g544500; MIPS:YLR210W
REFERENCE S14165
#authors Surana, U.; Robitsh, H.; Price, C.; Schuster, T.; Fitch, I.; Futcher, A.B.; Nasmyth, K.
#journal Cell (1991) 65:145-161
#title The role of CDC28 and cyclins during mitosis in the budding yeast *S. cerevisiae*.
#cross-references MIMD:9191554

##accession S14168
##status not compared with conceptual translation
##molecule_type DNA
##residues 233-254,'R',256-317,'S',319-327,'T',329-422 ##label SUR
GENETICS
#gene SGD:CLB4
##cross-references SGD:S004200; MIPS:YLR210w
#map_position 12R
CLASSIFICATION #superfamily cyclin
KEYWORDS cell cycle control
SUMMARY #length 460 #molecular-weight 53852 #checksum 6937

Query Match 71.8%; Score 51; DB 2; Length 460;
Best Local Similarity 62.5%; Pred. No. 1.82e+01;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 221 KYRNPY 228
||:||||
2 KYNSAPY 9

RESULT 9
ENTRY S19243 #type complete
TITLE tyrosinase-related protein TRP-2 - mouse
ALTERNATE_NAMES DOPACHROME tautomerase
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Sep-1997
S19243; S55476

ACCESSIONS
REFERENCE S19243
#authors Jackson, I.J.; Chambers, D.M.; Tsukamoto, K.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Hearing, V.
#journal EMBO J. (1992) 11:527-535
#title A second tyrosinase-related protein, TRP-2, maps to and is mutated at the mouse slaty locus.
#cross-references MIM:92164640
#accession S19243
##status preliminary
##molecule_type mRNA
##residues 1-517 ##label JAC
##cross-references EMBL:X63349; NID:955065; PID:955066

REFERENCE S55476
#authors Budd, P.S.
#submission submitted to the EMBL Data Library, March 1995
#accession S55476
##status preliminary
##molecule_type DNA
##residues 1-98 ##label BUD
##cross-references EMBL:X85126; NID:9854334; PID:9854335
CLASSIFICATION #superfamily monophenol monooxygenase
KEYWORDS transmembrane protein
SUMMARY #length 517 #molecular-weight 58569 #checksum 6717

Query Match 71.8%; Score 51; DB 2; Length 517;
Best Local Similarity 44.4%; Pred. No. 1.82e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 332 QKDSPPF 340
||:||||
1 QKNSAPY 9

RESULT 10
ENTRY GWS11 #type complete
TITLE Ig heavy chain V region (MPC 11) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Oct-1980 #sequence_revision 29-Jun-1981 #text_change 23-Aug-1996
A93708; A93711; A02027
A93708
#authors Zakut, R.; Cohen, J.; Givol, D.
#journal Nucleic Acids Res. (1980) 8:3591-3601
#title Cloning and sequence of the cDNA corresponding to the

variable region of immunoglobulin heavy chain MPC11.
##cross-references MIM:81053741
#accession A93708
##molecule_type mRNA
##residues 1-81,'D',83-103,'GD',106-121 ##label ZAK
#note this sequence was translated from an mRNA isolated from a myeloma that secretes IgG2b; the sequence of the C region has also been determined

REFERENCE A93711
#authors Zakut, R.; Cohen, J.; Givol, D.
#journal Nucleic Acids Res. (1980) 8:4839-4840
#accession A93711
#contents erratum
##residues 1-121 ##label ZA2
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 121 #molecular-weight 13135 #checksum 6524

Query Match 70.4%; Score 50; DB 1; Length 121;
Best Local Similarity 71.4%; Pred. No. 2.70e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 102 YNSSPY 108
||:||||
3 YNSAPY 9

RESULT 11
ENTRY JX0240 #type complete
TITLE antihemorrhagic factor HSF - habu
ORGANISM #formal_name Trimeresurus flavoviridis #common_name habu
DATE 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 12-Feb-1999
JX0240
ACCESSIONS JX0240
REFERENCE JX0240
#authors Yamakawa, Y.; Omori-Satoh, T.
#journal J. Biochem. (1992) 112:583-589
#title Primary structure of the antihemorrhagic factor in serum of the Japanese habu: A snake venom metalloproteinase inhibitor with a double-headed cystatin domain.
#accession JX0240
##molecule_type protein
##residues 1-323 ##label YAM
CLASSIFICATION #superfamily alpha-2-HS-glycoprotein; cystatin homology
KEYWORDS glycoprotein; metalloproteinase inhibitor
FEATURE 1-115
9-313,66-77,91-110, #domain cystatin homology #label CY1\
124-127,186-198, #disulfide_bonds #status predicted
211-234 #binding_site carbohydrate (Asn) (covalent) #status experimental
123,185,263
SUMMARY #length 323 #molecular-weight 37075 #checksum 2216

Query Match 70.4%; Score 50; DB 2; Length 323;
Best Local Similarity 44.4%; Pred. No. 2.70e+01;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 168 HYPEPAY 176
||:||||
1 QKNSAPY 9

RESULT 12
ENTRY S49009 #type complete
TITLE fork head protein 2 - African clawed frog
ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
S49009


```

REFERENCE          S49008
#authors           Lef, J.; Clement, J.H.; Oschwald, R.; Koester, M.; Knoechel,
#journal           Mech. Dev. (1994) 45:117-126
#title            Spatial and temporal transcription patterns of the forkhead
#cross-references  related XFD-2/XFD-2' genes in Xenopus laevis embryos.
#accession        S49009
#status           preliminary
#molecule-type  mRNA
#residues         1-367 ##label LEF
#cross-references EMBL:X74316; NID:9511161; PID:9511162
CLASSIFICATION    #superfamily unassigned fork head proteins; fork head
FEATURE           DNA-binding domain homology
SUMMARY           128-219 #domain fork head DNA-binding domain homology #label FHD
#length 367 #molecular-weight 40971 #checksum 6845

Query Match
Best Local Similarity 70.4%; Score 50; DB 2; Length 367;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 337 YNSAPY 343
||:||||
OY 3 YNSAPY 9

RESULT 13
ENTRY C29356 #type fragment
TITLE hydroxyproline-rich glycoprotein (clone HYP2.13) - kidney
ORGANISM #formal_name Phaseolus vulgaris #common_name kidney bean
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
09-Sep-1997
ACCESSION C29356
REFERENCE A29356
#authors Corbin, D.R.; Sauer, N.; Lamb, C.J.
#journal Mol. Cell. Biol. (1987) 7:4337-4344
#title Differential regulation of a hydroxyproline-rich glycoprotein
#cross-references NID:88142825
#accession C29356
#molecule-type mRNA
#residues 1-368 ##label COR
#cross-references EMBL:M18095; NID:9169348; PID:9169349
#experimental_source cv. Kleitsoobon Koekoek
KEYWORDS glycoprotein
SUMMARY #length 368 #checksum 4646

Query Match
Best Local Similarity 70.4%; Score 50; DB 2; Length 368;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 121 YNSAPY 127
||:||||
OY 3 YNSAPY 9

RESULT 14
ENTRY S49008 #type complete
TITLE fork head protein - African clawed frog
ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
17-Mar-1999
ACCESSION S49008; B56556
REFERENCE S49008
#authors Lef, J.; Clement, J.H.; Oschwald, R.; Koester, M.; Knoechel,
#journal Mech. Dev. (1994) 45:117-126
#title Spatial and temporal transcription patterns of the forkhead
#cross-references related XFD-2/XFD-2' genes in Xenopus laevis embryos.
#accession S49008

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#status           preliminary
#molecule-type  mRNA
#residues         1-370 ##label LEF
#cross-references EMBL:X74315; NID:9511159; PID:9511160
REFERENCE A56556
#authors Knoechel, S.; Lef, J.; Clement, J.; Klocke, B.; Hille, S.;
#journal Mech. Dev. (1992) 38:157-165
#title Activin A induced expression of a fork head related gene in
#cross-references posterior chordamesoderm (notochord) of Xenopus laevis
#accession B56556
#status           preliminary; not compared with conceptual translation
#molecule-type  mRNA
#residues         118-228 ##label KNO
#experimental_source gastrula
#note             sequence extracted from NCBI backbone (NCBP:118178)
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FEATURE           DNA-binding domain homology
SUMMARY           127-218 #domain fork head DNA-binding domain homology #label FHD
#length 370 #molecular-weight 41388 #checksum 6542

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Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 335 YNSAPY 341
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OY 3 YNSAPY 9

RESULT 15
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#formal_name Saccharomyces cerevisiae
#cross-references EMBL:Z73549; NID:91370402; PID:e246919; PID:91370403;
#accession S65212
#status           submitted to the Protein Sequence Database, May 1996
#authors Rieger, M.; Mueller-Auer, S.; Schaefer, M.
#journal Rieger, M.; Mueller-Auer, S.; Schaefer, M.
#title Submitted to the Protein Sequence Database, May 1996
#cross-references EMBL:Z73549; NID:91370402; PID:e246919; PID:91370403;
#experimental_source strain S288C (AB972)
GENETICS #map_position 16L
SUMMARY #length 381 #molecular-weight 43997 #checksum 8951

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Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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OY 1 QYNSAPY 9

Search completed: Thu Sep 2 11:46:45 1999
Job time : 15 secs.

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M E S S A G E (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 11:48:11 1999; Maspar time 1.38 Seconds
66.297 Million cell updates/sec
Modular output not generated.

Title: >US-08-599-226-17
Description: (1-9) from US08599226.Pep
Perfect Score: 71
Sequence: 1 QKYNAPY 9

Scoring table: PAM 150
Gap 15

Searched: 106580 segs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-1Issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:Backfiles1

Statistics: Mean 15.512; Variance 57.129; scale 0.272

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	51	71.8	124	2	US-08-476- Sequence 78, Applicati	7.59e+01
2	51	71.8	124	1	US-08-476- Sequence 78, Applicati	7.59e+01
3	50	70.4	454	3	PCT-US95-1 Sequence 33, Applicati	9.39e+01
4	50	70.4	454	2	US-08-420- Sequence 33, Applicati	9.39e+01
5	49	69.0	41	3	PCT-US93-1 Sequence 40, Applicati	1.16e+02
6	49	69.0	41	3	PCT-US95-0 Sequence 40, Applicati	1.16e+02
7	49	69.0	41	2	PCT-US95-0 Sequence 34, Applicati	1.16e+02
8	49	69.0	41	2	US-08-268- Sequence 34, Applicati	1.16e+02
9	49	69.0	41	1	US-07-998- Sequence 34, Applicati	1.16e+02
10	49	69.0	41	1	US-08-453- Sequence 34, Applicati	1.16e+02
11	49	69.0	41	1	US-08-453- Sequence 34, Applicati	1.16e+02
12	49	69.0	41	1	US-08-453- Sequence 40, Applicati	1.16e+02
13	49	69.0	41	2	US-08-268- Sequence 40, Applicati	1.16e+02
14	49	69.0	41	1	US-08-453- Sequence 34, Applicati	1.16e+02
15	49	69.0	41	1	PCT-US93-1 Sequence 34, Applicati	1.16e+02
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18	49	69.0	387	1	US-08-314- Sequence 40, Applicati	1.16e+02
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20	49	69.0	387	2	US-08-872- Sequence 6, Applicati	1.16e+02
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23	48	67.6	760	1	US-08-195- Sequence 2, Applicatio	1.43e+02

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29	47	66.2	107	3	PCT-US95-0 Sequence 82, Applicati	1.77e+02
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41	46	64.8	1408	1	US-08-612- Sequence 2, Applicati	2.18e+02
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45	44	62.0	596	3	PCT-US93-0 Sequence 8, Applicatio	3.29e+02

GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nadil
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.

CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-161
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO: 78:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 124 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC ORIGINAL SOURCE:
CC ORGANISM: Monkey
CC POSITION IN GENOME:
CC CHROMOSOME/SEGMENT: VH4 clone 4-16
SQ SEQUENCE 124 AA; 13147 MW; 95091 CN;

Query Match 71.8%; Score 51; DB 2; Length 124;
Best Local Similarity 71.4%; Pred. No. 7.59e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DE Sequence 78, Application US/08478039
CC Sequence 78, Application US/08478039
CC Patent No. 5681722
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A.
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Raab, Ronald W.
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
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CC FILING DATE: 23-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/735,064
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Teakin Esq., Robin L.
CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-160
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO: 78:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 124 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC ORIGINAL SOURCE:
CC ORGANISM: Monkey
CC POSITION IN GENOME:
CC CHROMOSOME/SEGMENT: VH4 clone 4-16
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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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CC GENERAL INFORMATION:
CC APPLICANT: The Trustees of Columbia University in the City of New York
CC APPLICANT: City
CC TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Cooper & Dunham LLP
CC STREET: 1185 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
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CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/10194
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: White, John P.
CC REGISTRATION NUMBER: 28,678
CC REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPW/MSC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 278-0400
CC TELEFAX: (212) 391-0525
CC INFORMATION FOR SEQ ID NO: 33:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 454 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein

SQ SEQUENCE 454 AA; 49525 MW; 1044348 CN;
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Patent No. 5801042
GENERAL INFORMATION:
CC APPLICANT: Chang, Yuan
CC APPLICANT: Moore, Patrick S.
CC TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
CC TITLE OF INVENTION: SEQUENCES AND USES THEREOF
CC NUMBER OF SEQUENCES: 47
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Cooper & Dunham LLP
CC STREET: 1185 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036
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CC FILING DATE:
CC CLASSIFICATION: 424
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CC NAME: White, John P.
CC REGISTRATION NUMBER: 28,678
CC REFERENCE/DOCKET NUMBER: 45185-B
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 278-0400
CC TELEFAX: (212) 391-0525
CC INFORMATION FOR SEQ ID NO: 33:
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CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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3 YNSAPY 9
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DE Sequence 40, Application PC/TUS9312588
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CC Sequence 40, Application PC/TUS9312588
CC GENERAL INFORMATION:
CC APPLICANT: Suzuki, Shintaro
CC TITLE OF INVENTION: Protocadherin Materials and Methods
CC NUMBER OF SEQUENCES: 107
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
CC ADDRESSEE: Borun
CC STREET: 6300 Sears Tower, 233 S. Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/12588
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/998,003
CC FILING DATE: 29 DEC 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31811
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6300
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 40:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 41 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 41 AA; 4393 MW; 8165 CN;
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Query Match 69.0%; Score 49; DB 3; Length 41;
Best Local Similarity 57.1%; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 5 YEATPY 11
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3 YNSAPY 9
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RESULT 6
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AC
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DE Sequence 40, Application PC/TUS9508071
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CC Sequence 40, Application PC/TUS9508071
CC GENERAL INFORMATION:
CC APPLICANT: Suzuki, Shintaro
CC TITLE OF INVENTION: Protocadherin Materials and Methods
CC NUMBER OF SEQUENCES: 115
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
CC ADDRESSEE: Borun
CC STREET: 6300 Sears Tower, 233 S. Wacker Drive

CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
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CC FILING DATE:
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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/12588
CC FILING DATE: 23 DEC 1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/998,003
CC FILING DATE: 29 DEC 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 32149
CC TELEPHONE: 312/474-6300
CC TELEFAX: 312/474-0448
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6300
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 40:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 41 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 41 AA: 4393 MW: 8165 CN;

Query Match 69.0%; Score 49; DB 3; Length 41;
Best Local Similarity 57.1%; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 5 YEATPY 11
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OY 3 YNSAPY 9

RESULT 7
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XX Sequence 34, Application PC/TUS9508071
CC GENERAL INFORMATION:
CC APPLICANT: Suzuki, Shintaro
CC TITLE OF INVENTION: Protocadherin Materials and Methods
CC NUMBER OF SEQUENCES: 115
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
CC ADDRESS: Borun
CC STREET: 6300 Sears Tower, 233 S. Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
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CC APPLICATION NUMBER: PCT/US95/08071
CC FILING DATE:
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CC APPLICATION NUMBER: PCT/US93/12588
CC FILING DATE: 23 DEC 1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/998,003
CC FILING DATE: 29 DEC 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 32149
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6300
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 41 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 41 AA: 4376 MW: 9295 CN;

Query Match 69.0%; Score 49; DB 3; Length 41;
Best Local Similarity 57.1%; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 5 YEATPY 11
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OY 3 YNSAPY 9

RESULT 8
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XX xxxxxx
AC
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DT
XX Sequence 34, Application US/08268161A
DE
XX Patent No. 5798224
CC GENERAL INFORMATION:
CC APPLICANT: Suzuki, Shintaro
CC TITLE OF INVENTION: Protocadherin Materials and Methods
CC NUMBER OF SEQUENCES: 115
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
CC ADDRESS: Borun
CC STREET: 233 South Wacker, 6300 Sears Tower
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/268,161A
CC FILING DATE: June 27, 1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Young J. Suh
CC REGISTRATION NUMBER: P-41,337
CC REFERENCE/DOCKET NUMBER: 27866/32149
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6300

CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 41 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
SQ SEQUENCE 41 AA; 4376 MW; 9295 CN;

Query Match 69.08; Score 49; DB 2; Length 41;
Best Local Similarity 57.18; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 5 YEATPY 11
ID 1:::111
QY 3 YNSAPY 9

US-07-998-003A-40 STANDARD; PRT; 41 AA.

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Sequence 40, Application US/07998003A

CC Sequence 40, Application US/07998003A
CC Patent No. 5643781

CC GENERAL INFORMATION:

CC APPLICANT: Suzuki, Shintaro

CC TITLE OF INVENTION: Protocadherin Materials and Methods

CC NUMBER OF SEQUENCES: 107

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

CC STREET: 20 South Clark Street

CC CITY: Chicago

CC STATE: Illinois

CC COUNTRY: USA

CC ZIP: 60603

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

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CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/998,003A

CC FILING DATE:

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: No. 5643781and, Greta E.

CC REGISTRATION NUMBER: 35,302

CC REFERENCE/DOCKET NUMBER: 30903

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 312/346-5750

CC TELEFAX: 312/984-9740

CC TELEX: 25-3856

CC INFORMATION FOR SEQ ID NO: 40:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 41 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: Protein

SQ SEQUENCE 41 AA; 4393 MW; 8165 CN;

Query Match 69.08; Score 49; DB 1; Length 41;
Best Local Similarity 57.18; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 5 YEATPY 11
ID 1:::111
QY 3 YNSAPY 9

US-07-998-003A-34 STANDARD; PRT; 41 AA.

xxxxxx

Sequence 34, Application US/07998003A

CC Sequence 34, Application US/07998003A
CC Patent No. 5643781

CC GENERAL INFORMATION:

CC APPLICANT: Suzuki, Shintaro

CC TITLE OF INVENTION: Protocadherin Materials and Methods

CC NUMBER OF SEQUENCES: 107

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

CC STREET: 20 South Clark Street

CC CITY: Chicago

CC STATE: Illinois

CC COUNTRY: USA

CC ZIP: 60603

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/998,003A

CC FILING DATE:

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: No. 5643781and, Greta E.

CC REGISTRATION NUMBER: 35,302

CC REFERENCE/DOCKET NUMBER: 30903

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 312/346-5750

CC TELEFAX: 312/984-9740

CC TELEX: 25-3856

CC INFORMATION FOR SEQ ID NO: 34:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 41 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: Protein

SQ SEQUENCE 41 AA; 4376 MW; 9295 CN;

Query Match 69.08; Score 49; DB 1; Length 41;
Best Local Similarity 57.18; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 5 YEATPY 11
ID 1:::111
QY 3 YNSAPY 9

US-08-453-274B-34 STANDARD; PRT; 41 AA.

xxxxxx

Sequence 34, Application US/08453274B

CC Sequence 34, Application US/08453274B

CC Patent No. 5663300
CC GENERAL INFORMATION:
CC APPLICANT: Suzuki, Shintaro
CC TITLE OF INVENTION: Protocadherin Materials and Methods
CC NUMBER OF SEQUENCES: 107
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/453,274B
CC FILING DATE: 30-MAY-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5663300and, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 32660
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6300
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 41 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 41 AA: 4376 MW: 9295 CN:

Query Match 69.0%; Score 49; DB 1; Length 41;
Best Local Similarity 57.1%; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 5 YEATPHY 11
|:::|
QY 3 YNSAPY 9

RESULT 12
ID US-08-453-695A-40 STANDARD: PRT; 41 AA.
xxxxxx

Sequence 40, Application US/08453695A
Patent No. 5708143
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
ADDRESSEE: Borun
STREET: 233 South Wacker, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/453,695A
CC FILING DATE:
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5708143and, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 32658
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6300
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 40:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 41 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 41 AA: 4393 MW: 8165 CN:

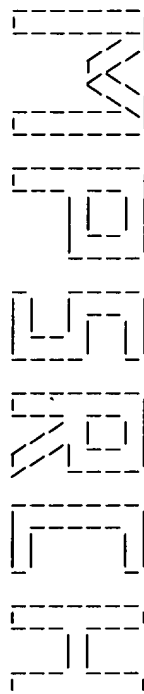
Query Match 69.0%; Score 49; DB 1; Length 41;
Best Local Similarity 57.1%; Pred. No. 1.16e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 5 YEATPHY 11
|:::|
QY 3 YNSAPY 9

RESULT 13
ID US-08-268-161A-40 STANDARD: PRT; 41 AA.
xxxxxx

Sequence 40, Application US/08268161A
Patent No. 5798224
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
ADDRESSEE: Borun
STREET: 233 South Wacker, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,161A
FILING DATE: June 27, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/32149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:

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(TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:45:52 1999; Maspar time 3.37 Seconds
56.763 Million cell updates/sec

Modular output not generated.

Title: >US-08-599-226-17
Description: (1-9) from US08599226.pep
Perfect Score: 71
Sequence: 1 OKNSAPY 9

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

a-geneseq5
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 16.503; Variance 58.002; scale 0.285

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	71	100.0	9	27	W27576	Anti-TNF-alpha antibo	1.51e+00
2	59	83.1	9	27	W27570	Anti-TNF-alpha antibo	2.41e+01
3	59	83.1	9	27	W27577	Anti-TNF-alpha antibo	2.41e+01
4	55	83.1	9	27	W27574	Anti-TNF-alpha antibo	2.41e+01
5	55	77.5	9	27	W27573	Anti-TNF-alpha antibo	5.91e+01
6	55	77.5	9	27	W27582	Anti-TNF-alpha antibo	5.91e+01
7	54	76.1	9	27	W27578	Anti-TNF-alpha antibo	7.38e+01
8	54	76.1	9	27	W27571	Anti-TNF-alpha antibo	7.38e+01
9	54	76.1	9	27	W27579	Anti-TNF-alpha antibo	7.38e+01
10	54	76.1	9	27	W27575	Anti-TNF-alpha antibo	7.38e+01
11	52	73.2	9	27	W27580	Anti-TNF-alpha antibo	1.15e+02
12	52	73.2	163	34	W42638	Protein sequence that	1.15e+02
13	51	71.8	9	27	W27584	Anti-TNF-alpha antibo	1.42e+02
14	51	71.8	9	27	W27562	Anti-TNF-alpha antibo	1.42e+02
15	51	71.8	9	27	W27585	Anti-TNF-alpha antibo	1.42e+02
16	51	71.8	9	27	W27583	Anti-TNF-alpha antibo	1.42e+02

17	51	71.8	107	27	W27568	Anti-TNF-alpha antibo	1.42e+02
18	51	71.8	124	31	W54005	Anti-CD4 antibody VH4	1.42e+02
19	50	70.4	454	17	R93616	Kaposi's sarcoma asso	1.77e+02
20	50	70.4	454	18	R97842	Kaposi's sarcoma asso	1.77e+02
21	49	69.0	9	27	W27572	Anti-TNF-alpha antibo	2.20e+02
22	49	69.0	40	11	R58878	Anti-551 cadherin part	2.20e+02
23	49	69.0	41	17	R87117	Protocadherin clone R	2.20e+02
24	49	69.0	41	17	R87120	Protocadherin clone R	2.20e+02
25	49	69.0	41	11	R58875	Ret-352 cadherin part	2.20e+02
26	49	69.0	387	10	R53702	Sequence of castor mi	2.20e+02
27	49	69.0	387	15	R79024	Wild type neopullulan	2.20e+02
28	49	69.0	588	2	R08255	Neo-pullulanase gene	2.20e+02
29	49	69.0	588	15	R79026	Y177F neopullulanase	2.20e+02
30	49	69.0	588	15	R79028	W275L neopullulanase	2.20e+02
31	49	69.0	588	15	R79027	M22V neopullulanase	2.20e+02
32	49	69.0	1301	6	R28304	Acid alpha-amylase en	2.20e+02
33	48	67.6	519	26	W30826	The novel tyrosinase	2.72e+02
34	48	67.6	760	26	W29490	Programmed cell death	2.72e+02
35	48	67.6	898	21	W14777	Granulosis virus infe	2.72e+02
36	47	66.2	107	19	W01261	VL region of HIV neut	3.37e+02
37	47	66.2	107	19	W01263	VL region of HIV neut	3.37e+02
38	47	66.2	107	10	R54305	Anti-HIV gp120 immuno	3.37e+02
39	47	66.2	107	10	W01266	VL region of HIV neut	3.37e+02
40	47	66.2	107	10	R54303	Anti-HIV gp120 immuno	3.37e+02
41	47	66.2	107	10	R54308	Anti-HIV gp120 immuno	3.37e+02
42	47	66.2	537	39	W87796	Tripeptidyl aminopept	3.37e+02
43	47	66.2	537	14	R80504	S. lividans protease	3.37e+02
44	46	64.8	826	5	R26042	P. yoelli SSP2 antige	4.16e+02
45	46	64.8	1408	32	W62871	Multiple drug resista	4.16e+02

ALIGNMENTS

RESULT 1
ID W27576 standard; peptide: 9 AA.

AC W27576;
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumor necrosis factor alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarily determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BAD) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Manukovich JA, McGuinness BT, Roberts AJ, Sakorats P,
PI Sallfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
PI WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 69; 102pp; English.
CC The present sequence is a novel anti-human tumor necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
Sequence 9 AA:

Query Match 100.0%; Score 71; DB 27; Length 9;
Best Local Similarity 100.0%; Pred. No. 1,51e+00;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gkyasnasy 9
| | | | | | | | |
QY 1 OKTNSAPY 9

RESULT 2
W2570 standard; peptide: 9 AA.

ID W2570: (first entry)
AC Anti-TNF-alpha antibody light chain CDR3.
DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-AL.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DV, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Sealfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
Claim 20; Page 67; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, malignancy, uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
Sequence 9 AA:

Query Match 83.1%; Score 59; DB 27; Length 9;
Best Local Similarity 100.0%; Pred. No. 2,41e+01;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 gkyasnasy 8
| | | | | | | | |
QY 1 OKTNSAPY 8

RESULT 3
W2577 standard; peptide: 9 AA.

ID W2577: (first entry)
AC Anti-TNF-alpha antibody light chain CDR3.
DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-AL.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DV, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Sealfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
Claim 20; Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, malignancy, uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
Sequence 9 AA:

Query Match 83.1%; Score 59; DB 27; Length 9;
Best Local Similarity 100.0%; Pred. No. 2,41e+01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 gkyasnasy 8
| | | | | | | | |
QY 1 OKTNSAPY 8

RESULT 4
W2574 standard; peptide: 9 AA.

ID W2574: (first entry)
AC Anti-TNF-alpha antibody light chain CDR3.
DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-AL.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DV, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Sealfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
Claim 20; Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, malignancy, uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
Sequence 9 AA:

Query Match 83.1%; Score 59; DB 27; Length 9;
Best Local Similarity 100.0%; Pred. No. 2,41e+01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AI.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SO

Query Match 83.1%; Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.41e+01;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gkyssapy 8
 |||
 1 QKTSAPY 8

RESULT 5
 ID W2573 standard; peptide: 9 AA.
 AC W2573;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AI.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SO

PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SO

Query Match 77.5%; Score 55; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 5.91e+01;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 gkyssapy 8
 |||
 1 QKTSAPY 8

RESULT 6
 ID W2582 standard; peptide: 9 AA.
 AC W2582;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HIVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AI.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 MPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC Sequence 9 AA:
 SO

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephritic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 77.5%; Score 55; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.91e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapy 8
||| |||
OY 1 OKYNSAPY 8

RESULT 7
ID W27578 standard; peptide: 9 AA.
AC W27578;
DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain: complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN MO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1986; US-031476.
PS 09-FEB-1996; US-599226.
PT (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephritic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 76.1%; Score 54; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 7.38e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapy 8
||| |||
OY 1 OKYNSAPY 8

RESULT 8
ID W27571 standard; peptide: 9 AA.
AC W27571;
DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain: complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN MO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1986; US-031476.
PS 09-FEB-1996; US-599226.
PT (BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 68; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephritic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 76.1%; Score 54; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 7.38e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapy 8
||| |||
OY 1 OKYNSAPY 8

RESULT 9

ID W27579 standard; peptide: 9 AA.

AC W27579;

DE 19-MAR-1998 (first entry)

KM Anti-TNF-alpha antibody light chain CDR3.

KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain: complementarity determining region 3; inhibition;

KM treatment; sepsis; disease; autoimmune disease; infectious disease;

KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KM cardiac disorder; inflammatory bone disorder; reperfusion injury;

KM bone resorption disease; coagulation disturbance; burn; ELAM-1;

KM keloid formation; scar tissue formation; pyrexia; HUVEC;

KM periodontal disease; obesity; radiation toxicity;

KM endothelial cell leukocyte adhesion molecule-1;

KM human umbilical vein endothelial cell.

OS Homo sapiens.

WO9729131-A1.

14-AUG-1997.

10-FEB-1997: U02219.

25-NOV-1996: US-031476.

09-FEB-1996: US-599226.

(BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,

PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 70; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

CC Sequence 9 AA;

SO

Query Match 76.1%; Score 54; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 7.38e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynraby 8
| | | | |
OY 1 QKXNSAPY 8

RESULT 10

ID W27575 standard; peptide: 9 AA.

AC W27575;

DE 19-MAR-1998 (first entry)

KM Anti-TNF-alpha antibody light chain CDR3.

KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain: complementarity determining region 3; inhibition;

KM treatment; sepsis; disease; autoimmune disease; infectious disease;

KM malignancy; pulmonary disorder; inflammatory bone disorder; reperfusion injury;

KM cardiac disorder; inflammatory bone disorder; reperfusion injury;

KM bone resorption disease; coagulation disturbance; burn; ELAM-1;

KM keloid formation; scar tissue formation; pyrexia; HUVEC;

KM periodontal disease; obesity; radiation toxicity;

KM endothelial cell leukocyte adhesion molecule-1;

KM human umbilical vein endothelial cell.

OS Homo sapiens.

WO9729131-A1.

14-AUG-1997.

10-FEB-1997: U02219.

25-NOV-1996: US-031476.

09-FEB-1996: US-599226.

(BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,

PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 69; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

CC Sequence 9 AA;

Query Match 76.1%; Score 54; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 7.38e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynraby 8
| | | | |
OY 1 QKXNSAPY 8

RESULT 11

ID W27580 standard; peptide: 9 AA.

AC W27580;

DE 19-MAR-1998 (first entry)

KM Anti-TNF-alpha antibody light chain CDR3.

KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain: complementarity determining region 3; inhibition;

KM treatment; sepsis; disease; autoimmune disease; infectious disease;

KM malignancy; pulmonary disorder; inflammatory bone disorder; reperfusion injury;

KM cardiac disorder; inflammatory bone disorder; reperfusion injury;

KM bone resorption disease; coagulation disturbance; burn; ELAM-1;

KM keloid formation; scar tissue formation; pyrexia; HUVEC;

KM periodontal disease; obesity; radiation toxicity;

KM endothelial cell leukocyte adhesion molecule-1;

KM human umbilical vein endothelial cell.

OS Homo sapiens.

WO9729131-A1.

14-AUG-1997.

10-FEB-1997: U02219.

25-NOV-1996: US-031476.

09-FEB-1996: US-599226.

(BADI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,

PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

DR WPI: 97-415302/38.

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 71; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 73.2%; Score 52; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.15e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsaay 8
 |||||:|
 QY 1 OKYNSAPY 8

RESULT 12
 ID W42638 standard: Protein; 162 AA.
 AC W42638;
 DT 22-OCT-1998 (first entry)
 DE Protein sequence that is specific for Neisseria meningitidis.
 KM N. gonorrhoeae; N. lactamica; chromosome 22491; region 1; region 2;
 KM region 3; pathogenicity; blood-brain barrier; diagnosis; infection;
 KM meningitis.
 OS Neisseria meningitidis.
 PN MO9802547-A2.
 PD 22-JAN-1998.
 PF 11-JUL-1997: F01295.
 PD 12-JUL-1996: FR-008768.
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
 (SMIR) SMITHKLINE BEECHAM.
 PA Nessif X, Tinsley C, Achman M, Merker P, Ruelle J,
 PI vinals C;
 DR WPI: 98-110594/10.
 CC Genes present in Neisseria meningitidis but not other Neisseria
 CC species - and related host cells, RNA, anti-sense sequences,
 CC polypeptide(s) and antibodies, useful for diagnosing Neisseria
 CC meningitidis infection and in protective vaccines
 PS Claim 8: Page 99: 150pp: French.
 CC The present sequence is isolated from Neisseria meningitidis.
 CC The specification describes DNA sequences that are found in
 CC N. meningitidis, but not in N. gonorrhoeae or N. lactamica,
 CC except for the genes involved in biosynthesis of the capsule
 CC polysaccharide, fliA or C, opc, porA, rotamase, sequence IC1106,
 CC IGA protease, pilin, pilC, proteins which bind transferrin and opacity
 CC proteins. The DNA sequences are found on chromosome 22491, mainly (or
 CC within 20 kb) between tufA and pili (region 1), pilQ and lambda-740
 CC (region 2) or argF and opaB (region 3). The DNA sequences are responsible
 CC for the differences in pathogenicity between N. meningitidis and
 CC N. gonorrhoeae, specifically they include the genes that allow
 CC N. meningitidis to cross the blood-brain barrier. DNA sequences common
 CC to N. meningitidis and N. gonorrhoeae, but absent from N. lactamica, are

CC responsible for colonisation and penetration of the mucosa. The DNA
 CC sequences can be used to produce probes and primers, and antibodies
 CC produced against the encoded proteins are used in standard
 CC hybridisation/immunoassay processes for diagnosis of N. meningitidis
 CC infection, particularly meningitis.
 CC Sequence 162 AA:

Query Match 73.2%; Score 52; DB 34; Length 162;
 Best Local Similarity 55.6%; Pred. No. 1.15e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 78 qkynsaay 86
 |||||:|
 QY 1 OKYNSAPY 9

RESULT 13
 ID W27584 standard: peptide; 9 AA.
 AC W27584;
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HUVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN MO9729131-AI.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Monkevich JA, McGulnass BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilson AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 72; 102pp: English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 71.8%; Score 51; DB 27; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.42e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynrpy 8
 |||||:|

OY 1 OKYNSAPY 8

RESULT 14
ID W27562 standard; peptide; 9 AA.
AC W27562;
DE 19-MAR-1998 (first entry)
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
Key Location/Qualifiers
Misc-difference 9 /label= Thr, Ala

PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuiness Br, Roberts AJ, Sakorafas P,
PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 9; Page 64; 102pp. English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 71.8%; Score 51; DB 27; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.42e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 grynrapy 8
1:11111
OY 1 OKYNSAPY 8

RESULT 15
ID W27585 standard; peptide; 9 AA.
AC W27585;
DE 19-MAR-1998 (first entry)
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Mankovich JA, McGuiness Br, Roberts AJ, Sakorafas P,
PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 72; 102pp. English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 71.8%; Score 51; DB 27; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.42e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 grynrapy 8
1:11111
OY 1 OKYNSAPY 8

Search completed: Thu Sep 2 11:46:12 1999
Job time : 20 secs.

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in - protein database search, using Smith-Waterman algorithm

MasPar time 4.28 Seconds

t generated.

1 QKYNAPYN 9

PAM 150

179066 seqs, 54579741 residues

Listing first 45 summaries

sptrembl9

13:sp_vertebrate 14:sp_virus

Mean 21.687; Variance 25.749; scale 0.842

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	57	89.1	337	2	034232	ORF40X1 PROTEIN.	5.45e-020
2	57	89.1	337	2	087136	ORF139-17 PROTEIN.	5.45e-020
3	50	78.1	560	5	044626	K1D12.1 PROTEIN.	2.22e+000
4	49	76.6	292	10	048821	PUTATIVE SERINE PROTEI	3.68e+000
5	49	76.6	496	2	087348	ILAK21 RESTRICTION EN	3.68e+000
6	48	75.0	336	5	P91524	COSMID T28A11.	6.07e+000
7	48	75.0	336	5	045161	C1787.1 PROTEIN.	6.07e+000
8	48	75.0	2896	5	061363	HEMOCYANIN G-TYPE SUBU	6.07e+000
9	47	73.4	16	14	079455	LIGHT-CHAIN COMPLEMEX	9.94e+000
10	47	73.4	16	14	079461	LIGHT-CHAIN COMPLEMEX	9.94e+000
11	47	73.4	278	2	047792	PLASMIN PAD1, OPEN REA	9.94e+000
12	47	73.4	450	2	050511	ZINC PROTEASE.	9.94e+000
13	47	73.4	644	4	012828	FUSE BINDING PROTEIN.	9.94e+000
14	46	71.9	305	5	018281	FK010.0 PROTEIN.	1.62e+010
15	46	71.9	320	2	068847	SITE-SPECIFIC RECOMBIN	1.62e+010
16	46	71.9	425	3	074477	HYPOTHEICAL 46.6 KD P	1.62e+010
17	46	71.9	521	2	044677	NEUTRAL PROTEASE.	1.62e+010
18	45	70.3	322	5	045024	AMPHIPHILIC OTX TRANSCR	2.61e+010
19	45	70.3	1129	5	002144	SIMILARITY TO HUMAN AT	2.61e+010
20	45	70.3	1175	5	002143	SIMILARITY TO HUMAN AT	2.61e+010

21	44	68.8	131.8	035865	NADH DEHYDROGENASE SUB	4.17e+01
22	44	68.8	292.14	065239	ORF. J155.	4.17e+01
23	44	68.8	292.2	056863	WBCE PROTEIN (ORF.5).	4.17e+01
24	44	68.8	301.14	065196	PROLIFERATING CELL NUC	4.17e+01
25	44	68.8	408.5	002441	GDP-DISSOCIATION INHIB	4.17e+01
26	44	68.8	533.6	028175	RETINAL PIGMENT EPITHE	4.17e+01
27	44	68.8	533.6	005661	RETINAL PIGMENT EPITHE	4.17e+01
28	44	68.8	725.10	004429	ARGININE DECARBOXYLASE	4.17e+01
29	44	68.8	808.5	024811	ABC FAMILY TRANSPORTER	4.17e+01
30	44	68.8	2270.4	014581	DIHYDROXYRIDINE-SENSIT	4.17e+01
31	44	68.8	2312.4	015878	VOLTAGE-OPERATED CALCI	4.17e+01
32	44	67.2	210.4	013179	PREGNANY-SPECIFIC GLY	6.63e+01
33	44	67.2	221.2	053073	HYPOTHETICAL 25.7 KD P	6.63e+01
34	43	67.2	301.6	086155	FORIN PROTEIN (FRAGMEN	6.63e+01
35	43	67.2	326.2	051946	OUTER MEMBRANE PROTEIN	6.63e+01
36	43	67.2	335.4	075237	PGSIIA-C.	6.63e+01
37	43	67.2	352.4	014503	PREGNANY-SPECIFIC PRO	6.63e+01
38	43	67.2	352.4	008266	PREGNANY-SPECIFIC BET	6.63e+01
39	43	67.2	417.4	075236	PBGL HUMAN.	6.63e+01
40	43	67.2	426.4	015231	PREGNANY-SPECIFIC BET	6.63e+01
41	43	67.2	428.4	008265	PREGNANY-SPECIFIC BET	6.63e+01
42	43	67.2	516.1	058456	HYPOTHETICAL PROTEIN M	6.63e+01
43	43	67.2	779.11	035269	POTENTIAL PHEROMONE REC	6.63e+01
44	43	67.2	890.5	020227	F4088.5 PROTEIN.	6.63e+01
45	43	67.2	1290.11	065295	LEUCOCYTE COMMON ANTIG	6.63e+01

ALIGNMENTS

RESULT	ID	034232	PRELIMINARY;	PRT;	337 AA.
AC	034232:				
DT	01-JAN-1998 (TREMBLREL. 05)	CREATED			
DT	01-JAN-1998 (TREMBLREL. 05)	LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL. 08)	LAST ANNOTATION UPDATE)			
DE	ORF40X1 PROTEIN.				
OS	VIBRIO CHOLERAE.				
CC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO				
PN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-A1-1837;				
RX	MEDLINE: 97252505.				
RA	STROEBER U. H., PARASIVAM G., DREDGE B. K., MANNING P. A.;				
RT	"Novel <i>Vibrio cholerae</i> O139 genes involved in lipopolysaccharide				
RT	biosynthesis".				
RL	J. BACTERIOL. 179:2740-2747(1997).				
DR	EMBL: Y07786; E274690.				
SO	SEQUENCE 337 AA; 40132 MW; 2D4A7939 CRC32;				

Query Match 89.18; Score 57; DB 2; Length 337;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db	147	OKYHSAPYK 155
Oy	1	OKYNSAPYN 9
RESULT	2	
ID	087136	PRELIMINARY; PRT; 337 AA.
AC	087136;	
DT	01-NOV-1998	(TREMBLREL. 08, CREATED)
DT	01-NOV-1998	(TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE	ORE139-17 PROTEIN.	
OS	VIBRIO CHOLERAE.	
OC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRATN-M045;	
RA	YAMASKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,	
RA	TAKEBA Y.;	
RT	"The genes responsible for O-antigen synthesis of <i>Vibrio cholerae</i>	

RT 0139 are closely related to those of *Vibrio cholerae* 022.;"
RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AB012956; D1034567; -
SQ SEQUENCE 337 AA; 40147 MW; 176B46EB CRC32;

Query Match 89.1%; Score 57; DB 2; Length 337;
Best Local Similarity 77.8%; Pred. No. 5,45e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 147 OKYNSAPYK 155
OY 1 OKYNSAPYK 9

RESULT 3 PRELIMINARY; PRT: 560 AA.
ID 044626.
AC 044626.
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
KL1D12.1.1 PROTEIN.

OS CAENORHABDITIS ELEGANS.
OC EURAROTIA; METAFOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERC C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMKNEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SOLTSON J.,
RA THERRIER-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMANN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA HEIKHAUS J., WOHLDMANN P., GILLAM B.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF039047; G2736445; -
DR PROSITE: PS00028; ZINC_FINGER_C2H2; 1.
KW ZINC-FINGER; METAL-BINDING; DNA-BINDING.
SQ SEQUENCE 560 AA; 61136 MW; 5906EB7D CRC32;

Query Match 78.1%; Score 50; DB 5; Length 560;
Best Local Similarity 75.0%; Pred. No. 2,22e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 81 OKYKAPY 88
OY 1 OKYNSAPYK 8

RESULT 4 PRELIMINARY; PRT: 292 AA.
ID 048821.
AC 048821.
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE PUTATIVE SERINE PROTEINASE.

GN TL31L6.3.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EURAROTIA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.

RN [1]
RP SEQUENCE FROM N.A.
RA DE LA BASTIDE M., HAMEED A., GNOJ L., JENSEN K., SHOHDY N.,
RA GOTTESMAN T., HABERMANN K., HUANG E.N., SCHUTZ K., KAPLAN N.,
RA LOHTE M., MARA M., DEBHIA N., PARNELL L.D., MARTIENSSEN R.,
RA MCCOMBIE W.R.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AC003952; G2708739; -
SQ SEQUENCE 292 AA; 33189 MW; F69680E1 CRC32;

Query Match 76.6%; Score 49; DB 10; Length 292;
Best Local Similarity 66.7%; Pred. No. 3,69e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 215 HYSAPYK 223
OY 1 OKYNSAPYK 9

RESULT 5 PRELIMINARY; PRT: 496 AA.
ID 087348.
AC 087348.
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LAKR21 RESTRICTION ENZYME.

GN LAKR21.
OS LACTOCOCCUS LACTIS (STREPTOCOCCUS LACTIS).
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
OC LACTOCOCCUS.

RN [1]
RP SEQUENCE FROM N.A.
RA TWOMEY D.P., MCKAY L.L., O'SULLIVAN D.J.;
RT "Molecular characterization of the *Lactococcus lactis* LAKR21
RT restriction-modification system and effect of an IS982 element
RT positioned between the restriction and modification genes.";
RL J. BACTERIOL. 180:0-0(1998).

DR EMBL: AF051563; G3702799; -
KW PLASMID.
SQ SEQUENCE 496 AA; 58081 MW; A04BA2A9 CRC32;

Query Match 76.6%; Score 49; DB 2; Length 496;
Best Local Similarity 55.6%; Pred. No. 3,69e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 33 EKYOSTPYK 41
OY 1 OKYNSAPYK 9

RESULT 6 PRELIMINARY; PRT: 336 AA.
ID P91524.
AC P91524.
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE COSMID T28A11.
GN T28A11.1.

OS CAENORHABDITIS ELEGANS.
OC EURAROTIA; METAFOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THERIERY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA ROHLFING T.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U80027; G1699135; -;
 SQ SEQUENCE 336 AA; 38484 MW; 04F43521 CRC32;

Query Match 75.0%; Score 48; DB 5; Length 336;
 Best Local Similarity 75.0%; Pred. No. 6.07e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 179 KYNITPYN 186
 ||| : |||
 QY 2 KYNAPYN 9

RESULT 7
 ID 045161 PRELIMINARY; PRT; 336 AA.
 AC 045161;
 DT 01-JUN-1998 (TREMBL:REL. 06, CREATED)
 DT 01-JUN-1998 (TREMBL:REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBL:REL. 08, LAST ANNOTATION UPDATE)
 DE C17B7.1 PROTEIN.
 GN C17B7.1.
 OS CAENORHABDITIS ELEGANS.
 CC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 CC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THERIERY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WILSON R.;
 RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF047655; G2911833; -;
 SQ SEQUENCE 336 AA; 38419 MW; E3D6B234 CRC32;

Query Match 75.0%; Score 48; DB 5; Length 336;
 Best Local Similarity 75.0%; Pred. No. 6.07e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 179 KYNITPYN 186
 ||| : |||
 QY 2 KYNAPYN 9

RESULT 8
 ID 061363 PRELIMINARY; PRT; 2896 AA.
 AC 061363;
 DT 01-AUG-1998 (TREMBL:REL. 07, CREATED)
 DT 01-AUG-1998 (TREMBL:REL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBL:REL. 08, LAST ANNOTATION UPDATE)
 DE HEMOCYANIN G-TYPE SUBUNIT (FRAGMENT).
 GN ODHXY.
 OS OCTOPUS DOFLEINI (GIANT OCTOPUS).
 CC EUKARYOTA; METAZOA; MOLLUSCA; CEPHALOPODA; COLEOIDEA; OCTOPODA;
 CC INCIRATA; OCTOPODIDA; OCTOPUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98277150.
 RA MILLER K.I., CUFF M.E., LANG W.F., VARGA-WEISZ P., FIELD K.G.,
 RA VAN HOLDE K.E.;
 RT "Sequence of the Octopus dofleini hemocyanin subunit: structural and
 evolutionary implications.";
 RL J. MOL. BIOL. 278:827-841(1998).
 DR EMBL; AF020548; G3132880; -;
 DR PROSITE; PS00497; TYROSINASE_1; 1.
 DR PROSITE; PS00498; TYROSINASE_2; 6.
 FT NON_TER 1 1
 SQ SEQUENCE 2896 AA; 331917 MW; 68BA6928 CRC32;

Query Match 75.0%; Score 48; DB 5; Length 2896;
 Best Local Similarity 66.7%; Pred. No. 6.07e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2716 QKXRGLEPYN 2724
 ||| : |||
 QY 1 QKXNAPYN 9

RESULT 9
 ID 079455 PRELIMINARY; PRT; 16 AA.
 AC 079455;
 DT 01-NOV-1996 (TREMBL:REL. 01, CREATED)
 DT 01-NOV-1996 (TREMBL:REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBL:REL. 08, LAST ANNOTATION UPDATE)
 DE LIGHT-CHAIN COMPLEMENTARITY-DETERMINING REGION 3 MRNA
 (CLONE 14), PARTIAL CDS (FRAGMENT).
 OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
 CC VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92052225.
 RA BURTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
 RA LERNER R.A.;
 RT "A large array of human monoclonal antibodies to type 1 human
 immunodeficiency virus from combinatorial libraries of asymptomatic
 seropositive individuals.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
 DR EMBL; M80720; G327942; -;
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1883 MW; 5462C8DD CRC32;

Query Match 73.4%; Score 47; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.94e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 QKXNSAP 10
 ||| : |||
 QY 1 QKXNSAP 7

RESULT 10

ID 079461 PRELIMINARY; PRT; 16 AA.
 AC 079461;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE LIGHT-CHAIN COMPLEMENT-1-DETERMINING REGION 3 mRNA
 DE (CLONE 31), PARTIAL CDS (FRAGMENT).
 OS HDVAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
 OC VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92052225.
 RA BURTON D.R., BARBAS C.F. III, PERSSON M.A., KOENIG S., CHANOCK R.M.,
 RA LERNER R.A.;
 RT "A large array of human monoclonal antibodies to type 1 human
 RT immunodeficiency virus from combinatorial libraries of asymptomatic
 RT seropositive individuals."
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
 DR EMBL; M80726; G327954; -.
 RN NON_TER 1 1
 RN NON_TER 16 16
 SQ SEQUENCE 16 AA; 1883 MW; 5462C8DD CRC32;

Query Match 73.4%; Score 47; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.94e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 OKYNSAP 10
 |||||
 QY 1 OKYNSAP 7

RESULT 11 PRELIMINARY; PRT; 278 AA.
 ID 047792
 AC 047792;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE PLASMID PAD1, OPEN READING FRAMES.
 OS ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS).
 OC PLASMID PAD1.
 CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; ENTEROCOCCACEAE;
 CC ENTEROCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-OGIX;
 RX MEDLINE; 97074879.
 RA HIRT H., WIRTH R., MUSCHOLL A.;
 RT "Comparative analysis of 18 sex pheromone plasmids from Enterococcus
 RT faecalis: detection of a new insertion element on pPD1 and
 RT implications for the evolution of this plasmid family."
 RL MOL. GEN. GENET. 252:640-647(1996).
 DR EMBL; X96977; E236596; -.
 KW PLASMID.
 SQ SEQUENCE 278 AA; 30520 MW; 67892F0F CRC32;

Query Match 73.4%; Score 47; DB 2; Length 278;
 Best Local Similarity 55.6%; Pred. No. 9.94e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 227 OKYNSAPK 235
 |||:|:
 QY 1 OKYNSAPYN 9

RESULT 12 PRELIMINARY; PRT; 450 AA.
 ID 050511
 AC 050511;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ZINC PROTEASE.
 GN SC9B10.04.

OS STREPTOMYCES COELICOLOR.
 CC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 CC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA OLIVER K., HARRIS D.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE; 97000351.
 RA REDENBACH M., KIESER H.M., DENAPATE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL MOL. MICROBIOL. 21:77-96(1996).
 DR EMBL; AL009204; E1202335; -.
 KW PROTEASE.
 SQ SEQUENCE 450 AA; 49045 MW; 3E30B71A CRC32;

Query Match 73.4%; Score 47; DB 2; Length 450;
 Best Local Similarity 50.0%; Pred. No. 9.94e+00;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 147 OKYNDVPY 154
 ||:|:|
 QY 1 OKYNSAPY 8

RESULT 13 PRELIMINARY; PRT; 644 AA.
 ID 012828
 AC 012828;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE FUSE BINDING PROTEIN.
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94170991.
 RA DUNCAN R., BAZAR T., MICHELOTTI G., TOMONAGA T., KRUTZSCH H.,
 RA AVIGAN M., LEVENS D.;
 RT "A sequence-specific, single-strand binding protein activates the far
 RT upstream element of c-myc and defines a new DNA-binding motif."
 RL GENES DEV. 8:465-480(1994).
 DR EMBL; U05040; G460152; -.
 DR PFM; PF00013; KH-domain; 4.
 SQ SEQUENCE 644 AA; 67534 MW; C499E251 CRC32;

Query Match 73.4%; Score 47; DB 4; Length 644;
 Best Local Similarity 85.7%; Pred. No. 9.94e+00;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 484 YNPAPYN 490
 ||:|:|
 QY 3 YNSAPYN 9

RESULT 14 PRELIMINARY; PRT; 305 AA.
 ID 018281
 AC 018281;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE ZK1010.2 PROTEIN.

GN ZK1010.2.
 OS CAENORHABDITIS ELEGANS.
 CC EUKARYOTA; METAZOA; NEMATODA; SECCERNITEA; RHABDITIA; RHABDITIDA;
 CC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA GARDNER A.;
 RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 94150718.
 RX WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.*;
 RL NATURE 368:32-38(1994).
 DR EMBL; 282083; E1350959; -
 SQ SEQUENCE 305 AA; 34863 MM; 7607532C CRC32;

Query Match 71.9%; Score 46; DB 5; Length 305;
 Best Local Similarity 44.4%; Pred. No. 1.62e+01;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 149 ERYADAPD 157
 QY 1 OKNSAPYN 9

RESULT 15
 ID 068847 PRELIMINARY; PRT; 320 AA.
 AC 068847;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SITE-SPECIFIC RECOMBINASE INT14.
 GN INT14.
 OS VIRBIO CHOLERAE.
 CC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TRANSPONSON-INVCH;
 RA MEDLINE; 98221242.
 RA MAKEL D., DYCHINCO B., WEBB V.A., DAVIES J.;
 RT *A distinctive class of integron in the Vibrio cholerae genome.*;
 RL SCIENCE 280:605-608(1998).
 DR EMBL; AF055586; G3095165; -
 SQ SEQUENCE 320 AA; 37505 MM; CBF0F9CD CRC32;

Query Match 71.9%; Score 46; DB 2; Length 320;
 Best Local Similarity 55.6%; Pred. No. 1.62e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 208 EKPAPYE 216
 QY 1 OKNSAPYN 9

Search completed: Thu Sep 2 11:51:22 1999
 Job time : 27 secs.

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 W E S E R E (TM)

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 Msearch.p protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:50:30 1999; Maspar time 2.13 Seconds
 Molecular output not generated. 119.220 Million cell updates/sec

Title: >US-08-599-226-18
 Description: (1-9) from US08599226.pep
 Perfect Score: 64
 Sequence: 1 OKYNAPYN 9

Scoring table: PAM 150
 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 22.593; Variance 24.957; scale 0.905

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	48	75.0	392	1	YHBB_BACU HYPOTHEICAL 45.3 KD P	2.87e+00
2	48	75.0	500	1	AR08_YEAS AROMATIC AMINO ACID AM	2.87e+00
3	48	75.0	1233	1	HCY_OCTDO HEMOCYANIN, UNITS ODE	2.87e+00
4	47	73.4	469	1	GLN1_RHME GLUTAMINE SYNTHETASE I	4.79e+00
5	47	73.4	469	1	GLN1_RHIV GLUTAMINE SYNTHETASE I	4.79e+00
6	47	73.4	1673	1	CO3_LAMJA COMPLEMENT C3 PRECURSOR	4.79e+00
7	46	71.9	530	1	PRO9_YEAS PRE-MRNA SPLICING FACT	7.92e+00
8	46	71.9	863	1	GLND_HAETN [PROTEIN-P11] URIDYLAT	7.92e+00
9	46	71.9	887	1	GLND_HAETN [PROTEIN-P11] URIDYLAT	7.92e+00
10	46	71.9	890	1	GLND_HAETN [PROTEIN-P11] URIDYLAT	7.92e+00
11	46	71.9	1385	1	YMS5_CAEEL HYPOTHEICAL 159.2 KD	7.92e+00
12	45	70.3	376	1	OPPC_MYCPN OLIGOPEPTIDE TRANSPORT	1.30e+01
13	45	70.3	410	1	HCYB_HELPD HEMOCYANIN, BETA-C CHA	1.30e+01
14	45	70.3	689	1	YBP3_YEAS HYPOTHEICAL 77.3 KD P	1.30e+01
15	45	70.3	2148	1	VITL1_AEDAE VITELLOGENIN A1 PRECUR	2.11e+01
16	44	68.8	114	1	KV4A_HUMAN IG KAPPA CHAIN V-IV RE	2.11e+01
17	44	68.8	121	1	PA2B_PSETE PHOSPHOLIPASE A2 HOMOL	2.11e+01
18	44	68.8	128	1	KV3K_HUMAN IG KAPPA CHAIN PRECUR	2.11e+01
19	44	68.8	348	1	CHLI_EUGER MAGNESIUM-CHLORIDE SU	2.11e+01
20	44	68.8	376	1	YNN4_YEAS HYPOTHEICAL 41.2 KD P	2.11e+01
21	44	68.8	515	1	GGPD_YEAS GLUTOCOSE-6-PHOSPHATE 1-	2.11e+01
22	44	68.8	517	1	TYR2_MOUSE DOPACHROME TAUOMERASE	2.11e+01
23	44	68.8	725	1	SPE1_DIACA ARGININE DECARBOXYLASE	2.11e+01

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
24	44	68.8	846	1	NRT_DROME NEUROFACIN.	2.11e+01
25	44	68.8	1262	1	GNRP_MOUSE GRANINE NUCLEOTIDE REL	2.11e+01
26	44	68.8	2259	1	CB21_RABIT BRAIN CALCIUM CHANNEL	2.11e+01
27	43	67.2	108	1	KV1V_HUMAN IG KAPPA CHAIN V-I REG	3.40e+01
28	43	67.2	121	1	HV01_MOUSE IG HEAVY CHAIN V-REGIO	3.40e+01
29	43	67.2	210	1	REPB_STRPN REPLICATION PROTEIN RE	3.40e+01
30	43	67.2	331	1	OMB2_NEIME MAJOR OUTER MEMBRANE P	3.40e+01
31	43	67.2	335	1	PBGE_HUMAN PREGNANCY-SPECIFIC BET	3.40e+01
32	43	67.2	406	1	BHMT_HUMAN BETAINE--HOMOCYSTEINE	3.40e+01
33	43	67.2	407	1	BHMT_HUMAN BETAINE--HOMOCYSTEINE	3.40e+01
34	43	67.2	417	1	PBGI_HUMAN PREGNANCY-SPECIFIC BET	3.40e+01
35	43	67.2	419	1	PBGC_HUMAN PREGNANCY-SPECIFIC BET	3.40e+01
36	43	67.2	428	1	VIT2_DROME VITELLOGENIN II PRECUR	3.40e+01
37	43	67.2	442	1	EYAL_MOUSE EYES ABSENT HOMOLOG 1.	3.40e+01
38	43	67.2	591	1	EYAL_MOUSE EYES ABSENT HOMOLOG 1.	3.40e+01
39	43	67.2	592	1	EYAL_HUMAN EYES ABSENT HOMOLOG 1.	3.40e+01
40	43	67.2	615	1	ALBU_CHICK SERUM ALBUMIN PRECURSOR	3.40e+01
41	43	67.2	895	1	PMAL_CANAL PLASMA MEMBRANE ATPASE	3.40e+01
42	43	67.2	1139	1	KPCI_TRIPE PROTEIN KINASE C-LIKE	3.40e+01
43	43	67.2	1897	1	PTPE_HUMAN LAR PROTEIN PRECURSOR	3.40e+01
44	42	65.6	252	1	XUG6_YEAS HYPOTHEICAL 28.5 KD P	5.43e+01
45	42	65.6	1279	1	APU_THESA AMILOPOLYLINASE PRECU	5.43e+01

ALIGNMENTS

RESULT 1
 ID YHBB_BACU STANDARD; PRT; 392 AA.

AC P45742;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE HYPOTHEICAL 45.3 KD PROTEIN IN PKA-CSPB INTERGENIC REGION (ORF4).

GN YHBB.

OS BACILLUS SUBTILIS.

OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;

OC BACILLUS.

OC BACILLUS.

RP SEQUENCE FROM N.A.

RC STRAIN-168;

RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [2]

RP SEQUENCE OF 1-309 FROM N.A.

RC STRAIN-168;

RA DEUTSCHER J., BERGSTEDT U., BOHRSON C., PANAYOTOVA-HEIERMANN M.;

RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- SIMILARITY: TO E.COLI YEAS.

CC

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Query Match 75.0%; Score 48; DB 1; Length 392;
 Best local similarity 66.7%; Pred. No. 2.87e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 294 OKYNAPYN 302
 QY 1 OKYNAPYN 9

RESULT 2

ID ARO8_YEAST STANDARD: PRT: 500 AA.
AC P53090;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE AROMATIC AMINO ACID AMINOTRANSFERASE I (EC 2.6.1.-).
GN ARO8 OR YGL202M.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCCHAROMYCETALES;
CC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SIGMA 1278B;
RX MEDLINE: 98151783.
RA IRAQUI I., VISSERS S., CARTIAUX M., URRESTARAZU A.;
RT "Characterisation of Saccharomyces cerevisiae ARO8 and ARO9 genes
encoding aromatic aminotransferases I and II reveals a new
aminotransferase subfamily";
RL MOL. GEN. GENET. 257:238-248(1998).
[2]
SEQUENCE FROM N.A.
BJOURSON A.J., MOREYNOUDS A.D.K., WRIGHT L.F.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: TO YEAST ARO9.

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CC or send an email to license@isb-sib.ch).

CC EMBL: Y13624; E321594; -
CC DR EMBL: 272724; E243502; -
CC KW SGD: L0003949; ARO8
CC TRANSFERASE; AMINOTRANSFERASE.
CC SEQUENCE 500 AA; 56177 MW; B42B3B85 CRC32;
SO
Query Match 75.0%; Score 48; DB 1; Length 500;
Best Local Similarity 85.7%; Pred. No. 2.87e+00;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 415 KYNSDPY 421
OY 2 KYNSAPY 8

SUBMIT 3
AC HCX_OCTDO STANDARD: PRT: 1233 AA.
AC P12659;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE HEMOCYANIN, UNITS ODE TO ODS (FRAGMENT).
OS OCTOPUS DOFLEINI (GIANT OCTOPUS).
OC EUKARYOTA; METAZOA; MOLUSCA; CEPHALOPODA; COLEOIDEA; OCTOPODA;
CC INCIRRATA; OCTOPODIDA; OCTOPUS.
RN [1]
RP SEQUENCE OF 1-834 FROM N.A.
RC MEDLINE: 91095437.
RX LANG W.H., VAN HOLDE K.E.;
RT "Cloning and sequencing of Octopus dofleini hemocyanin cDNA: derived
RT sequences of functional units Ode and Odf";
RL PROC. NATL. ACAD. SCI. U.S.A. 88:244-248(1991).
RN [2]
RP SEQUENCE OF 835-1233 FROM N.A.
RX MEDLINE: 89088084.
RA LANG W.H.;
RT "cDNA cloning of the Octopus dofleini hemocyanin: sequence of the
RT carboxyl-terminal domain";
RL BIOCHEMISTRY 27:7276-7282(1988).
CC -1- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS

CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSCS AND
CC ARTHROPODS.
CC -1- SUBUNIT: DECATERS OF LARGE IDENTICAL SUBUNITS (350 KD), EACH
CC CONTAINING 7 GLOBULAR OXYGEN-BINDING DOMAINS: ODA, ODB, ODC, ODD,
CC ODE, ODF, AND ODG.
CC -1- SIMILARITY: TO HELIX POMATIA HEMOCYANIN AND TO TYROSINASES.

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CC EMBL: M57288; E37715; -
CC DR EMBL: J02835; G159737; -
CC DR PIR: A31137; A31137.
CC PIR: A28786; A28786.
CC DR PROSITE: PS00497; TYROSINASE_1; 1.
CC DR PROSITE: PS00498; TYROSINASE_2; 3.
CC DR PFAM: PF00264; Tyrosinase; 4.
CC KW RESPIRATORY PROTEIN; OXYGEN TRANSPORT; COPPER; GLYCOPROTEIN;
CC HEMOLYMPH; DUPLICATION.
CC NON_TER 1
CC FT DOMAIN 1 413
CC FT DOMAIN 414 834
CC FT DOMAIN 835 1233
CC FT DOMAIN 45 45
CC FT METAL 65 65
CC FT METAL 74 74
CC FT METAL 186 186
CC FT METAL 190 190
CC FT METAL 217 217
CC FT METAL 463 463
CC FT METAL 481 481
CC FT METAL 490 490
CC FT METAL 599 599
CC FT METAL 603 603
CC FT METAL 630 630
CC FT METAL 880 880
CC FT METAL 899 899
CC FT METAL 908 908
CC FT METAL 1008 1008
CC FT METAL 1012 1012
CC FT METAL 1039 1039
CC FT CARBOHYD 392 392
CC FT CARBOHYD 538 538
CC FT CARBOHYD 890 890
CC SEQUENCE 1233 AA; 141523 MW; 2D91A9CB CRC32;
SO
Query Match 75.0%; Score 48; DB 1; Length 1233;
Best Local Similarity 66.7%; Pred. No. 2.87e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 1053 QKXRGIPYN 1061
OY 1 QKXNSAPYN 9

RESULT 4
AC GLN1_RHIME STANDARD: PRT: 469 AA.
AC Q59747;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE GLUTAMINE SYNTHETASE I (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE 1)
DE (GSI).
GN GLNA.
OS RHIZOBIUM MELILOTI.
CC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
CC RHIZOBIACEAE; SINORHIZOBIUM.
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-2011;
 RX MEDLINE: 97085050.
 RA ARCONDEGUY T., HUEZ I., FOURMENT J., KAHN D.;
 RT "Symiotic nitrogen fixation does not require adenylation of
 glutamine synthetase I in Rhizobium meliloti.";
 RL FEMS MICROBIOL. LETT. 145:33-40(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 ORTHOPHOSPHATE.
 CC -1- ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED
 BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE
 (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 HEXAGON (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII) CAN BE FOUND IN
 THIS NITROGEN FIXING BACTERIA, GSI IS A TYPICAL PROKARYOTIC
 GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE EUKARYOTIC
 ENZYME.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U50385; G1245379; -
 DR PROSITE: PS00180; GLNA_1; 1.
 DR PROSITE: PS00181; GLNA_ATP; 1.
 DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
 DR PFAM: PF00120; gln-synt; 1.
 DR HSSP: P06201; 2LGS.
 KW NITROGEN FIXATION; LIGASE; MULTIGENE FAMILY.
 FT BINDING 397 AMP (UNDER CONDITIONS OF ABUNDANT
 GLUTAMINE) (BY SIMILARITY).
 SQ SEQUENCE 469 AA; 52035 MW; 7E3044A9 CRC32;
 Query Match 73.4%; Score 47; DB 1; Length 469;
 Best Local Similarity 62.5%; Pred. No. 4.79e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 141 KYRADPYN 148
 Oy 2 KYNAPYN 9
 ID GUNT_RHILV STANDARD; PRT; 469 AA.
 AC P09826;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GLUTAMINE SYNTHETASE I (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE I)
 DE (GSI).
 GN GLNA.
 OS RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE).
 OC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
 OC RHIZOBIACEAE; RHIZOBIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RCC1001;
 RX MEDLINE: 87174729.
 RA COLONNA-ROMANO S., RICCIO A., GUIDA M., DEFEEZ R., LAMBERTI A.,
 RA IACCARINO M., ARNOLD W., PRIEFER U., PUHLER A.;
 RT "tight linkage of glna and a putative regulatory gene in Rhizobium
 leguminosarum.";
 RL MOLECULAR ACIDS RES. 15:1951-1964(1987).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 ORTHOPHOSPHATE.
 CC -1- ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED

CC BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 HEXAGON.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII) CAN BE FOUND IN
 THIS NITROGEN FIXING BACTERIA, GSI IS A TYPICAL PROKARYOTIC
 GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE EUKARYOTIC
 ENZYME.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X04880; G46193; -
 DR PIR: A26567; AJZROL.
 DR PROSITE: PS00180; GLNA_1; FALSE_NEG.
 DR PROSITE: PS00181; GLNA_ATP; 1.
 DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
 DR PFAM: PF00120; gln-synt; 1.
 DR HSSP: P06201; 2LGS.
 KW NITROGEN FIXATION; LIGASE; MULTIGENE FAMILY.
 FT BINDING 398 AMP (UNDER CONDITIONS OF ABUNDANT
 GLUTAMINE) (BY SIMILARITY).
 SQ SEQUENCE 469 AA; 52232 MW; 9B59505D CRC32;
 Query Match 73.4%; Score 47; DB 1; Length 469;
 Best Local Similarity 62.5%; Pred. No. 4.79e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 141 KYRADPYN 148
 Oy 2 KYNAPYN 9
 ID CO3_LAMOA STANDARD; PRT; 1673 AA.
 AC Q00685;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN] (FRAGMENT).
 DE C3.
 GN LAMPEPTRA JAPONICA (JAPANESE LAMPEPTRA).
 OS LAMPEPTRA JAPONICA (JAPANESE LAMPEPTRA).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CEPHALASPIDOMORPHI;
 OC PETROMYZONTIFORMES; PETROMYZONTIDAE; LAMPEPTRA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 92251197.
 RA NONAKA M., TAKAHASHI M.;
 RT "complete complementary DNA sequence of the third component of
 complement of lamprey. Implication for the evolution of thioester
 containing proteins.";
 RL J. IMMUNOL. 148:3290-3295(1992).
 CC -1- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
 COMPLEMENT SYSTEM. AFTER ACTIVATION (C3b), IT CAN BIND COVALENTLY,
 VIA ITS REACTIVE THIOESTER, TO CELL SURFACE CARBOHYDRATES OR
 IMMUNE AGGREGATES. CYCLOSTOMATES C3 APPEARS TO REPRESENT THE
 COMMON ANCESTOR OF MAMMALIAN C3 AND C4, SHOWING SIMILARITIES TO
 BOTH PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -----
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DR EMBL: D10087; G22888; -
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PFAM; PF00207; A2M; 1.
 DR HSP; P01024; IC3D.
 KM COMPLEMENT PATHWAY; PLASMA; INFLAMMATORY RESPONSE; GLYCOPROTEIN;
 KW SIGNAL.
 FT SIGNAL. 1
 FT SIGNAL. <1 13 POTENTIAL.
 FT CHAIN 14 1673 COMPLEMENT C3.
 FT CHAIN 14 653 BETA CHAIN (BY SIMILARITY).
 FT CHAIN 657 1375 ALPHA CHAIN (BY SIMILARITY).
 FT CHAIN 1379 1673 GAMMA CHAIN (BY SIMILARITY).
 FT PEPTIDE 657 732 C3A ANAPHYLATOXIN (BY SIMILARITY).
 FT DOMAIN 678 713 ANAPHYLATOXIN-LIKE.
 FT DISULEID 678 705 BY SIMILARITY.
 FT DISULEID 679 712 BY SIMILARITY.
 FT DISULEID 692 713 BY SIMILARITY.
 FT THIOLEST 986 990 BY SIMILARITY.
 SO SEQUENCE 1673 AA; 187767 MW; D857446F CRC32;

Query Match 73.4%; Score 47; DB 1; Length 1673;
 Best Local Similarity 75.0%; Pred. No. 4.79e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 443 OKYASASY 450
 Oy 1 OKYNSAPY 8

RESULT 7
 ID PRO9_YEAST STANDARD; PRT; 530 AA.
 AC P19736;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PRE-MRNA SPLICING FACTOR PRP9.
 OS PRP9 OR YD1030W OR D2773.
 GN SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OS SACCAROMYCES CEREVISIAE; SACCAROMYCETALES;
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
 RN SACCAROMYCETACEAE; SACCAROMYCES.
 RP SEQUENCE FROM N.A.
 RP STRAIN-S288C / GRF88;
 MEDLINE; 90360988.
 RT "The molecular characterization of PRP6 and PRP9 yeast genes reveals
 RT a new cysteine/histidine motif common to several splicing factors.";
 RL EMBL J. 9:2775-2781(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN-S288C;
 RA PAULIN L., SAREN A.M., LAAMANEN P.;
 RA SUBMITTED (APR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: INVOLVED IN PRE-MRNA SPLICING. REQUIRED FOR U2 SNRNP
 CC BINDING TO THE PRE-MRNA. ACTS EARLY DURING SPLICOSOME ASSEMBLY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: TO MAMMALIAN SPLICOSOME ASSOCIATED PROTEIN 61
 CC (SF360).

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DR EMBL: Z71781; E237299; -
 DR EMBL: Z74078; E253198; -
 DR PIR: S12320; S12320.
 DR SGD: L0001501; PRP9.
 DR PFAM; PF00096; zfc2R2; 2.
 KM mRNA PROCESSING; MRNA SPLICING; SPLICOSOME; NUCLEAR PROTEIN.
 SO SEQUENCE 530 AA; 63029 MW; 11741EAC CRC32;

Query Match 71.9%; Score 46; DB 1; Length 530;
 Best Local Similarity 44.4%; Pred. No. 7.92e+00;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 359 OKYEPAPYD 367
 Oy 1 OKYNSAPY 9

RESULT 8
 ID GLND_HAEIN STANDARD; PRT; 863 AA.
 AC P43919;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE [PROTEIN-PII] URIDYLTRANSFERASE (EC 2.7.7.59) (PII URIDYL-
 DE TRANSFERASE) (URIDYL REMOVING ENZYME) (UTASE).
 GN GLND OR H11719.
 OS HAEMOPHILUS INFLUENZAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
 OC HAEMOPHILUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN-RD / RW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BUTT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,
 RA UETTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRICHTMAN J.L., FUHRMAN J.L., GEORGHEN N.S.M.,
 RA GHEM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL SCIENCE 269:496-512(1995).
 CC -1- FUNCTION: MODIFIES, BY URIDYLATION OR DEURIDYLATION THE PII
 CC (GLNB) REGULATORY PROTEIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: UTP + [PROTEIN-PII] = PYROPHOSPHATE +
 CC URIDYL- [PROTEIN-PII].
 CC -1- SIMILARITY: TO OTHER BACTERIAL GLND.
 CC -----
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DR EMBL: U32844; G1574572; -
 DR TIGR; H11719; -
 KM TRANSFERASE; NUCLEOTIDYLTRANSFERASE.
 SO SEQUENCE 863 AA; 100173 MW; AFBF5FD CRC32;

Query Match 71.9%; Score 46; DB 1; Length 863;
 Best Local Similarity 44.4%; Pred. No. 7.92e+00;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 OKYNSAPY 193
 Oy 1 OKYNSAPY 9

RESULT 9
ID GLND_KLEPN STANDARD: PRT: 887 AA.
AC P41393:
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE [PROTEIN-PII] URIDYLTRANSFERASE (EC 2.7.7.59) (PII URIDYL-
TRANSFERASE) (URIDYL REMOVING ENZYME) (UTASE).
GN GLND.
OS KLEBSIELLA PNEUMONIAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC KLEBSIELLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M5A1:
RX MEDLINE; 95272528.
RA EDWARDS R.A., MERRICK M.J.;
RT "The role of uridylyltransferase in the control of Klebsiella
pneumoniae nif gene regulation."
MOL. GEN. GENET. 247:189-198(1995).
CC -1- FUNCTION: MODIFIES, BY URIDYLATION OR DEURIDYLATION THE PII
(GLND) REGULATORY PROTEIN.
CC -1- CATALYTIC ACTIVITY: UTP + [PROTEIN-PII] - PYROPHOSPHATE +
URIDYL-[PROTEIN-PII].
CC -1- SIMILARITY: TO OTHER BACTERIAL GLND.
CC -----
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CC -----
DR EMBL; X7685; G470140; -
KW TRANSFERASE; NUCLEOTIDYLTRANSFERASE.
SQ SEQUENCE 887 AA; 102343 MW; C2C8386A CRC32;
Query Match 71.9%; Score 46; DB 1; Length 887;
Best Local Similarity 44.4%; Pred. No. 7.92e+00;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Db 203 ORYHGTSYN 211
QY 1 OKNSAPYN 9
RESULT 10
ID GLND_ECOLI STANDARD: PRT: 890 AA.
AC P27249:
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE [PROTEIN-PII] URIDYLTRANSFERASE (EC 2.7.7.59) (PII URIDYL-
TRANSFERASE) (URIDYL REMOVING ENZYME) (UTASE).
GN GLND.
OS ESCHERICHIA COLI.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC ESCHERICHIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RA PARK S.-C., KIM I.H., RHEE S.G.;
RL SUBMITTED (XXX-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94018640.
RA VAN HESSEN W.C., RABENBERG M., WESTERHOFF H.V., KAHN D.;
RT "The genes of the glutamine synthetase adenylation cascade are not
regulated by nitrogen in Escherichia coli."
MOL. MICROBIOL. 9:443-458(1993).
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94261430.
RA FUJITA N., MORI H., YURA T., ISHIGAMA A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
the 2.4-4.1 min (110,917-193,643 bp) region."
RL NUCLEIC ACIDS RES. 22:1637-1639(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426157.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12."
SCIENCE 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA SCHRAMM S., DUNCAN M., ALLEN E., ARAUJO R., APARICIO A., CHUNG E.,
RA DAVIS K., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O.,
RA LASHKARI D., LEW H., LIN D., NAWATH A., OEFNER P., ROBERTS D.,
RA DAVIS R.W.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MODIFIES, BY URIDYLATION OR DEURIDYLATION THE PII
(GLND) REGULATORY PROTEIN.
CC -1- CATALYTIC ACTIVITY: UTP + [PROTEIN-PII] - PYROPHOSPHATE +
URIDYL-[PROTEIN-PII].
CC -1- SIMILARITY: TO OTHER BACTERIAL GLND.
CC -1- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 703
ONWARD AND IS SHORTER (727 AA) DUE TO A FRAMESHIFT.
CC -----
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CC -----
DR EMBL; M96431; G146155; -
DR EMBL; 221842; G49393; -
DR EMBL; D26562; G473822; ALT FRAME.
DR EMBL; A6000126; G1786363; -
DR EMBL; U70214; G1552744; -
DR PIR; S31962; S31962.
DR PIR; S36254; S36254.
DR ECOGENE; EG11411; GLND.
KW TRANSFERASE; NUCLEOTIDYLTRANSFERASE.
FT CONFLICT 47 47
FT CONFLICT 225 225
FT CONFLICT 357 358
FT CONFLICT 523 523
FT CONFLICT 703 703
SQ SEQUENCE 890 AA; 102390 MW; 96599666 CRC32;
Query Match 71.9%; Score 46; DB 1; Length 890;
Best Local Similarity 44.4%; Pred. No. 7.92e+00;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Db 206 ORYHGTSYN 214
QY 1 OKNSAPYN 9
RESULT 11
ID YMS5_CAEEL STANDARD: PRT: 1385 AA.
AC P34501:
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III.
GN K03H1.5.

OS CAENORHABDITIS ELEGANS.
CC EKKAROTIA; METAZOA; SECERNENTEA; RHABDITIA; RHABDITIDA;
CC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BUTTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA FULLON L., GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSIER N.,
RA LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SAMS M., SMALDON N., SMITH A., SMITH M., SONNEMMER E., STADEN R.,
RA SULLIVAN J., THIRREY-MIEG J., THOMAS K., VAIDIN M., VAUGHAN K.,
RA WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA WOLDMAN P.,
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans".
NATURE 368:32-38(1994).

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DR EMBL: Z29560; E1347842; -.
DR PIR: S41028; S41028.
DR MORPEP: K03H1.5; CE03459.
DR PFAM: PF00084; sushi; 1.
KM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 1385 AA; 159181 MW; A2134063 CRC32;

Query Match
Best Local Similarity 71.9%; Score 46; DB 1; Length 1385;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 797 HRYGAPY 804
OY 1 OKNSAPY 8

RESULT 12
OPPC MYCPN STANDARD; PRT; 376 AA.
P75553;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC.
GN OPPC
OS MYCOPLASMA PNEUMONIAE.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLICUTES;
OC MYCOPLASMATACEAE; MYCOPLASMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE: 97105885.
RA HILBERT R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
RA HERRMANN R.,
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae".
RL NUCLEIC ACIDS RES. 24:4420-4449(1996).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF
CC THE SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPC
CC SUBFAMILY.

CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: A6000058; G1674317; -.
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER. 1.
DR PFAM: PF00528; BPD_transp; 1.
KM TRANSPORT; PEPTIDE TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
FT TRANSMEM 341 361 POTENTIAL.
SQ SEQUENCE 376 AA; 41233 MW; 151AF8C3 CRC32;

Query Match
Best Local Similarity 70.3%; Score 45; DB 1; Length 376;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 134 KYNTAPY 140
OY 2 KYNSAPY 8

RESULT 13
ID HCXB_HELPD STANDARD; PRT; 410 AA.
AC P12031;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE HEMOCYANIN, BETA-C CHAIN UNIT D (FRAGMENT).
OS EKKAROTIA; METAZOA; MOLLUSCA; GASTROPODA; PULMONATA; STYLOMATOPHORA;
OC HELICIDAE; HELIX.
RN [1]
RP SEQUENCE.
RX MEDLINE: 87299002.
RA DREXEL R., SIEGMUND S., SCHNEIDER H.J., LINZEN B., GIELENS C.,
RA PREAU G., LONTJE R., KELLERMANN J., LOTSPRECH F.,
RT "Complete amino-acid sequence of a functional unit from a molluscan
RT hemocyanin (Helix pomatia)".
RL BIOL. CHEM. HOPE-SEYLER 368:617-635(1987).
CC -1- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSCS AND
CC ARTHROPODS.
CC -1- SUBUNIT: DECAMERS OF LARGE IDENTICAL SUBUNITS (350 KD), EACH
CC CONTAINING 7 GLOBULAR OXYGEN-BINDING DOMAINS.
CC -1- SIMILARITY: TO OCTOPUS DOFLEINI HEMOCYANIN AND TO TYROSINASES.
DR PROSITE: PS00498; TYROSINASE_2; 1.
DR PFAM: PF00264; tyrosinase; 1.
KM RESPIRATORY PROTEIN; OXYGEN TRANSPORT; COPPER; GLYCOPROTEIN;
KM HEMOLYMPH.
FT NON_TER 1 1
FT CHAIN 1 410 BETA-C HEMOCYANIN FUNCTIONAL UNIT D.
FT METAL 44 44 COPPER A (BY SIMILARITY).
FT METAL 55 55 COPPER A (BY SIMILARITY).
FT METAL 71 71 COPPER A (BY SIMILARITY).
FT METAL 175 175 COPPER B (BY SIMILARITY).
FT METAL 179 179 COPPER B (BY SIMILARITY).
FT METAL 206 206 COPPER B (BY SIMILARITY).
FT CARBOHYD 253 253 COPPER B (BY SIMILARITY).
FT NON_TER 410 410
SQ SEQUENCE 410 AA; 46964 MW; 04A3B076 CRC32;

Query Match
70.3%; Score 45; DB 1; Length 410;

Best Local Similarity 55.6%; Pred. No. 1.30e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 220 ORYGLPYN 228

OY 1 OKYNAPYN 9

RESULT 14
ID VAP3 YEAST STANDARD; PRT; 689 AA.

AC P38227;

DT 01-OCT-1994 (REL. 30, CREATED)

DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE HYPOTHEICAL 77.3 KD PROTEIN IN FIG1-G1P1 INTERGENIC REGION.

GN YBR043C OR YBR0413

OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCAROMYCETALES;

OC SACCAROMYCETACEAE; SACCAROMYCES.

[1] SEQUENCE FROM N.A.

STRAIN-8288C; HEIN C., JAUNIAUX J.C., URESTARAZU A.,

RA VISSERS S.;

RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN

AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE

CAR/CYR SUBFAMILY.

CC -----

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CC -----

DR EMBL: Z35912; G536268; -

DR PIR: S45901; S45901.

KW HYPOTHEICAL PROTEIN; TRANSPORT; TRANSMEMBRANE.

FT TRANSMEM 109 131 POTENTIAL.

FT TRANSMEM 140 163 POTENTIAL.

FT TRANSMEM 176 193 POTENTIAL.

FT TRANSMEM 236 256 POTENTIAL.

FT TRANSMEM 266 283 POTENTIAL.

FT TRANSMEM 476 493 POTENTIAL.

FT TRANSMEM 511 532 POTENTIAL.

FT TRANSMEM 559 577 POTENTIAL.

FT TRANSMEM 587 609 POTENTIAL.

FT TRANSMEM 625 642 POTENTIAL.

FT TRANSMEM 649 668 POTENTIAL.

SO SEQUENCE 689 AA; 77300 MW; 3616EDAE CRC32;

Query Match 70.3%; Score 45; DB 1; Length 689;

Best Local Similarity 62.5%; Pred. No. 1.30e+01;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 500 KYSRPPYN 507

OY 2 KYNAPYN 9

RESULT 15
ID VIT1_AEDAE STANDARD; PRT; 2148 AA.

AC Q16927; Q16927;

DT 15-JUL-1998 (REL. 36, CREATED)

DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE VITELLOGENIN A1 PRECURSOR (Vg) (PVG1) [CONTAINS: VITELLIN LIGHT CHAIN

(Vg); VITELLIN HEAVY CHAIN (Vh)].

GN VEG1.

OS AEDES AEGYPTI (YELLOW FEVER MOSQUITO).

OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;

OC PTERRIGOTA; DIPTERA; NEMATOCERA; CULICOIDA; AEDES.

RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE: 96035842.

RA ROMANS P., TU Z., KE Z., HAGEDORN H.H.;

RT "Analysis of a vitellogenin gene of the mosquito, Aedes aegypti and

RL comparisons to vitellogenins from other organisms."

INSECT BIOCHEM. MOL. BIOL. 25:939-958(1995).

RN [2] SEQUENCE FROM N.A., AND SEQUENCE OF 17-24 AND 469-477.

RC STRAIN-UGALS; TISSUE-FAT BODY;

RX MEDLINE: 94210487.

RA CHEN J.-S., CHO W.-L., RAIKHEL A.S.;

RT "Analysis of mosquito vitellogenin cDNA. Similarity with vertebrate

phosphatids and arthropod serum proteins."

J. MOL. BIOL. 237:641-647(1994).

RN [3] TISSUE-FAT BODY;

RX MEDLINE: 90277688.

RA DHADIALA T.S., RAIKHEL A.S.;

RT "Biosynthesis of mosquito vitellogenin."

J. BIOL. CHEM. 265:9924-9933(1990).

CC -1- FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES OF

NUTRIENTS DURING EMBRYONIC DEVELOPMENT. MAY SUPPLY AROMATIC AMINO

ACIDS TO THE CUTICLE OF RAPIDLY DEVELOPING EMBRYOS.

CC -1- TISSUE SPECIFICITY: PRODUCED BY THE FAT BODY, WHERE IT IS CLEAVED

IN THE ROUGH ENDOPASMIC RETICULUM OR CIS-GOLGI BEFORE BEING

SECRETED INTO HEMOLYPH. IT IS THEN STORED BY A SINGLE CLASS

CC -1- INDUCTION: SYNTHESIZED ONLY BY SEXUALLY MATURE FEMALE AFTER

CC -1- INGESTION OF BLOOD. PHOSPHORYLATED AND SULFATED. THE LARGE SUBUNIT

CC IS GLYCOSYLATED MORE EXTENSIVELY THAN THE SMALL ONE.

CC -1- POLYMORPHISM: ALLELIC VARIATIONS DETECTED IN THE MOSQUITO

CC POPULATION.

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CC -----

DR EMBL: I41842; G790835; -

DR PIR: U02548; G472308; -

KW GLYCOPROTEIN; PHOSPHORYLATION; STORAGE PROTEIN; SIGNAL; POLYMORPHISM;

FT SIGNAL 1 16

FT CHAIN 17 2148

FT CHAIN 17 468

FT CHAIN 469 2148

FT CARBOHYD 86 86

FT CARBOHYD 104 104

FT CARBOHYD 339 339

FT CARBOHYD 370 370

FT CARBOHYD 414 414

FT CARBOHYD 493 493

FT CARBOHYD 517 517

FT CARBOHYD 566 566

FT CARBOHYD 742 742

FT CARBOHYD 760 760

FT CARBOHYD 1119 1119

FT CARBOHYD 1212 1212

FT CARBOHYD 1315 1315

FT CARBOHYD 1631 1631

FT CARBOHYD 1675 1675

FT CARBOHYD 1956 1956

FT DOMAIN 5 10

FT DOMAIN 417 440

FT DOMAIN 496 512

FT DOMAIN 520 548 POLY-SER.
 FT DOMAIN 2007 2025 POLY-SER.
 FT DOMAIN 2033 2042 POLY-SER.
 FT CONFLICT 39 47 MISSING (IN REF. 2).
 FT CONFLICT 906 906 R -> S (IN REF. 2).
 FT CONFLICT 1367 1367 F -> Y (IN REF. 2).
 FT CONFLICT 1576 1576 C -> Y (IN REF. 2).
 FT CONFLICT 1757 1757 N -> Y (IN REF. 2).
 FT CONFLICT 1935 1935 A -> P (IN REF. 2).
 FT CONFLICT 2031 2031 G -> S (IN REF. 2).
 SQ SEQUENCE 2148 AA; 250249 MW; A5ADCFM4 CRC32;

Query Match 70.3%; Score 45; DB 1; Length 2148;
 Best Local Similarity 62.5%; Pred. No. 1.30e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1849 KYNGRPD 1856
 0Y 11:11:
 2 KNSAPYN 9

Search completed: Thu Sep 2 11:50:38 1999
 Job time : 8 secs.

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March pp. protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:49:57 1999; Maspar time 3.06 Seconds
 117.719 Million cell updates/sec
 Molecular output not generated.

Title: >US-08-599-226-18
 Description: (1-9) from US08599226.pep
 Perfect Score: 64
 Sequence: 1 OKNSAPYN 9

Scoring table: PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: PIGSO
 1:PIR1 2:PIR2 3:PIR3 4:PIR4

Statistics: Mean 21.995; Variance 27.782; scale 0.792

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	49	76.6	292	2	T00829	homeodomain transcrip	5.23e+00
2	48	75.0	392	2	B69821	conserved hypothetical	8.35e+00
3	48	75.0	399	2	A31137	hemocyanin - giant oc	8.35e+00
4	48	75.0	500	2	S64220	hypothetical protein	8.35e+00
5	47	73.4	95	2	PH0863	ig kappa chain V reg1	1.32e+01
6	47	73.4	107	2	S40366	ig kappa chain V-J re	1.32e+01
7	47	73.4	278	2	S72385	hypothetical protein	1.32e+01
8	47	73.4	469	1	AJZRL	glutamate--ammonia li	1.32e+01
9	47	73.4	644	2	A53184	myc far upstream elem	1.32e+01
10	47	73.4	1673	2	150806	complement component	1.32e+01
11	46	71.9	407	2	JC5632	hemocyanin dioxygen-b	2.08e+01
12	46	71.9	521	2	139956	neutral proteinase (E	2.08e+01
13	46	71.9	530	2	S12330	PRP9 protein - yeast	2.08e+01
14	46	71.9	863	2	B64138	uridylyltransferase h	2.08e+01
15	46	71.9	887	2	S43196	uridylyltransferase (2.08e+01
16	46	71.9	890	2	G64740	hypothetical protein	2.08e+01
17	46	71.9	1409	2	S41028	hypothetical protein	2.08e+01
18	45	70.3	91	2	S67940	ig kappa chain V reg1	3.25e+01
19	45	70.3	92	2	S37513	ig kappa chain V reg1	3.25e+01
20	45	70.3	109	2	H30601	ig kappa chain V-III	3.25e+01
21	45	70.3	109	2	A30608	ig kappa chain V-III	3.25e+01
22	45	70.3	376	2	S73941	oligopeptide transpor	3.25e+01
23	45	70.3	410	2	A29393	hemocyanin beta-c cha	3.25e+01

24	45	70.3	689	2	S45901	probable membrane pro	3.25e+01
25	45	70.3	2139	2	S46404	vitellogenin - yellow	3.25e+01
26	44	68.8	114	1	K4H1LN	ig kappa chain V-IV r	5.05e+01
27	44	68.8	121	1	S29652	textiloxin chain B	5.05e+01
28	44	68.8	128	1	K3H041	ig kappa chain precu	5.05e+01
29	44	68.8	216	2	JE0241	ig kappa chain Am37 p	5.05e+01
30	44	68.8	348	2	S34494	ccsa protein - Euglen	5.05e+01
31	44	68.8	376	2	S55149	hypothetical protein	5.05e+01
32	44	68.8	515	2	S57785	glucose-6-phosphate 1	5.05e+01
33	44	68.8	517	2	S19243	lysinease-related pr	5.05e+01
34	44	68.8	533	2	A47143	retinal pigment micro	5.05e+01
35	44	68.8	846	2	S13795	neurotactin - fruit f	5.05e+01
36	44	68.8	846	2	S12005	neurotactin - fruit f	5.05e+01
37	44	68.8	1260	2	S28407	guanine nucleotide-ex	5.05e+01
38	44	68.8	2251	2	S54972	voltage-dependent cal	5.05e+01
39	44	68.8	2259	2	S29236	calcium channel prote	5.05e+01
40	44	68.8	2270	2	A54972	voltage-dependent cal	5.05e+01
41	43	67.2	107	2	B28195	ig kappa chain V reg1	7.78e+01
42	43	67.2	332	2	JN0067	pregnancy-specific be	7.78e+01
43	43	67.2	436	2	A35964	pregnancy-specific gl	7.78e+01
44	43	67.2	442	1	VJPF2	vitellogenin II precu	7.78e+01
45	43	67.2	1139	2	S61918	protein kinase C (EC	7.78e+01

ALIGNMENTS

RESULT 1
 ENTRY T00829 #type complete
 TITLE homeodomain transcription factor homolog - Arabidopsis thaliana
 ALTERNATE_NAMES T1316.3 protein: wuschel protein
 ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear cress

DATE 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 12-Feb-1999

ACCESSIONS T00829
 REFERENCE Z14205
 #authors

#submission submitted to the EMBL Data Library, January 1999
 #description A. thaliana BAC T1316 from chromosome IV, top arm.
 #accession T00829
 #status Preliminary; translated from GE/EMBL/DBJ
 ##molecule_type DNA
 ##residues 1-292 ##label DEL
 ##cross-references EMBL:AC003952; NID:g2708736; PID:g2708739
 ##experimental_source cultivar Columbia

GENETICS

#map_position 2
 #introns 166/1; 195/3
 #note T1316.3

SUMMARY #length 292 #molecular_weight 33189 #checksum 7184

Query Match 76.6%; Score 49; DB 2; Length 292;
 Best Local Similarity 66.7%; Pred. No. 5.23e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 215 HHXSAAPYN 223
 QY 1 OKNSAPYN 9

RESULT 2

ENTRY B69821 #type complete
 TITLE conserved hypothetical protein ynhb - Bacillus subtilis
 ORGANISM #formal_name Bacillus subtilis
 DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
 ACCESSIONS B69821
 REFERENCE A69580
 #authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;

Alloinl, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Bourcier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Brox, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoedt, A.; Ehrlich, S.D.; Emerson, P.T.; Enliam, K.D.; Erlington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleon, N.; Gilh, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grand, G.; Giuseppe, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaer-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moesli, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle, D.; Portolick, S.; Prescott, A.M.; Presseau, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serro, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandendol, M.; Vannier, F.; Vassarotti, A.; Viati, A.; Wambull, R.; Wedler, E.; Wedler, H.; Wellenreger, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Yoshida, A.

#journal Nature (1997) 390:249-256
#title The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
#cross-references MUID:98044033
#accession B69821
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-392 ##label RUN
#cross-references GB:J09108; GB:AL009126; NID:g2633055; PID:e1182887; PID:g2633221
#experimental_source strain 168

GENETICS
#gene yhhH
#length 392 #molecular-weight 4533 #checksum 173

Query Match 75.0%; Score 48; DB 2; Length 392;
Best Local Similarity 66.7%; Pred. No. 8.35e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 294 EKINPARYN 302
QY 1 OKYNSAPYN 9

RESULT 3
ENTRY A31137 #type fragment
TITLE hemocyanin - giant octopus (*fragment*)
ORGANISM #formal_name Octopus dofleini #common_name giant octopus
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 01-Aug-1997
ACCESSIONS A31137; A28786
REFERENCE A31137
#authors Lang, W.H.
#journal Blochometry (1988) 27:7276-7282
#title cDNA cloning of the Octopus dofleini hemocyanin: sequence of the carboxyl-terminal domain.
#cross-references MUID:89088084
#accession A31137

##molecule_type mRNA
##residues 1-399 ##label LAN
#cross-references GB:J02835; NID:g159736; PID:g159737
#note the author translated the codon CCT for residue 346 as Leu

REFERENCE A94629
#authors Lang, W.H.
#submission submitted to the Protein Sequence Database, July 1988
#accession A28786
##molecule_type mRNA
##residues 1-263,265-345,'L',347-399 ##label LA2
KEYWORDS copper; oxygen carrier
SUMMARY #length 399 #checksum 154

Query Match 75.0%; Score 48; DB 2; Length 399;
Best Local Similarity 66.7%; Pred. No. 8.35e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 219 OKYRGLPYN 227
QY 1 OKYNSAPYN 9

RESULT 4
ENTRY S64220 #type complete
TITLE hypothetical protein YGL202w - yeast (*Saccharomyces cerevisiae*)
ALTERNATE_NAMES hypothetical protein G1253
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 17-May-1996 #sequence_revision 17-May-1996 #text_change 06-Feb-1998

ACCESSIONS S64220
#authors Bjournson, A.J.; McReynolds, A.D.K.; Wright, L.F.
#submission submitted to the Protein Sequence Database, May 1996
#accession S64220
##molecule_type DNA
##residues 1-500 ##label BJO
#cross-references EMBL:Z72724; NID:g1322833; PID:e243502; PID:g1322834; MIPs:YGL202w
#experimental_source strain S288c

GENETICS
#gene SCD:ARO8
#cross-references SGD:S0003170; MIPs:YGL202w
#map_position 7L
SUMMARY #length 500 #molecular-weight 56177 #checksum 3537

Query Match 75.0%; Score 48; DB 2; Length 500;
Best Local Similarity 85.7%; Pred. No. 8.35e+00;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 415 KYNSDPY 421
QY 2 KYNSAPY 8

RESULT 5
ENTRY PH0863 #type fragment
TITLE Ig kappa chain V region (anti-DNA, IIT-2R) - human (*fragment*)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
ACCESSIONS PH0863
REFERENCE PH0862
#authors Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosein, C.; Smith, A.; Diamond, B.
#journal J. Exp. Med. (1991) 174:1639-1652
#title Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.
#cross-references MUID:9207875
#accession PH0863
##molecule_type DNA
##residues 1-95 ##label MAN

COMMENT This antibody is produced by Epstein-Barr virus-transformed B cell that bears the 3i idiotype expressed on anti-DNA antibody.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotetramer; immunoglobulin

FEATURE

1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-95 #region complementarity-determining 3

SUMMARY #length 95 #checksum 6652

Query Match 73.4%: Score 47; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.32e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 OKYNSAP 95
1 OKYNSAP 7

RESULT 6

ENTRY S40366 #type complete
TITLE Ig kappa chain V-J region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-May-1994 #sequence_revision 26-May-1995 #text_change 20-Mar-1998

ACCESSIONS S40366
REFERENCE S40312 Klein, R.; Jaenichen, R.; Zachau, H.G.
#authors Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chl genes and their hypermutation.

#accession S40366
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-107 #label KLE
#cross-references EMBL:X72476; NID:g441420; PID:g441421
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 107 #molecular_weight 11556 #checksum 9149

Query Match 73.4%: Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.32e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

101 OKYNSAP 107
1 OKYNSAP 7

RESULT 7

ENTRY S72385 #type complete
TITLE hypothetical protein 9 - Enterococcus faecalis plasmid PAD1
ORGANISM #formal_name Enterococcus faecalis
DATE 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Jun-1998

ACCESSIONS S72385
REFERENCE S72375 Hirt, H.; Wirth, R.; Muscholl, A.
#authors Mol. Gen. Genet. (1996) 252:640-647
#journal Comparative analysis of 18 sex pheromone plasmids from Enterococcus faecalis: detection of a new insertion element on PPD1 and implications for the evolution of this plasmid family.

#cross-references MIMD:97074879
#accession S72385
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-278 #label HIR
#cross-references EMBL:X96977; NID:g1279406; PID:e236596; PID:g1279411
#experimental_source strain OG1X

#note the nucleotide sequence was submitted to the EMBL Data Library, February 1996

GENETICS #genome
SUMMARY plasmid PAD1
#length 278 #molecular_weight 30520 #checksum 877

Query Match 73.4%: Score 47; DB 2; Length 278;
Best Local Similarity 55.6%; Pred. No. 1.32e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 227 OKYNSAPFN 235
1 OKYNSAPFN 9

QY

RESULT 8

ENTRY A26567 #type complete
TITLE glutamate--ammonia ligase (EC 6.3.1.2) I - Rhizobium leguminosarum
ALTERNATE_NAMES glutamine synthetase I
ORGANISM #formal_name Rhizobium leguminosarum
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Apr-1998

ACCESSIONS A26567
REFERENCE A26566 Colonna-Romano, S.; Riccio, A.; Guida, M.; Defez, R.; Lamberti, A.; Iaccarino, M.; Arnold, W.; Priefer, U.; Puhler, A.
#journal Nucleic Acids Res. (1987) 15:1951-1964
#title Tight linkage of glnA and a putative regulatory gene in Rhizobium leguminosarum.

#cross-references MIMD:87174729
#accession A26567
#molecule_type DNA
#residues 1-469 #label COL
#cross-references GB:M16626
#note the authors translated the codon TTC for residue 54 as Ser, CGC for residues 106 and 130 as Pro, and TTC for residue 323 as Leu
COMMENT This enzyme catalyzes the formation of glutamine from ammonia and glutamic acid in the presence of ATP.

GENETICS glnA
CLASSIFICATION #superfamily glutamate--ammonia ligase
KEYWORDS ligase; phosphoprotein
FEATURE
398 #binding_site AMP (Tyr) (covalent) #status predicted
SUMMARY #length 469 #molecular_weight 52232 #checksum 3184

Query Match 73.4%: Score 47; DB 1; Length 469;
Best Local Similarity 62.5%; Pred. No. 1.32e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 141 KYRADPYN 148
2 KYRADPYN 9

QY

RESULT 9

ENTRY A53184 #type complete
TITLE myc far upstream element-binding protein - human
ALTERNATE_NAMES FUSE-binding protein
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997

ACCESSIONS A53184
REFERENCE A53184 Duncan, R.; Bazar, L.; Michelotti, G.; Tomonaga, T.; Krutzsch, H.; Avigan, M.; Levens, D.
#journal Genes Dev. (1994) 8:465-480
#title A sequence-specific, single-strand binding protein activates the far upstream element of c-myc and defines a new DNA-binding motif.

#cross-references MUID:94170991
#accession A53184
#status Preliminary
#molecule_type mRNA
#residues 1-644 ##label DUN
#cross-references GB:U05040; NID:9460151; PID:9460152
KEYWORDS DNA binding
SUMMARY #length 644 #molecular-weight 67534 #checksum 798

Query Match 73.4%; Score 47; DB 2; Length 644;
Best Local Similarity 85.7%; Pred. No. 1.32e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 484 YNPAPYN 490
|||:||||
OY 3 YNSAPYN 9

RESULT 10
ENTRY 150806 #type fragment
TITLE complement component C3 - Japanese lamprey (fragment)
ORGANISM #formal_name Lampetra japonica #common_name Japanese lamprey
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Aug-1998

ACCESSIONS 150806
REFERENCE 150806
#authors Nonaka, M.; Takahashi, M.
#journal J. Immunol. (1992) 148:3290-3295
#title Complete complementary DNA sequence of the third component of complement of lamprey; implication for the evolution of thioester containing protein.

#cross-references MUID:92251197
#accession 150806
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-1673 ##label NON
#cross-references GB:D10087; NID:9222887; PID:9222888
CLASSIFICATION #superfamily alpha-2-macroglobulin
SUMMARY #length 1673 #checksum 8983

Query Match 73.4%; Score 47; DB 2; Length 1673;
Best Local Similarity 75.0%; Pred. No. 1.32e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 443 OKYASAY 450
|||:||||
OY 1 OKYNSAPY 8

RESULT 11
ENTRY JC5632 #type complete
TITLE hemocyanin dioxygen-binding functional unit - grosse
ORGANISM #formal_name Rapana thomasiانا #common_name grosse
DATE 27-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 07-Nov-1997

ACCESSIONS JC5632
REFERENCE JC5632
#authors Stoeva, S.; Idakieva, K.; Genov, N.; Voelker, W.
#journal Biochem. Biophys. Res. Commun. (1997) 238:403-410
#title Complete amino acid sequence of dioxygen-binding functional unit of the Rapana thomasianna hemocyanin.

#accession JC5632
#molecule_type protein
#residues 1-407 ##label SNO
SUMMARY #length 407 #molecular-weight 46755 #checksum 3652

Query Match 71.9%; Score 46; DB 2; Length 407;
Best Local Similarity 55.6%; Pred. No. 2.08e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 216 OKYGLPYD 224
|||:||||
OY 1 OKYNSAPYN 9

RESULT 12
ENTRY I39956 #type complete
TITLE neutral proteinase (EC 3.4.24.-) - Bacillus amyloliquefaciens
ORGANISM #formal_name Bacillus amyloliquefaciens
DATE 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 18-Mar-1997

ACCESSIONS I39956
REFERENCE I39956
#authors Shimada, H.; Honjo, M.; Mita, I.; Nakayama, A.; Akaoka, A.; Mandae, K.; Furutani, Y.
#journal J. Biotechnol. (1985) 2:75-85
#title The nucleotide sequence and some properties of the neutral protease gene of Bacillus amyloliquefaciens.

#accession I39956
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-521 ##label RES
#cross-references GB:M36723; NID:9143352; PID:9143353

GENETICS #start_codon GTG
CLASSIFICATION #superfamily thermolysin
KEYWORDS hydrolase; metalloproteinase
SUMMARY #length 521 #molecular-weight 56725 #checksum 6816

Query Match 71.9%; Score 46; DB 2; Length 521;
Best Local Similarity 55.6%; Pred. No. 2.08e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 308 OKYNSPYD 316
|||:||||
OY 1 OKYNSAPYN 9

RESULT 13
ENTRY S12320 #type complete
TITLE PRP9 protein - yeast (Saccharomyces cerevisiae) (strain S288C)
ORGANISM #formal_name Saccharomyces cerevisiae
#variety strain S288C
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 06-Feb-1998

ACCESSIONS S12320; S67563
REFERENCE S12319
#authors Legrain, P.; Choulika, A.
#journal EMBO J. (1990) 9:2775-2781
#title The molecular characterization of PRP6 and PRP9 yeast genes reveals a new cysteine/histidine motif common to several splicing factors.

#cross-references MUID:90360988
#accession S12320
#molecule_type DNA
#residues 1-530 ##label LEG
#cross-references EMBL:X53466; NID:94240; PID:94241
#experimental_source strain S288C

REFERENCE S67560
#authors Paulin, L.; Saren, A.M.; Laananen, P.
#submission submitted to the Protein Sequence Database, July 1996
#accession S67563
#molecule_type DNA
#residues 1-530 ##label PAU
#cross-references EMBL:Z74078; NID:91431007; PID:e253198; PID:91431008; MIPS:YDL030v
#experimental_source strain S288C

GENETICS #gene SCD:PRP9
#cross-references SGD:S0002188; MIPS:YDL030v
#map_position 4L
KEYWORDS nucleus; RNA binding; zinc finger
SUMMARY #length 530 #molecular-weight 63029 #checksum 402

Query Match 71.9%; Score 46; DB 2; Length 530;
Best Local Similarity 44.4%; Pred. No. 2.08e+01;

Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 359 QKXEAAPYD 367

QY 1 QKXNSAPYN 9

RESULT 14

ENTRY B64138 #type complete
TITLE uridylyltransferase homolog - Haemophilus influenzae (strain Rd KW20)

ORGANISM #formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998

ACCESSIONS
REFERENCE

#authors

A64000
B64138
Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirsness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, J.L.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
#cross-references MUID:95350630

#accession B64138

##status nucleic acid sequence not shown; translation not shown

##molecule_type DNA

##residues 1-863 #label TIGR

##cross-references GB:U32844; GB:L42023; NID:g1574563; PID:g1574572;

TIGR:HI1719

CLASSIFICATION #superfamily uridylyltransferase

SUMMARY #length 863 #molecular_weight 100172 #checksum 231

Query Match 71.9%; Score 46; DB 2; Length 863;
Best Local Similarity 44.4%; Pred. No. 2.08e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 185 QRYHNTAYN 193

QY 1 QKXNSAPYN 9

RESULT 15

ENTRY S43196 #type complete
TITLE uridylyltransferase (EC 2.7.7.59) - Klebsiella pneumoniae

ALTERNATE_NAMES PII-uridylyltransferase

ORGANISM #formal_name Klebsiella pneumoniae

DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Sep-1998

ACCESSIONS S43196

REFERENCE S43196

#journal Edwards, R.; Merrick, M.

#title Mol. Gen. Genet. (1995) 247:189-198

The role of uridylyltransferase in the control of Klebsiella pneumoniae nif gene regulation.

#cross-references MUID:95272528

#accession S43196

##status preliminary

##molecule_type DNA

##residues 1-887 #label ED2

##cross-references EMBL:X78685; NID:g470138; PID:g470140

GENETICS

KEYWORDS

gene glnd
#superfamily uridylyltransferase
nucleotidyltransferase

SUMMARY #length 887 #molecular_weight 102343 #checksum 41

Query Match 71.9%; Score 46; DB 2; Length 887;

Best Local Similarity 44.4%; Pred. No. 2.08e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

DB 203 QRYHGTSYN 211

QY 1 QKXNSAPYN 9

Search completed: Thu Sep 2 11:50:13 1999
Job time : 16 secs.

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Sep 2 11:51:40 1999; M\$Par time 1.35 Seconds
Regular output not generated. 67.800 Million cell updates/sec

Scoring table: PAM 150

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

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Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1
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Statistics: Mean 14.636; Variance 44.740; scale 0.327

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Test No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	47	73.4	107	3	PCT-US55-0		Sequence 87, Applicat1	5.09e+01
2	47	73.4	107	3	PCT-US55-0		Sequence 82, Applicat1	5.09e+01
3	47	73.4	107	3	PCT-US55-0		Sequence 84, Applicat1	5.09e+01
4	47	73.4	107	2	US-08-899-		Sequence 82, Applicat1	5.09e+01
5	47	73.4	107	1	US-08-8776-		Sequence 84, Applicat1	5.09e+01
6	47	73.4	107	1	US-08-899-		Sequence 82, Applicat1	5.09e+01
7	47	73.4	107	2	US-08-899-		Sequence 82, Applicat1	5.09e+01
8	47	73.4	107	2	US-08-899-		Sequence 84, Applicat1	5.09e+01
9	47	73.4	107	2	US-08-899-		Sequence 84, Applicat1	5.09e+01
10	47	73.4	107	2	US-08-899-		Sequence 87, Applicat1	5.09e+01
11	47	73.4	107	2	US-08-899-		Sequence 87, Applicat1	5.09e+01
12	47	73.4	107	1	US-08-8776-		Sequence 87, Applicat1	5.09e+01
13	47	73.4	243	1	US-08-8726-		Sequence 6, Applicatio	5.09e+01
14	47	73.4	243	1	US-08-8726-		Sequence 6, Applicatio	5.09e+01
15	47	73.4	243	3	PCT-US54-0		Sequence 6, Applicatio	5.09e+01
16	47	73.4	590	1	US-08-8726-		Sequence 8, Applicatio	5.09e+01
17	47	73.4	590	1	US-08-8726-		Sequence 8, Applicatio	5.09e+01
18	47	73.4	590	3	PCT-US54-0		Sequence 8, Applicatio	5.09e+01
19	47	73.4	643	1	US-08-8726-		Sequence 10, Applicat1	5.09e+01
20	47	73.4	643	1	US-08-8726-		Sequence 10, Applicat1	5.09e+01
21	47	73.4	644	3	PCT-US54-0		Sequence 10, Applicat1	5.09e+01
22	47	73.4	644	3	US-08-8726-		Sequence 2, Applicatio	5.09e+01
23	47	73.4	644	1	US-08-8726-		Sequence 2, Applicatio	5.09e+01

[illegible]

ALIGNMENTS

RESULT	ID	PCT-US95-08743-87	STANDARD;	PRT:	107 AA.
XX	AC	xxxxxx			
XX	D7				
XX	DE	Sequence 87, Application PC/TUS9508743			
CC	CC	Sequence 87, Application PC/TUS9508743			
CC	CC	GENERAL INFORMATION:			
CC	CC	APPLICANT:			
CC	CC	TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES			
CC	CC	TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS			
CC	CC	NUMBER OF SEQUENCES: 170			
CC	CC	COMPUTER READABLE FORM:			
CC	CC	MEDIUM TYPE: Floppy disk			
CC	CC	COMPUTER: IBM PC compatible			
CC	CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	CC	SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)			
CC	CC	CURRENT APPLICATION DATA:			
CC	CC	APPLICATION NUMBER: PCT/US95/08743			
CC	CC	FILING DATE: 11-JUL-1995			
CC	CC	PRIOR APPLICATION DATA:			
CC	CC	APPLICATION NUMBER: US 08/276,852			
CC	CC	FILING DATE: 18-JUL-1994			
CC	CC	INFORMATION FOR SEQ ID NO: 87:			
CC	CC	SEQUENCE CHARACTERISTICS:			
CC	CC	LENGTH: 107 amino acids			
CC	CC	TYPE: amino acid			
CC	CC	TOPOLOGY: linear			
CC	CC	MOLECULE TYPE: protein			
SQ	SEQ	SEQUENCE 107 AA; 11654 MW; 62438 CN;			
	DB	Query Match	73.4%;	Score 47;	DB 3;
	QY	Best Local Similarity 62.5%;		Pred. No. 5.09e+01;	Length 107;
		Matches 5;	Conservative 2;	Mismatches 1;	Indels 0;
					Gaps 0;
	DB	88 QQHSSPY 95			
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	QY	1 QKYNASPY 8			
RESULT	ID	PCT-US95-08743-82	STANDARD;	PRT:	107 AA.
XX	AC	xxxxxx			

XX DE Sequence 82, Application PC/TUS9508743
XX CC Sequence 82, Application PC/TUS9508743
XX CC GENERAL INFORMATION:
XX CC APPLICANT:
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US95/08743
XX CC FILING DATE: 11-JUL-1995
XX CC PRIORITY APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC INFORMATION FOR SEQ ID NO: 82:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 107 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 107 AA: 11570 MW: 65513 CN;
SO
DB 87 QKYNAP 93
OY 1 QKYNAP 7
RESULT 3
ID PCT-US95-08743-84 STANDARD: PRT: 107 AA.
XX AC xxxxxx
XX DT
XX DT
XX DE Sequence 84, Application PC/TUS9508743
XX CC Sequence 84, Application PC/TUS9508743
XX CC GENERAL INFORMATION:
XX CC APPLICANT:
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US95/08743
XX CC FILING DATE: 11-JUL-1995
XX CC PRIORITY APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC INFORMATION FOR SEQ ID NO: 84:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 107 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 107 AA: 11532 MW: 65997 CN;
SO

XX DE Query Match 73.4%; Score 47; DB 3; Length 107;
XX CC Best Local Similarity 100.0%; Pred. No. 5.09e+01;
XX CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 87 QKYNAP 93
OY 1 QKYNAP 7
RESULT 4
ID US-08-899-575-82 STANDARD: PRT: 107 AA.
XX AC xxxxxx
XX DT
XX DT
XX DE Sequence 82, Application US/08899575
XX CC Sequence 82, Application US/08899575
XX CC Patent No. 5804440
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Burton, Dennis R
XX CC APPLICANT: Barbas, Carlos F
XX CC APPLICANT: Letner, Richard A
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: The Scripps Research Institute, Office of
XX CC ADDRESSEE: Patent Counsel
XX CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
XX CC CITY: La Jolla
XX CC STATE: CA
XX CC COUNTRY: USA
XX CC ZIP: 92037
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patentin Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/899,575
XX CC FILING DATE: 24-JUL-1997
XX CC CLASSIFICATION:
XX CC PRIORITY APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC APPLICATION NUMBER: US 08/178,302
XX CC FILING DATE: 30-SEP-1993
XX CC PRIORITY APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/954,148
XX CC FILING DATE: 30-SEP-1992
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Fitting, Thomas
XX CC REGISTRATION NUMBER: 34,163
XX CC REFERENCE/DOCKET NUMBER: SCR1452P
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 619-554-2937
XX CC TELEFAX: 619-554-6312
XX CC INFORMATION FOR SEQ ID NO: 82:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 107 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 107 AA: 11570 MW: 65513 CN;
SO
DB 87 QKYNAP 93
OY 1 QKYNAP 7
RESULT 4
ID US-08-899-575-82 STANDARD: PRT: 107 AA.
XX AC xxxxxx
XX DT
XX DT
XX DE Query Match 73.4%; Score 47; DB 2; Length 107;
XX CC Best Local Similarity 100.0%; Pred. No. 5.09e+01;
XX CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 87 QKYNAP 93
OY 1 QKYNAP 7
RESULT 4
ID US-08-899-575-82 STANDARD: PRT: 107 AA.
XX AC xxxxxx
XX DT
XX DT
XX DE Sequence 82, Application US/08899575
XX CC Sequence 82, Application US/08899575
XX CC Patent No. 5804440
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Burton, Dennis R
XX CC APPLICANT: Barbas, Carlos F
XX CC APPLICANT: Letner, Richard A
XX CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
XX CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
XX CC NUMBER OF SEQUENCES: 170
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: The Scripps Research Institute, Office of
XX CC ADDRESSEE: Patent Counsel
XX CC STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
XX CC CITY: La Jolla
XX CC STATE: CA
XX CC COUNTRY: USA
XX CC ZIP: 92037
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patentin Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/899,575
XX CC FILING DATE: 24-JUL-1997
XX CC CLASSIFICATION:
XX CC PRIORITY APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/276,852
XX CC FILING DATE: 18-JUL-1994
XX CC APPLICATION NUMBER: US 08/178,302
XX CC FILING DATE: 30-SEP-1993
XX CC PRIORITY APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/954,148
XX CC FILING DATE: 30-SEP-1992
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Fitting, Thomas
XX CC REGISTRATION NUMBER: 34,163
XX CC REFERENCE/DOCKET NUMBER: SCR1452P
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 619-554-2937
XX CC TELEFAX: 619-554-6312
XX CC INFORMATION FOR SEQ ID NO: 82:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 107 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC MOLECULE TYPE: protein
XX CC SEQUENCE 107 AA: 11570 MW: 65513 CN;
SO

OY 1 OKYNSAP 7

RESULT 5 STANDARD: PRT: 107 AA.

AC XXXXX

DE Sequence 84, Application US/08276852

CC Sequence 84, Application US/08276852

CC Patent No. 5652138

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R

CC APPLICANT: Barbas, Carlos F

CC APPLICANT: Lerner, Richard A

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC NUMBER OF SEQUENCES: 170

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute, Office of

CC ADDRESSEE: Patent Counsel

CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

CC STREET: Mail Drop TPC8

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276,852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCRI452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 84:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 107 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 107 AA; 11532 MW; 65997 CN;

Query Match 73.4%; Score 47; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 5.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 OKYNSAP 93

OY 1 OKYNSAP 7

RESULT 6 STANDARD: PRT: 107 AA.

ID US-08-276-852-82

AC XXXXX

DE Sequence 82, Application US/08276852

CC Sequence 82, Application US/08276852

CC Patent No. 5652138

CC GENERAL INFORMATION:

CC APPLICANT: Burton, Dennis R

CC APPLICANT: Barbas, Carlos F

CC APPLICANT: Lerner, Richard A

CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC NUMBER OF SEQUENCES: 170

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: The Scripps Research Institute, Office of

CC ADDRESSEE: Patent Counsel

CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,

CC STREET: Mail Drop TPC8

CC CITY: La Jolla

CC STATE: CA

CC COUNTRY: USA

CC ZIP: 92037

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: IBM PC compatible

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/276,852

CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US 08/178,302

CC FILING DATE: 30-SEP-1993

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Fitting, Thomas

CC REGISTRATION NUMBER: 34,163

CC REFERENCE/DOCKET NUMBER: SCRI452P

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312

CC INFORMATION FOR SEQ ID NO: 82:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 107 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 107 AA; 11570 MW; 65513 CN;

Query Match 73.4%; Score 47; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 5.09e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 OKYNSAP 93

OY 1 OKYNSAP 7

RESULT 7 STANDARD: PRT: 107 AA.

ID US-08-899-575-82

Sequence 82, Application US/08899575
Sequence 82, Application US/08899575

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CC PatentNo. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbos, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 82:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11570 MW; 65513 CN;
CC
CC Query Match 73.4%; Score 47; DB 2; Length 107;
CC Match Local Similarity 100.0%; Pred. NO. 5.09e+01;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 87 QKNSAP 93
CC |||||
CC 1 QKNSAP 7
CC
CC RESULT 8
CC ID US-08-899-575-84 STANDARD: PRT; 107 AA.
CC AC xxxxxx
CC DT
CC DE Sequence 84, Application US/08899575
CC XX
CC Sequence 84, Application US/08899575
CC Patent No. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbos, Carlos F
CC APPLICANT: Lerner, Richard A

```

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CC CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC CC NUMBER OF SEQUENCES: 170
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: The Scripps Research Institute, Office of
CC CC ADDRESSEE: Patent Counsel
CC CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC CC STREET: Mail Drop TPC8
CC CC CITY: La Jolla
CC CC STATE: CA
CC CC COUNTRY: USA
CC CC ZIP: 92037
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/08/899,575
CC CC FILING DATE: 24-JUL-1997
CC CC CLASSIFICATION: 435
CC CC PRIORITY APPLICATION DATA:
CC CC APPLICATION NUMBER: US 08/276,852
CC CC FILING DATE: 18-JUL-1994
CC CC APPLICATION NUMBER: US 08/178,302
CC CC FILING DATE: 30-SEP-1993
CC CC PRIORITY APPLICATION DATA:
CC CC APPLICATION NUMBER: US 07/954,148
CC CC FILING DATE: 30-SEP-1992
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Fitting, Thomas
CC CC REGISTRATION NUMBER: 34,163
CC CC REFERENCE/DOCKET NUMBER: SCR1452P
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: 619-554-2937
CC CC TELEFAX: 619-554-6312
CC CC INFORMATION FOR SEQ ID NO: 84:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 107 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: Protein
CC CC SEQUENCE 107 AA; 11532 MW; 65997 CN;
SQ
Query Match 73.4%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 87 OKNSAP 93
QY 1 OKNSAP 7
RESULT 9
SD US-08-899-575-84 STANDARD; PRT; 107 AA.
XX xxxxxx
XX
DE Sequence 84, Application US/08899575
CC CC
CC CC Sequence 84, Application US/08899575
CC CC Patent No. 580440
CC CC GENERAL INFORMATION:
CC CC APPLICANT: Burton, Dennis R
CC CC APPLICANT: Barbas, Carlos F
CC CC APPLICANT: Ierner, Richard A
CC CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC CC NUMBER OF SEQUENCES: 170
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: The Scripps Research Institute, Office of

```

CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 84:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11532 MW; 65997 CN;
SQ

Query Match 73.4%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.09e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 87 QKYNAP 93
QY 1 QKYNAP 7
|111111|
|111111|
US-08-899-575-87 STANDARD; PRT; 107 AA.
XX
AC xxxxxx
XX
DE Sequence 87, Application US/08899575
XX
CC Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESS: Patent Counsel
CC STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC

CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ

Query Match 73.4%; Score 47; DB 2; Length 107;
Best Local Similarity 62.5%; Pred. No. 5.09e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 88 QYHSSPY 95
QY 1 QKYNAPY 8
|111111|
|111111|
US-08-899-575-87 STANDARD; PRT; 107 AA.
XX
AC xxxxxx
XX
DE Sequence 87, Application US/08899575
XX
CC Patent No. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESS: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ
Db 88 QOYHSPY 95
| | : | : | : |
QY 1 QKYSAPY 8
RESULT 12
ID US-08-276-852-87 STANDARD: PRT: 107 AA.
XX xxxxxx
DE
DT
DX
DE
XX
Sequence 87, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Ierner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994

CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ
Db 88 QOYHSPY 95
| | : | : | : |
QY 1 QKYSAPY 8
RESULT 13
ID US-08-021-608D-6 STANDARD: PRT: 243 AA.
XX xxxxxx
DE
DT
DX
DE
XX
Sequence 6, Application US/08021608D
Patent No. 5580760
GENERAL INFORMATION:
CC APPLICANT: LEVENS, DAVID L., DUNCAN,
CC APPLICANT: ROBERT C., AND AVIGAN, MARK I.
CC TITLE OF INVENTION: NOVEL FUSE BINDING
CC TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: MORGAN & FINNEGAN
CC STREET: 345 PARK AVENUE
CC CITY: NEW YORK
CC STATE: NEW YORK
CC COUNTRY: USA
CC ZIP: 10154
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC COMPATIBLE
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/021,608D
CC FILING DATE: 22-FEB-1993
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILLIAM S. FEILER
CC REGISTRATION NUMBER: 26,728
CC REFERENCE/DOCKET NUMBER: 2026-4063
CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (212) 758-4800
CC TELEFAX: (212) 751-6849
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 243
CC TYPE: Amino Acid
CC STRANDEDNESS: Single
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: Peptide/Protein
CC HYPOTHETICAL: No
CC ORIGINAL SOURCE:
CC ORGANISM: Human
CC CELL TYPE: HL60
CC SEQUENCE 243 AA; 25407 MW; 306126 CN;

Query Match 73.4%; Score 47; DB 1; Length 243;
Best Local Similarity 85.7%; Pred. No. 5.09e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

207 YNPAPYN 213
11:1111
3 YNSAPYN 9

RESULT 14
ID US-08-726-160-6 STANDARD; PRT; 243 AA.
XX xxxxxx

Sequence 6, Application US/08726160
Patent No. 5734016
GENERAL INFORMATION:
CC APPLICANT: LEVENS, DAVID L., DUNCAN,
CC APPLICANT: ROBERT C., AND AVIGAN, MARK I.
CC TITLE OF INVENTION: NOVEL FUSE BINDING
CC TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: MORGAN & FINNEGAN
CC STREET: 345 PARK AVENUE
CC CITY: NEW YORK
CC STATE: NEW YORK
CC COUNTRY: USA
CC ZIP: 10154
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: FLOPPY DISK
CC COMPUTER: IBM PC COMPATIBLE
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/726,160
CC FILING DATE: 04-OCT-1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/021,608
CC FILING DATE: 22-FEB-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILLIAM S. FEILER
CC REGISTRATION NUMBER: 26,728
CC REFERENCE/DOCKET NUMBER: 2026-4063US1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 758-4800
CC TELEFAX: (212) 751-6849
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 243
CC TYPE: Amino Acid
CC STRANDEDNESS: Single

CC TOPOLOGY: Unknown
CC MOLECULE TYPE: Peptide/Protein
CC HYPOTHETICAL: No
CC ORIGINAL SOURCE:
CC ORGANISM: Human
CC CELL TYPE: HL60
CC SEQUENCE 243 AA; 25407 MW; 306126 CN;

Query Match 73.4%; Score 47; DB 1; Length 243;
Best Local Similarity 85.7%; Pred. No. 5.09e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

207 YNPAPYN 213
11:1111
3 YNSAPYN 9

RESULT 15
ID PCT-US94-01782-6 STANDARD; PRT; 243 AA.
XX xxxxxx

Sequence 6, Application PC/TUS9401782
GENERAL INFORMATION:
CC APPLICANT: THE GOVERNMENT OF THE UNITED STATES
CC APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
CC APPLICANT: HEALTH AND HUMAN SERVICES
CC TITLE OF INVENTION: NOVEL FUSE BINDING
CC TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
CC NUMBER OF SEQUENCES: 10
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: MORGAN & FINNEGAN
CC STREET: 345 PARK AVENUE
CC CITY: NEW YORK
CC STATE: NEW YORK
CC COUNTRY: USA
CC ZIP: 10154
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: FLOPPY DISK
CC COMPUTER: IBM PC COMPATIBLE
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01782
CC FILING DATE: 22-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: U.S. 08/021,608
CC FILING DATE: 22-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILLIAM S. FEILER
CC REGISTRATION NUMBER: 26,728
CC REFERENCE/DOCKET NUMBER: 2026-4063PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 758-4800
CC TELEFAX: (212) 751-6849
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 243
CC TYPE: Amino Acid
CC STRANDEDNESS: Single
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: Peptide/Protein
CC HYPOTHETICAL: No
CC ORIGINAL SOURCE:
CC ORGANISM: Human
CC STRAIN:
CC INDIVIDUAL ISOLATE:
CC DEVELOPMENTAL STAGE:

CC HAPLOTYPE:
 CC TISSUE TYPE:
 CC CELL TYPE: HL60
 CC CELL LINE:
 CC ORGANELLE:
 CC FEATURE:
 CC NAME/KEY:
 CC LOCATION:
 CC IDENTIFICATION METHOD:
 CC OTHER INFORMATION:
 SQ SEQUENCE 243 AA; 25407 MW; 306126 CN;

Query Match 73.4%; Score 47; DB 3; Length 243;
 Best Local Similarity 85.7%; Pred. No. 5.09e+01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 207 YNPAPYN 213
 07 11:1111
 3 YNSAPYN 9

Search completed: Thu Sep 2 11:51:47 1999
 Job time : 7 secs.

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 100.0% Score 64; DB 27; Length 9;
 Best Local Similarity 100.0% Pred. No. 1.33e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynsapy 9
 |||||
 QY 1 QKYNsAPYN 9

W2570 standard; peptide: 9 AA.
 W2570:
 19-MAR-1998 (first entry)
 Anti-TNF-alpha antibody light chain CDR3.

Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 light chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.

OS Homo sapiens.
 PN WO9729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DV, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakoraitas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

Claim 20; Page 67; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, malignancy, uveitis or nephrotic
 syndrome, infectious diseases, inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 92.2% Score 59; DB 27; Length 9;
 Best Local Similarity 100.0% Pred. No. 5.10e+00;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 qkynsapy 8
 |||||
 QY 1 QKYNsAPY 8

W2579 standard; peptide: 9 AA.
 W2579:
 19-MAR-1998 (first entry)
 Anti-TNF-alpha antibody light chain CDR3.

Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 light chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.

OS Homo sapiens.
 PN WO9729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DV, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankevich JA, McGuinness BT, Roberts AJ, Sakoraitas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.

High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer

Claim 20; Page 70; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 less and has a Koff rate constant of 1x10 power -3 s power -1 or
 less (both determined by surface plasmon resonance), and
 neutralises human TNF-alpha cytotoxicity in a standard in vitro
 L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 inhibits TNF-alpha activity, can be used to treat sepsis,
 autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 sclerosis, autoimmune diabetes, malignancy, uveitis or nephrotic
 syndrome, infectious diseases, inflammatory bone disorders, bone resorption disease,
 alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 burns, reperfusion injury, keloid formation, scar tissue formation,
 pyrexia, periodontal disease, obesity and radiation toxicity. The
 Ab also inhibits TNF-alpha induced expression of endothelial cell
 leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 92.2% Score 59; DB 27; Length 9;
 Best Local Similarity 88.9% Pred. No. 5.10e+00;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapy 9
 |||||
 QY 1 QKYNsAPYN 9

W2576 standard; peptide: 9 AA.
 W2576:
 19-MAR-1998 (first entry)
 Anti-TNF-alpha antibody light chain CDR3.

Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 light chain; complementarity determining region 3; inhibition;
 treatment; sepsis; disease; autoimmune disease; infectious disease;
 malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 cardiac disorder; inflammatory bone disorder; reperfusion injury;
 bone resorption disease; coagulation disturbance; burn; ELAM-1;
 keloid formation; scar tissue formation; pyrexia; HUVEC;
 periodontal disease; obesity; radiation toxicity;
 endothelial cell leukocyte adhesion molecule-1;
 human umbilical vein endothelial cell.

KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; pyrexia; HIVEC;
 KW keloid formation; scar tissue formation; burn; ELAM-1;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 CC Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 92.28; Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.10e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 qkynsapy 8
 1 | | | | | | | |
 1 QKYNsAPY 8

RESULT 5
 ID W2574 standard; peptide: 9 AA.
 AC W2574;
 DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 CC Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 CC Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ

Query Match 92.28; Score 59; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.10e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 qkynsapy 8
 1 | | | | | | | |
 1 QKYNsAPY 8

RESULT 6
 ID W2573 standard; peptide: 9 AA.
 AC W2573;
 DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PE 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PS 09-FEB-1996; US-599226.
 PA (BAD1) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 CC TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 CC Claim 20; Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC Sequence 9 AA:
 SQ

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralizes human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).

Sequence 9 AA:

Query Match 85.9%; Score 55; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.47e+01;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysapy 8
| | | | |
QY 1 QKNSAPY 8

RESULT 7
ID W27582 standard; peptide; 9 AA.

AC W27582;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997; 002219.

PR 25-NOV-1996; US-031476.

PS 09-FEB-1996; US-599226.

PT High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 71; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralizes human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).

Sequence 9 AA:

Query Match 85.9%; Score 55; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysapy 8
| | | | |
QY 1 QKNSAPY 8

RESULT 8
ID W27575 standard; peptide; 9 AA.

AC W27575;

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3; light chain; complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN WO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997; 002219.

PR 25-NOV-1996; US-031476.

PS 09-FEB-1996; US-599226.

PT High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 69; 102pp; English.

CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralizes human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).

Sequence 9 AA:

Query Match 84.4%; Score 54; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.91e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysapy 8
| | | | |
QY 1 QKNSAPY 8

RESULT 9

ID W27571 standard; peptide: 9 AA.

AC W27571;

DE 19-MAR-1998 (first entry)

DT Anti-TNF-alpha antibody light chain CDR3.

DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN MO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PR 09-FEB-1996: US-599226.

PA (BABI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,

PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 68; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

SO Sequence 9 AA;

Query Match 84.4%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.91e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkytasy 8
 ||| |||
 QY 1 OKYNSAPY 8

RESULT 10
 ID W27578 standard; peptide: 9 AA.

AC W27578;

DE 19-MAR-1998 (first entry)

DT Anti-TNF-alpha antibody light chain CDR3.

DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN MO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PR 09-FEB-1996: US-599226.

PA (BABI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,

PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 70; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

SO Sequence 9 AA;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN MO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PR 09-FEB-1996: US-599226.

PA (BABI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,

PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 70; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

SO Sequence 9 AA;

Query Match 84.4%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.91e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gkytasy 8
 ||| |||
 QY 1 OKYNSAPY 8

RESULT 11
 ID W27580 standard; peptide: 9 AA.

AC W27580;

DE 19-MAR-1998 (first entry)

DT Anti-TNF-alpha antibody light chain CDR3.

DE Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain: complementarity determining region 3; inhibition;

KW treatment; sepsis; disease; autoimmune disease; infectious disease;

KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;

KW cardiac disorder; inflammatory bone disorder; reperfusion injury;

KW bone resorption disease; coagulation disturbance; burn; ELAM-1;

KW keloid formation; scar tissue formation; pyrexia; HUVEC;

KW periodontal disease; obesity; radiation toxicity;

KW endothelial cell leukocyte adhesion molecule-1;

KW human umbilical vein endothelial cell.

OS Homo sapiens.

PN MO9729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PR 09-FEB-1996: US-599226.

PA (BABI) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,

PI Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

PI WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20; Page 70; 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis

CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and

CC neutralises human TNF-alpha cytotoxicity in a standard in vitro

CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,

CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid

CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,

CC alcoholic, viral or fulminant hepatitis, coagulation disturbance,

CC burns, reperfusion injury, keloid formation, scar tissue formation,

CC pyrexia, periodontal disease, obesity and radiation toxicity. The

CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

CC endothelial cells (HUVEC).

SO Sequence 9 AA;

PI Salfield JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 CC High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 71; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 82.8%; Score 53; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.48e+01;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysaays 9
 |||||:
 QY 1 OKVNSAPYN 9

RESULT 12
 ID W27583 standard; peptide; 9 AA.
 AC W27583;

DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PI Salfield JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 72; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 79.7%; Score 51; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 4.15e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysapy 8
 |||||:
 QY 1 OKVNSAPY 8

RESULT 13
 ID W27562 standard; peptide; 9 AA.
 AC W27562;

DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PI Salfield JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9: Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell

FT Key location/Qualifiers
 FT Misc-difference 9 /label- Thr, Ala
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADT) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9: Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell

CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 79.7%: Score 51; DB 27; Length 9;
Best Local Similarity 75.0%: Pred. No. 4.15e+01;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 grynary 8
1:11111
QY 1 OKYNSAPY 8

RESULT 14
ID W27584 standard; peptide; 9 AA.
AC W27584;

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
KW Homo sapiens.
PN W09729131-AL.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
DR WPI; 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity; e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 72; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholism, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 79.7%: Score 51; DB 27; Length 9;
Best Local Similarity 75.0%: Pred. No. 4.15e+01;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 grynary 8
1:11111
QY 1 OKYNSAPY 8

RESULT 15
ID W27585 standard; peptide; 9 AA.
AC W27585;

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
KW Homo sapiens.
PN W09729131-AL.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Manovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Willton AJ;
DR WPI; 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity; e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 72; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholism, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 79.7%: Score 51; DB 27; Length 9;
Best Local Similarity 75.0%: Pred. No. 4.15e+01;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 grynary 8
1:11111
QY 1 OKYNSAPY 8

Search completed: Thu Sep 2 11:49:40 1999
Job time : 19 secs.

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MARCH 1999 protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 11:52:54 1999; Maspar time 3.73 Seconds
51.313 Million cell updates/sec

Molecular output not generated.

Title: >US-08-599-226-19
Description: (1-9) from US08599226.pep
Perfect Score: 64
Sequence: 1 OKYSAPYR 9
Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a.genseq35
1:part1 2:part3 3:part4 4:part5 5:part6 6:part7 7:part8
8:part9 9:part10 11:part12 13:part13
14:part15 15:part16 17:part18 18:part19
19:part20 21:part22 23:part24
24:part25 26:part27 27:part28
29:part30 31:part32 33:part33
34:part34 35:part36 37:part38
39:part39

Statistics: Mean 15.783; Variance 48.977; scale 0.322

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	64	100.0	9 27	W27578	Anti-TNF-alpha antibo	1.99e+00
2	61	95.3	9 27	W27573	Anti-TNF-alpha antibo	4.35e+00
3	59	92.2	9 27	W27574	Anti-TNF-alpha antibo	7.35e+00
4	56	87.5	9 27	W27583	Anti-TNF-alpha antibo	7.28e+00
5	55	85.9	9 27	W27570	Anti-TNF-alpha antibo	1.57e+01
6	54	84.4	9 27	W27582	Anti-TNF-alpha antibo	2.02e+01
7	54	84.4	9 27	W27577	Anti-TNF-alpha antibo	2.60e+01
8	54	84.4	9 27	W27576	Anti-TNF-alpha antibo	2.60e+01
9	54	84.4	9 27	W27575	Anti-TNF-alpha antibo	2.60e+01
10	52	81.3	9 27	W27572	Anti-TNF-alpha antibo	4.28e+01
11	51	79.7	9 27	W27584	Anti-TNF-alpha antibo	5.49e+01
12	51	79.7	9 27	W27571	Anti-TNF-alpha antibo	5.49e+01
13	51	79.7	9 27	W27568	Anti-TNF-alpha antibo	5.49e+01
14	49	76.6	9 27	W27580	Anti-TNF-alpha antibo	8.98e+01
15	49	76.6	9 27	W27579	Anti-TNF-alpha antibo	8.98e+01
16	49	76.6	129 7	R38672	VK325-Jk2.	8.98e+01

17	48	75.0	9 27	W27585	Anti-TNF-alpha antibo	1.15e+02
18	48	75.0	107 28	W31726	Alpha light chain ami	1.15e+02
19	48	75.0	533 9	R44617	Human retinol binding	1.15e+02
20	47	73.4	9 23	W24551	CCR #3 of r101-2 ligh	1.46e+02
21	47	73.4	107 19	W01266	VL region of HIV neut	1.46e+02
22	47	73.4	107 19	R54308	Anti-HIV gp120 immuno	1.46e+02
23	47	73.4	108 19	W01278	VL region of HIV neut	1.46e+02
24	47	73.4	108 10	R54316	Anti-HIV gp120 immuno	1.46e+02
25	47	73.4	124 23	W24539	Immunoglobulin r101-2	1.46e+02
26	47	73.4	144 2	R06431	N-terminal of SPI-1ix	1.46e+02
27	47	73.4	360 13	R75006	Tomato S-adenosyl-met	1.46e+02
28	47	73.4	419 2	R06428	SP1-like protein enco	1.46e+02
29	47	73.4	426 3	R12458	Pregnancy-specific be	1.46e+02
30	47	73.4	428 7	R35208	Sequence of human tro	1.46e+02
31	47	73.4	2251 14	R71009	Human neuronal calciu	1.46e+02
32	47	73.4	2270 14	R71010	Human neuronal calciu	1.46e+02
33	47	73.4	2270 14	R69604	Calcium channel alpha	1.46e+02
34	46	71.9	9 27	W27562	Anti-TNF-alpha antibo	1.86e+02
35	46	71.9	109 10	R50218	HSV glycoprotein F bl	1.86e+02
36	46	71.9	653 33	W69845	Amino acid sequence o	2.35e+02
37	45	70.3	92 39	W95480	Mouse derived RT3 pha	2.35e+02
38	45	70.3	92 39	W95476	Mouse derived RT3 pha	2.35e+02
39	45	70.3	109 9	R47041	Sequence of the conse	2.35e+02
40	45	70.3	145 39	W87593	Antibody 11D10 light	2.35e+02
41	45	70.3	153 13	R77307	Mouse monoclonal anti	2.35e+02
42	45	70.3	540 17	R96102	Hepatitis E virus (ME	2.35e+02
43	45	70.3	660 3	R14619	Protein encoded by OR	2.35e+02
44	45	70.3	660 37	W81520	Hepatitis E virus (HE	2.35e+02
45	45	70.3	808 25	W32911	Castor bean phospholi	2.35e+02

ALIGNMENTS

RESULT 1
ID W27578 standard; peptide: 9 AA.
AC W27578;

DE 19-MAR-1998 (first entry)
KW Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha; antitumor; light chain; complementarity determining region 3; inhibition; treatment; sepsis; disease; autoimmune disease; infectious disease; malignancy; pulmonary disorder; intestinal disorder; hepatitis; cardiac disorder; inflammatory bone disorder; reperfusion injury; bone resorption disease; coagulation disturbance; burn; ELAM-1; keloid formation; scar tissue formation; pyrexia; HIVEC; peridontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN MO9729131-A1.
PD 14-ARG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BAD) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B, Mankevich JA, McGuinness BT, Roberts AJ, Sakorafas F, Salfield UG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 100.0% Score 64; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.99e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|||||
 QY 1 QKTSAPPT 9

RESULT 2
 W2573 standard; peptide: 9 AA.

AC W2573:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Seifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 68; 102pp; English.
 The present sequence is a novel anti-human tumour necrosis
 factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 95.3% Score 61; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.35e+00;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 qkysappt 9
 |||:|||||
 QY 1 QKTSAPPT 9

RESULT 3
 W2574 standard; peptide: 9 AA.

AC W2574:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-AL.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Seifeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 CC Sequence 9 AA:

Query Match 92.2% Score 59; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.28e+00;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkysappt 9
 |||:|||||
 QY 1 QKTSAPPT 9

RESULT 4
 W2583 standard; peptide: 9 AA.

AC W2583:
 DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious diseases;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: 002219.
 PR 25-NOV-1996: US-031476.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20, Page 72: 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 CC Sequence 9 AA:
 SQ

Query Match 92.2% Score 59; DB 27; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.28e+00; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1;

1 qkyisapyt 9
 ||| |||||
 1 OKYTSAPYT 9

RESULT 5
 ID W27570 standard; peptide: 9 AA.
 AC W27570:
 DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: 002219.

PR 25-NOV-1996: US-031476.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20, Page 67: 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEC).
 CC Sequence 9 AA:
 SQ

Query Match 87.5% Score 56; DB 27; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.57e+01; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1;

1 qkyusapya 9
 ||| |||||
 1 OKYTSAPYT 9

RESULT 6
 ID W27582 standard; peptide: 9 AA.
 AC W27582:
 DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody light chain CDR3.
 KM Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: 002219.
 PR 25-NOV-1996: US-031476.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 PI WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 Claim 20, Page 71: 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 85.9%; Score 55; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 2.02e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkynsapyt 9
||| |||
Qy 1 OKYNSAPYT 9

RESULT 7
ID W2577 standard; peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha: TNF-alpha: antibody: CDR3:
KW light chain: complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PS 09-FEB-1996; US-599226.
(BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 70; 102pp: English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).

CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 84.4%; Score 54; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 2.60e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapyt 8
||| |||
Qy 1 OKYNSAPY 8

RESULT 8
ID W2576 standard; peptide; 9 AA.

DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha: TNF-alpha: antibody: CDR3:
KW light chain: complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN WO9729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PS 09-FEB-1996; US-599226.
(BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 69; 102pp: English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).

Query Match 84.4%; Score 54; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 2.60e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 qkynsapyt 8
||| |||
Qy 1 OKYNSAPY 8

RESULT 9
ID W27575 standard; peptide; 9 AA.
AC W27575;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha: antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI: 97-415302/38.
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 69; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
CC Sequence 9 AA:
SO

Query Match 84.4%; Score 54; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 2,60e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkyrpyt 9
||| |||
Oy 1 OKYTSAPYT 9

RESULT 10
ID W27572 standard; peptide; 9 AA.
AC W27572;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha: antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI: 97-415302/38.
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 68; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
CC Sequence 9 AA:
SO

keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI: 97-415302/38.
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 68; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
CC Sequence 9 AA:
SO

Query Match 81.3%; Score 52; DB 27; Length 9;
Best Local Similarity 77.8%; Pred. No. 4,28e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 qkyrpyt 9
||| |||
Oy 1 OKYTSAPYT 9

RESULT 11
ID W27584 standard; peptide; 9 AA.
AC W27584;
DT 19-MAR-1998 (first entry)
DE Anti-TNF-alpha antibody light chain CDR3.
KW Human: tumour necrosis factor-alpha; TNF-alpha: antibody; CDR3;
light chain; complementarity determining region 3; inhibition;
treatment; sepsis; disease; autoimmune disease; infectious disease;
malignancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; reperfusion injury;
bone resorption disease; coagulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodontal disease; obesity; radiation toxicity;
endothelial cell leukocyte adhesion molecule-1;
human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-A1.
PD 14-AUG-1997.
PF 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
Mankovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
WPI: 97-415302/38.
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 68; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. Rheumatoid arthritis, Rheumatoid
spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
CC Sequence 9 AA:
SO

PI Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
PT High affinity antibodies against human TNF alpha - useful to inhibit
TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20: Page 72: 102pp: English.
CC The present sequence is a novel anti-human tumour necrosis
factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
less and has a Koff rate constant of 1x10 power -3 s power -1 or
less (both determined by surface plasmon resonance), and
neutralises human TNF-alpha cytotoxicity in a standard in vitro
L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 79.7%: Score 51: DB 27: Length 9:
Best Local Similarity 66.7%: Pred. No. 5.49e+01:

Matches 6: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

Db 1 qkynrpyt 9
||| |||
Oy 1 OKYTSAPYT 9

RESULT 12
ID W21571 standard; peptide: 9 AA.
AC W21571:

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain CDR3.

KW Human: tumour necrosis factor-alpha; TNF-alpha: antibody; CDR3;

light chain; complementarity determining region 3; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

malignancy; pulmonary disorder; intestinal disorder; hepatitis;

cardiac disorder; inflammatory bone disorder; reperfusion injury;

bone resorption disease; coagulation disturbance; burn; ELAM-1;

keloid formation; scar tissue formation; pyrexia; HUVEC;

periodontal disease; obesity; radiation toxicity;

endothelial cell leukocyte adhesion molecule-1;

human umbilical vein endothelial cell.

OS Homo sapiens.

PN W09729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PR 09-FEB-1996: US-599226.

PA (BAD1) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,

Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,

Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit

TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 20: Page 68: 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis

factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity

determining region 3 (CDR3).

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

less and has a Koff rate constant of 1x10 power -3 s power -1 or

less (both determined by surface plasmon resonance), and

neutralises human TNF-alpha cytotoxicity in a standard in vitro

L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

CC inhibits TNF-alpha activity, can be used to treat sepsis,
autoimmune diseases, e.g. rheumatoid arthritis, allergy, multiple
sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
syndrome, infectious diseases, malignancy, pulmonary, intestinal,
cardiac or inflammatory bone disorders, bone resorption disease,
alcoholic, viral or fulminant hepatitis, coagulation disturbances,
burns, reperfusion injury, keloid formation, scar tissue formation,
pyrexia, periodontal disease, obesity and radiation toxicity. The
Ab also inhibits TNF-alpha induced expression of endothelial cell
leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
endothelial cells (HUVEC).
SQ Sequence 9 AA:

Query Match 79.7%: Score 51: DB 27: Length 9:
Best Local Similarity 66.7%: Pred. No. 5.49e+01:

Matches 6: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

Db 1 qkynrpyt 9
||| |||
Oy 1 OKYTSAPYT 9

RESULT 13
ID W21568 standard; protein: 107 AA.
AC W21568:

DT 19-MAR-1998 (first entry)

DE Anti-TNF-alpha antibody light chain variable region.

KW Human: tumour necrosis factor-alpha; TNF-alpha: antibody;

light chain; variable region; inhibition;

treatment; sepsis; disease; autoimmune disease; infectious disease;

malignancy; pulmonary disorder; intestinal disorder; hepatitis;

cardiac disorder; inflammatory bone disorder; reperfusion injury;

bone resorption disease; coagulation disturbance; burn; ELAM-1;

keloid formation; scar tissue formation; pyrexia; HUVEC;

periodontal disease; obesity; radiation toxicity;

endothelial cell leukocyte adhesion molecule-1;

human umbilical vein endothelial cell.

OS Homo sapiens.

PN W09729131-A1.

PD 14-AUG-1997.

PF 10-FEB-1997: U02219.

PR 25-NOV-1996: US-031476.

PR 09-FEB-1996: US-599226.

PA (BAD1) BASF AG.

PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,

Markovitch JA, McGuinness BT, Roberts AJ, Sakorafas P,

Salfield JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;

DR WPI: 97-415302/38.

DR N-PSDB: T88403.

PT High affinity antibodies against human TNF alpha - useful to inhibit

TNF alpha activity, e.g. to treat autoimmune diseases and cancer

PS Claim 15: Page 75: 102pp: English.

CC The present sequence is a novel anti-human tumour necrosis

factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.

CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or

less and has a Koff rate constant of 1x10 power -3 s power -1 or

less (both determined by surface plasmon resonance), and

neutralises human TNF-alpha cytotoxicity in a standard in vitro

L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which

inhibits TNF-alpha activity, can be used to treat sepsis,

autoimmune diseases, e.g. rheumatoid arthritis, allergy, multiple

spondylitis, osteoarthritis, gouty arthritis, rheumatoid

sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic

syndrome, infectious diseases, malignancy, pulmonary, intestinal,

cardiac or inflammatory bone disorders, bone resorption disease,

alcoholic, viral or fulminant hepatitis, coagulation disturbances,

burns, reperfusion injury, keloid formation, scar tissue formation,

pyrexia, periodontal disease, obesity and radiation toxicity. The

Ab also inhibits TNF-alpha induced expression of endothelial cell

leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein

endothelial cells (HUVEC).
Sequence 107 AA;

Query Match 79.7%; Score 51; DB 27; Length 107;
 Best Local Similarity 66.7%; Pred. No. 5.49e+01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 89 qyrnarypt 97
 ||| |||
 OY 1 QKYSAPYT 9

RESULT 14
 ID W27580 standard; peptide; 9 AA.
 AC W27580;
 DE 19-MAR-1998 (first entry)
 DT Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Saifeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 71, 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 76.6%; Score 49; DB 27; Length 9;
 Best Local Similarity 66.7%; Pred. No. 8.98e+01;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkynsaays 9
 ||| |||
 OY 1 QKYSAPYT 9

RESULT 15
 ID W27579 standard; peptide; 9 AA.
 AC W27579;

DT 19-MAR-1998 (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HIVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Saifeld JG, Schoenhaut D, Vaughan TV, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 70, 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA:

Query Match 76.6%; Score 49; DB 27; Length 9;
 Best Local Similarity 75.0%; Pred. No. 8.98e+01;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 qkynary 8
 ||| |||
 OY 1 QKYSAPYT 8

Search completed: Thu Sep 2 11:53:24 1999
 Job time : 30 secs.

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Molecular output not generated.

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
on: Thu Sep 2 11:55:26 1999; Maspar time 1.38 Seconds
66.145 Million cell updates/sec

Title: >US-08-599-226-19
Description: (1-9) from US08599226.pep
Perfect Score: 64
Sequence: 1 OKTSAAPT 9

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:Issued
1:5A:COMB 2:5B:COMB 3:PCT9:COMB 4:backfiles1

Statistics: Mean 14.775; Variance 46.692; scale 0.316
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	48	75.0	533	1	US-08-488-Sequence 6, Applicatio	5.05e+01
2	47	73.4	93	4	5169835-26 Patent No. 5169835.	6.45e+01
3	47	73.4	107	3	PCT-US95-0 Sequence 87, Applicati	6.45e+01
4	47	73.4	107	1	US-08-276-Sequence 87, Applicati	6.45e+01
5	47	73.4	107	2	US-08-899-Sequence 87, Applicati	6.45e+01
6	47	73.4	107	2	US-08-899-Sequence 87, Applicati	6.45e+01
7	47	73.4	108	3	PCT-US95-0 Sequence 99, Applicati	6.45e+01
8	47	73.4	108	2	US-08-899-Sequence 99, Applicati	6.45e+01
9	47	73.4	108	2	US-08-899-Sequence 99, Applicati	6.45e+01
10	47	73.4	108	1	US-08-276-Sequence 99, Applicati	6.45e+01
11	47	73.4	144	4	5169835-8 Patent No. 5169835.	6.45e+01
12	47	73.4	230	4	5169835-13 Patent No. 5169835.	6.45e+01
13	47	73.4	419	4	5169835-2 Patent No. 5169835.	6.45e+01
14	46	71.9	53	2	US-08-162-Sequence 44, Applicati	8.23e+01
15	46	71.9	109	2	US-08-162-Sequence 24, Applicati	8.23e+01
16	46	71.9	109	3	PCT-US93-0 Sequence 24, Applicati	8.23e+01
17	45	70.3	92	2	US-08-273-Sequence 45, Applicati	1.05e+02
18	45	70.3	92	2	US-08-273-Sequence 53, Applicati	1.05e+02
19	45	70.3	106	2	US-08-652-Sequence 1, Applicatio	1.05e+02
20	45	70.3	106	2	US-08-652-Sequence 48, Applicati	1.05e+02
21	45	70.3	109	2	US-07-934-Sequence 3, Applicatio	1.05e+02
22	45	70.3	153	2	US-08-652-Sequence 41, Applicati	1.05e+02
23	45	70.3	435	1	US-08-259-Sequence 18, Applicati	1.05e+02

RESULT	ID	STANDARD	PRT	533 AA.
1	US-08-488-305A-6			
xxxxxx				
Sequence 6, Application US/08488305A				
Sequence 6, Application US/08488305A				
Patent No. 5679772				
GENERAL INFORMATION:				
APPLICANT: B vix, Claes Olaf, Eriksson, Ulf; Peterson, Per A.				
TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which				
TITLE OF INVENTION: blind Thereto, Nucleic Acid Sequence Coding				
Patent No. 5679772				
TITLE OF INVENTION: Therefor, And Uses Thereof				
NUMBER OF SEQUENCES: 6				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Felte & Lynch				
STREET: 805 Third Avenue				
CITY: New York City				
STATE: New York				
COUNTRY: USA				
ZIP: 10022				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage				
COMPUTER: IBM PS/2				
OPERATING SYSTEM: PC-DOS				
SOFTWARE: Wordperfect				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/08/488,305A				
FILING DATE: 7-JUNE-1995				
CLASSIFICATION: 530				
ATTORNEY/AGENT INFORMATION:				
NAME: Kohli, Vineet				
REGISTRATION NUMBER: 37,003				
REFERENCE/DOCKET NUMBER: LTD 5280.3				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: (212) 688-9200				
TELEFAX: (212) 838-3884				
INFORMATION FOR SEQ ID NO: 6:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 533 amino acids				
TYPE: amino acid				
TOPOLOGY: linear				
SEQUENCE 533 AA: 60970 MW: 1558915 CN:				

Query Match 75.0%; Score 48; DB 1; Length 533;
Best Local Similarity 66.7%; Pred. No. 5.05e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 424 OKYGSAPT 432
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QY 1 OKYTSAPT 9

RESULT 2
ID 5169835-26 STANDARD; PRT: 101 AA.

XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Patent No. 5169835.

Patent No. 5169835
APPLICANT: WAI-YEE, CHAN
TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
NUMBER OF SEQUENCES: 48
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/390,409
FILING DATE: 07-AUG-1989
SEQ ID NO:26:
LENGTH: 93
SEQUENCE 101 AA; 11225 MW; 64082 CN;

Query Match 73.4%; Score 47; DB 4; Length 93;
Best Local Similarity 71.4%; Pred. No. 6.45e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 66 KYTAGPY 72
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QY 2 KYTSAPT 8

RESULT 3
ID PCT-US95-08743-87 STANDARD; PRT: 107 AA.

XX AC xxxxxx
XX DT
XX DE
Sequence 87, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 107 AA; 11654 MW; 62438 CN;

Query Match 73.4%; Score 47; DB 3; Length 107;
Best Local Similarity 66.7%; Pred. No. 6.45e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYHSAPT 96
| | | | |
QY 1 OKYTSAPT 9

RESULT 4
ID US-08-276-852-87 STANDARD; PRT: 107 AA.

XX AC xxxxxx
XX DT
XX DE
Sequence 87, Application US/08276852

Sequence 87, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 107 AA; 11654 MW; 62438 CN;

Query Match 73.4%; Score 47; DB 1; Length 107;
Best Local Similarity 66.7%; Pred. No. 6.45e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 88 QOYHSAPT 96
| | | | |
QY 1 OKYTSAPT 9

RESULT 5
ID US-08-899-575-87 STANDARD; PRT: 107 AA.
XX
AC xxxxxx
DT
XX
XX
DE Sequence 87, Application US/08899575
CC
CC Sequence 87, Application US/08899575
CC Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Letner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRL452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ
Query Match 73.48; Score 47; DB 2; Length 107;
Best Local Similarity 66.78; Pred. No. 6.45e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

AC
XX
XX
DT
XX
XX
DE Sequence 87, Application US/08899575
CC
CC Sequence 87, Application US/08899575
CC Patent No. 5770440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Letner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRL452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 87:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
SQ
Query Match 73.48; Score 47; DB 2; Length 107;
Best Local Similarity 66.78; Pred. No. 6.45e+01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 7
ID PCT-US95-08743-99 STANDARD; PRT: 108 AA.
XX
AC xxxxxx
DT
XX
XX
DE Sequence 99, Application PC/TUS9508743

XX Sequence 99: Application PC/TUS508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC CC
CC SEQUENCE 108 AA; 11738 MW; 63142 CN;
SQ

Query Match 73.4%; Score 47; DB 3; Length 108;
Best Local Similarity 55.6%; Pred. No. 6.45e+01;
Matches 5; Conservatively 2; Mismatches 2; Indels 0; Gaps 0

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Db      88 QQYGTSPYT 96
      | | : : | |
QY      1 QKYTSAPYT 9

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CC	FILING DATE:	18-JUL-1994
CC	APPLICATION NUMBER:	US 08/178,302
CC	FILING DATE:	30-SEP-1993
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 07/954,148
CC	FILING DATE:	30-SEP-1992
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Fitting, Thomas
CC	REGISTRATION NUMBER:	34,163
CC	REFERENCE/DOCKET NUMBER:	SCA1452P
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	619-554-2937
CC	TELEFAX:	619-554-6312
CC	INFORMATION FOR SEQ ID NO:	99:
CC	SEQUENCE CHARACTERISTICS:	
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CC	TYPE:	amino acid
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	protein
CC	SEQUENCE	108 AA; 11738 MW; 63142 CN;
QY	Query Match	73.4% Score 47; DB 2; Length 108; Best Local Similarity 55.6%; Pred. No. 6.45e+01; Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0.
Dd	88 QQRYSPT 96 : 1 QKRSAPYT 9	
RESULT 9		
ID US-08-899-575-99	STANDARD;	PRT; 108 AA.
EX		

RESULT	8	STANDARD;	PRT;	108 AA
ID	US-08-899-575-99			

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ID	US-08-839-575-99	STANDARD;	PRT;	108	AA
XX	xxxxxx				
XX	AC				
XX					
DT					
XX					

AC XXXXXX

XX

DE Sequence 99, Application US/08899575
xx
CC Sequence 99, Application US/08899575
CC Patent No. 5804440
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Ierner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESS: Patent Counsel
CC STREET: 10666 NO. 5804440th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/899,575
CC FILING DATE: 24-JUL-1997
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852

CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
 CC STREET: Mail Drop TPC8
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/899,575
 CC FILING DATE: 24-JUL-1993
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148

CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCRI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-2937
 CC INFORMATION FOR SEQ ID NO: 99:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 108 AA; 11738 MW; 63142 CN;
 SQ
 Query Match 73.4%; Score 47; DB 2; Length 108;
 Best Local Similarity 55.6%; Pred. No. 6.45e+01;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QYTSAPY 9
 88 QOYGTSPY 96
 | | : : |||
 1 QYTSAPY 9
 RESULT 10
 ID US-08-276-852-99 STANDARD; PRT; 108 AA.
 XX
 AC xxxxxx
 DE
 XX
 DE Sequence 99, Application US/08276852
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESSES:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCRI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937

CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 99:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 108 AA; 11738 MW; 63142 CN;
 SQ
 Query Match 73.4%; Score 47; DB 1; Length 108;
 Best Local Similarity 55.6%; Pred. No. 6.45e+01;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QYTSAPY 9
 88 QOYGTSPY 96
 | | : : |||
 1 QYTSAPY 9
 RESULT 11
 ID 5169835-8 STANDARD; PRT; 156 AA.
 XX
 AC xxxxxx
 DE
 XX
 DE Patent No. 5169835.
 CC Patent No. 5169835
 CC APPLICANT: WAI-YEE, CHAN
 CC TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
 CC NUMBER OF SEQUENCES: 48
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/390,409
 CC FILING DATE: 07-AUG-1989
 CC SEQ ID NO: 8:
 CC LENGTH: 144
 CC SEQUENCE 156 AA; 17234 MW; 149812 CN;
 SQ
 Query Match 73.4%; Score 47; DB 4; Length 144;
 Best Local Similarity 71.4%; Pred. No. 6.45e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYTSAPY 8
 115 KYTAGPY 121
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 2 QYTSAPY 8
 RESULT 12
 ID 5169835-13 STANDARD; PRT; 249 AA.
 XX
 AC xxxxxx
 DE
 XX
 DE Patent No. 5169835.
 CC Patent No. 5169835
 CC APPLICANT: WAI-YEE, CHAN
 CC TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
 CC NUMBER OF SEQUENCES: 48
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/390,409
 CC FILING DATE: 07-AUG-1989
 CC SEQ ID NO: 13:
 CC LENGTH: 230
 CC SEQUENCE 249 AA; 27757 MW; 380603 CN;
 SQ
 Query Match 73.4%; Score 47; DB 4; Length 230;
 Best Local Similarity 71.4%; Pred. No. 6.45e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 65 KYTAGPY 71
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QY 2 KYTSAPY 8

RESULT 13
ID 5169835-2 STANDARD; PRT; 454 AA.
XX AC xxxxxx
XX 01-JAN-1900
DE Patent No. 5169835.
XX
CC Patent No. 5169835
CC APPLICANT: WAI-YEE, CHAN
CC TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
CC NUMBER OF SEQUENCES: 48
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/390,409
CC FILING DATE: 07-AUG-1989
CC SEQ ID NO:2:
CC LENGTH: 419
CC SEQUENCE 454 AA; 51077 MW; 1273311 CN;

Query Match 73.4%; Score 47; DB 4; Length 419;
Best Local Similarity 71.4%; Pred. No. 6,45e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
QY 2 KYTSAPY 8

RESULT 14
ID US-08-162-102C-44 STANDARD; PRT; 53 AA.
XX AC xxxxxx
XX
DE Sequence 44, Application US/08162102C
CC
CC Sequence 44, Application US/08162102C
CC Patent No. 5762905
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Barbas, III, Carlos F.
CC APPLICANT: Chanock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr., James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/162,102C
CC FILING DATE: 10-DEC-1993
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07300/007001
CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 678-5070
CC TELEFAX: (619) 678-5099
CC INFORMATION FOR SEQ ID NO: 44:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 53 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 53 AA; 5857 MW; 16217 CN;

Query Match 71.9%; Score 46; DB 2; Length 53;
Best Local Similarity 55.6%; Pred. No. 8,23e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 33 QOYGSPYT 41
QY 1 QKTSAPYT 9

RESULT 15
ID US-08-162-102C-24 STANDARD; PRT; 109 AA.
XX AC xxxxxx
XX
DE Sequence 24, Application US/08162102C
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CC Sequence 24, Application US/08162102C
CC Patent No. 5762905
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Barbas, III, Carlos F.
CC APPLICANT: Chanock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr., James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/162,102C
CC FILING DATE: 10-DEC-1993
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07300/007001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 678-5099
CC TELEFAX: (619) 678-5070
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: tsv 23L
CC FEATURE:

CC NAME/KEY: Peptide
CC LOCATION: 1..109
SQ SEQUENCE 109 AA; 11858 MW; 64524 CN;

Query Match 71.9%; Score 46; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. NO. 8.23e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 89 QOYGSPYT 97
| | : |||
QY 1 QKTSAPYT 9

Search completed: Thu Sep 2 11:55:32 1999
Job time : 6 secs.

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 WIRESETH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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 Distribution rights by Oxford Molecular Ltd

Mpsrch.pp protein - protein database search, using Smith-Waterman algorithm
 on: Thu Sep 2 11:53:42 1999; Maspar time 3.13 Seconds
 115.080 Million cell updates/sec
 Molecular output not generated.

Title: >US-08-599-226-19
 Description: (1-9) from US08599226.pep
 Perfect Score: 64
 Sequence: 1 OKYTSAPYR 9

Scoring table: PAM 150
 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r60
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 22.062; Variance 27.728; scale 0.796

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
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2	49	76.6	91	2	S67940	Ig kappa chain V regi 5.27e+00
3	49	76.6	92	2	S37513	Ig kappa chain V regi 5.27e+00
4	49	76.6	109	2	A30608	Ig kappa chain V-III 5.27e+00
5	49	76.6	109	2	H30601	Ig kappa chain V-III 5.27e+00
6	49	76.6	1673	2	I50806	complement component 5.27e+00
7	48	75.0	533	2	A47143	retinal pigment micro 8.42e+00
8	47	73.4	182	2	A34647	pregnancy-specific be 1.34e+01
9	47	73.4	210	2	UC4122	pregnancy-specific g1 1.34e+01
10	47	73.4	273	2	B28928	pregnancy-specific be 1.34e+01
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14	47	73.4	326	2	F43354	pregnancy-specific g1 1.34e+01
15	47	73.4	332	2	UN0067	pregnancy-specific be 1.34e+01
16	47	73.4	333	2	A43354	pregnancy-specific be 1.34e+01
17	47	73.4	335	2	H43354	pregnancy-specific g1 1.34e+01
18	47	73.4	336	2	C27658	pregnancy-specific be 1.34e+01
19	47	73.4	352	2	I77374	pregnancy-specific be 1.34e+01
20	47	73.4	360	2	S28047	Tub13 protein - post 1.34e+01
21	47	73.4	360	2	S52662	S-adenosylmethionine 1.34e+01
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23	47	73.4	397	2	C43354	pregnancy-specific g1 1.34e+01

24	47	73.4	406	2	E43354	pregnancy-specific g1 1.34e+01
25	47	73.4	417	2	A28277	pregnancy-specific be 1.34e+01
26	47	73.4	419	2	A33258	pregnancy-specific g1 1.34e+01
27	47	73.4	426	2	A31135	pregnancy-specific be 1.34e+01
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33	47	73.4	428	2	J50032	pregnancy-specific be 1.34e+01
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37	46	71.9	101	2	B37262	Ig kappa chain V regi 2.10e+01
38	46	71.9	106	2	A49138	IgA kappa rheumatoid 2.10e+01
39	46	71.9	615	1	ABCHS	serum albumin precurs 2.10e+01
40	46	71.9	1290	2	A56493	leucocyte common anti 2.10e+01
41	46	71.9	1897	1	TDHUK	leukocyte antigen-rel 2.10e+01
42	46	71.9	1898	2	S46216	leukocyte antigen-rel 2.10e+01
43	45	70.3	268	2	A56446	Ig heavy chain V regi 3.29e+01
44	45	70.3	841	2	B71212	hypothetical protein 3.29e+01
45	45	70.3	1042	2	G64514	type I restriction en 3.29e+01

ALIGNMENTS

RESULT 1
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 TITLE Ig kappa chain precursor V-III region (IARC/BL41) - human
 ORGANISM Homo sapiens #common_name man
 DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997

ACCESSIONS A01899
 REFERENCE A93588
 #authors Klobbeck, H.G.; Melndl, A.; Combrlato, G.; Solomon, A.; Zachau, H.G.

#journal Nucleic Acids Res. (1985) 13:6499-6513
 #title Human immunoglobulin kappa light chain genes of subgroups II and III

#cross-references MUID:86041852

#accession A01899

#molecule_type DNA

#residues 1-128 #label KLO

#note the sequence was determined from the differentiated gene

GENETICS GDB:IGKV3

#gene #cross-references GDB:136266

#map_position 2p12-2p11

#introns 17/1

COMPLEX An immunoglobulin heterotrimer subunit consists of two

identical light (kappa or lambda) and two identical heavy

(alpha, delta, epsilon, gamma, or mu) chains usually

stabilized by interchain disulfide bonds. In some cases,

such as IgA and IgM, the subunits associate into larger

oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotrimer; immunoglobulin

FEATURE 1-20

21-43 #domain signal sequence #status predicted #label SIG

44-54 #product Ig kappa chain V-III region (IARC/BL41) #status predicted #label MAT

55-69 #region framework 1\

70-76 #region framework 2\

77-108 #region framework 3\

109-117 #region framework 4\

118-128 #region complementarity-determining 3\

43-108 #region framework 4\

SUMMARY #disulfide_bonds #status predicted

Query Match 78.1%; Score 50; DB 1; Length 128;

Best Local Similarity 55.6%; Pred. No. 3.28e+00;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 109 QOYGSAPT 117
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OY 1 OKYTSAPT 9

RESULT 2
ENTRY S67940 #type fragment
TITLE Ig kappa chain V region, subgroup III (clone MH52) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998

ACCESSIONS S67940
REFERENCE S67940
#authors Hexham, J.M.; Furmanik, J.; Pegg, C.; Burton, D.R.; Smith, B.R.

#journal Autoimmunity (1992) 12:135-141
#file Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial approach.

#cross-references MUID:92314301
#accession S67940
#status preliminary
#molecule_type mRNA
#residues 1-91 #label HEX
#cross-references EMBL:X73852

CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology
SUMMARY #length 91 #checksum 3259

Query Match 76.6%; Score 49; DB 2; Length 91;
Best Local Similarity 66.7%; Pred. No. 5.27e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 71 QOYGSAPT 79
| | | | |
OY 1 OKYTSAPT 9

RESULT 3
ENTRY S37513 #type fragment
TITLE Ig kappa chain V region (V-kappa 3) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

ACCESSIONS S37513
REFERENCE S37501
#authors Klein, U.; Kueppers, R.; Rajewsky, K.
#submission submitted to the EMBL Data Library, September 1993
#description Human IgM(+) IgD(+) cells, the major B cell subset in the peripheral blood, expresses V(kappa) genes with no or little somatic mutation throughout life.

#accession S37513
#status preliminary
#molecule_type mRNA
#residues 1-92 #label KLE
#cross-references EMBL:226598; NID:9405668; PID:9405669

CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 92 #checksum 6096

Query Match 76.6%; Score 49; DB 2; Length 92;
Best Local Similarity 66.7%; Pred. No. 5.27e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 73 QOYGSAPT 81
| | | | |
OY 1 OKYTSAPT 9

RESULT 4
ENTRY A30608 #type fragment

TITLE Ig kappa chain V-III region (Soc) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS A30608
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonailla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.

#journal J. Immunol. (1989) 142:3158-3163
#file Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.

#cross-references MUID:89215279
#accession A30608
#status preliminary
#molecule_type protein
#residues 1-109 #label GON

CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6031

Query Match 76.6%; Score 49; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 5.27e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 90 QOYGSAPT 98
| | | | |
OY 1 OKYTSAPT 9

RESULT 5
ENTRY H30601 #type fragment
TITLE Ig kappa chain V-III region (Gar and Flo) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996

ACCESSIONS H30601; E30601
REFERENCE A30601
#authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonailla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.

#journal J. Immunol. (1989) 142:3158-3163
#file Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.

#cross-references MUID:89215279
#accession H30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON1
#accession E30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON2

CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5951

Query Match 76.6%; Score 49; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 5.27e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 90 QOYGSAPT 98
| | | | |
OY 1 OKYTSAPT 9

RESULT 6
ENTRY I50806 #type fragment
TITLE complement component C3 - Japanese lamprey (fragment)
ORGANISM #formal_name Lampetra japonica #common_name Japanese lamprey
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Aug-1998

ACCESSIONS I50806

REFERENCE 150806
#authors Nonaka, M.; Takahashi, M.
#journal J. Immunol. (1992) 148:3290-3295
#title Complete complementary DNA sequence of the third component of thioester containing protein.
#cross-references MIM:92251197
#accession 150806
#status preliminary; translated from GB/EMBL/DBJ
#molecule-type mRNA
#residues 1-1673 ##label NON
#cross-references GB:DI0087; NID:9222887; PID:9222888
CLASSIFICATION #superfamily alpha-2-macroglobulin
SUMMARY #length 1673 #checksum 8983

Query Match 76.6%; Score 49; DB 2; Length 1673;
Best Local Similarity 75.0%; Pred. No. 5.2/e+00;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

443 OKYASAPY 450
1 OKYASAPY 8

RESULT 7
ENTRY A47143 #type complete
TITLE retinal pigment microsomal protein RPE65, epithelium-specific
ALTERNATE_NAMES bovine
ORGANISM membrane receptor p65; retinol-binding protein receptor
DATE #formal_name Bos primigenius taurus #common_name cattle
03-May-1994 #sequence_revision 03-May-1994 #text_change 10-Sep-1997
A47143; A48017; S28503

ACCESSIONS A47143
REFERENCE A47143
#authors Hamel, C.P.; Tsiou, E.; Pfeiffer, B.A.; Hooks, J.J.; Detrick, B.; Redmond, T.M.
#journal J. Biol. Chem. (1993) 268:15751-15757
#title Molecular cloning and expression of RPE65, a novel retinal pigment epithelium-specific microsomal protein that is post-translationally regulated in vitro.
#cross-references MIM:93340181
#accession A47143
#status preliminary
#molecule-type mRNA
#residues 1-533 ##label HAM
#cross-references GB:L11356; NID:9163656; PID:9163657
REFERENCE A48017
#authors Baviik, C.O.; Levy, F.; Hellman, U.; Wernstedt, C.; Eriksson, U.
#journal J. Biol. Chem. (1993) 268:20540-20546
#title The retinal pigment epithelial membrane receptor for plasma retinol-binding protein. Isolation and cDNA cloning of the 63-kDa protein.
#cross-references MIM:93388633
#accession A48017
#status preliminary
#molecule-type mRNA
#residues 1-340; 'L', 342-533 ##label BA2
#cross-references EMBL:X66277; NID:9563; PID:9564
KEYWORDS membrane protein
SUMMARY #length 533 #molecular-weight 60944 #checksum 3885

Query Match 75.0%; Score 48; DB 2; Length 533;
Best Local Similarity 66.7%; Pred. No. 8.42e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 424 OKYASAPY 432
1 OKYASAPY 9

RESULT 8
ENTRY A34647 #type fragment

TITLE pregnancy-specific beta-1-glycoprotein 1 - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 31-Oct-1997

ACCESSIONS A34647
REFERENCE A34647
#authors Borjigin, J.; Tease, L.A.; Barnes, W.; Chan, W.Y.; Blochem, B.ophys. Res. Commun. (1990) 166:622-629
#title Expression of the pregnancy-specific beta 1-glycoprotein genes in human testis.
#cross-references MIM:90147764
#accession A34647
#status preliminary
#molecule-type mRNA
#residues 1-182 ##label BOR
#cross-references GB:M30629; NID:9806596; PID:9337671
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology
KEYWORDS glycoprotein
FEATURE 18-75
SUMMARY #domain immunoglobulin homology #label IMM1
#domain immunoglobulin homology #label IMM2
#length 182 #checksum 2511

Query Match 73.4%; Score 47; DB 2; Length 182;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 65 KYTAGPY 71
1 KYTAGPY 8

RESULT 9
ENTRY JCA122 #type complete
TITLE pregnancy-specific glycoprotein 13' precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 26-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
JCA122
ACCESSIONS JCA122
REFERENCE JCA122
#authors Teiglund, S.; Zhou, G.O.; Hammarstrom, S.
#journal Biochem. Biophys. Res. Commun. (1995) 211:656-664
#title Characterization of cDNA encoding novel pregnancy-specific glycoprotein variants.
#cross-references MIM:95314639
#accession JCA122
#status preliminary
#molecule-type mRNA
#residues 1-210 ##label TEG
#cross-references GB:U25988; NID:9862682; PID:9984306
COMMENT #experimental_source fetal liver
This protein belongs to the carcinoembryonic antigen family. This protein is a molecule synthesized by the placental syncytiotrophoblasts and released to the maternal circulation during pregnancy.

GENETICS GDB:PSG13
#gene
#cross-references GDB:128243; OMIM:176401
CLASSIFICATION #map_position 19q13.2-19q13.2
#superfamily carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology glycoprotein
KEYWORDS
FEATURE 1-22
SUMMARY #domain signal sequence #status predicted #label SIG
#product pregnancy-specific glycoprotein 13' #status predicted #label MAR
#domain immunoglobulin homology #label IMM1
#domain immunoglobulin homology #label IMM2
#binding_site carbohydrate (Asn) (covalent) #status predicted
#length 210 #molecular-weight 23093 #checksum 3459

Query Match 73.4%; Score 47; DB 2; Length 210;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 87 KYTAGPY 93
|||:|
2 KYTSAPY 8

RESULT 10
ENTRY B28928 #type fragment
TITLE pregnancy-specific beta-1 glycoprotein C2 - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Sep-1998

ACCESSIONS B28928
REFERENCE A28928
#authors Oikawa, S.; Inuzuka, C.; Kosaki, G.; Nakazato, H.
#journal Biochem. Biophys. Res. Commun. (1988) 156:68-77
#title Exon-intron organization of a gene for pregnancy-specific beta-1-glycoprotein, a subfamily member of CEA family: implications for its characteristic repetitive domains and C-terminal sequences.

#cross-references MUID:89025910

#accession B28928

#molecule_type mRNA

#residues 1-273 #label OIK

GENETICS #cross-references GB:M2311; GB:M2312

#gene GDB:PSG1; PSBG1; PSGGA
#cross-references GDB:I20321; OMIM:176390

#map_position 19q13.2-19q13.2

#introns 93/1; 178/1

CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology

glycoprotein

KEYWORDS #domain immunoglobulin homology #label IMM1\

FEATURE 18-75 #domain immunoglobulin homology #label IMM2

SUMMARY 11-168 #length 273 #checksum 6283

Query Match 73.4%; Score 47; DB 2; Length 273;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 65 KYTAGPY 71
|||:|
2 KYTSAPY 8

RESULT 11
ENTRY A28928 #type fragment
TITLE pregnancy-specific beta-1 glycoprotein C1 - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Sep-1998

ACCESSIONS A28928
REFERENCE A28928
#authors Oikawa, S.; Inuzuka, C.; Kosaki, G.; Nakazato, H.
#journal Biochem. Biophys. Res. Commun. (1988) 156:68-77
#title Exon-intron organization of a gene for pregnancy-specific beta-1-glycoprotein, a subfamily member of CEA family: implications for its characteristic repetitive domains and C-terminal sequences.

#cross-references MUID:89025910

#accession A28928

#molecule_type mRNA

#residues 1-275 #label OIK

GENETICS #cross-references GB:M2311; GB:M2312

#gene GDB:PSG1; PSBG1; PSGGA
#cross-references GDB:I20321; OMIM:176390

#map_position 19q13.2-19q13.2
#introns 93/1; 178/1
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology

glycoprotein

KEYWORDS #domain immunoglobulin homology #label IMM1\
FEATURE 18-75 #domain immunoglobulin homology #label IMM2

SUMMARY 11-168 #length 275 #checksum 4824

Query Match 73.4%; Score 47; DB 2; Length 275;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 65 KYTAGPY 71
|||:|
2 KYTSAPY 8

RESULT 12
ENTRY C28928 #type fragment
TITLE pregnancy-specific beta-1 glycoprotein C3 - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Sep-1998

ACCESSIONS C28928
REFERENCE A28928
#authors Oikawa, S.; Inuzuka, C.; Kosaki, G.; Nakazato, H.
#journal Biochem. Biophys. Res. Commun. (1988) 156:68-77
#title Exon-intron organization of a gene for pregnancy-specific beta-1-glycoprotein, a subfamily member of CEA family: implications for its characteristic repetitive domains and C-terminal sequences.

#cross-references MUID:89025910

#accession C28928

#molecule_type mRNA

#residues 1-282 #label OIK

GENETICS #cross-references GB:M2311; GB:M2312

#gene GDB:PSG1; PSBG1; PSGGA
#cross-references GDB:I20321; OMIM:176390

#map_position 19q13.2-19q13.2

#introns 93/1; 178/1

CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology; immunoglobulin homology

glycoprotein

KEYWORDS #domain immunoglobulin homology #label IMM1\
FEATURE 18-75 #domain immunoglobulin homology #label IMM2

SUMMARY 11-168 #length 282 #checksum 4005

Query Match 73.4%; Score 47; DB 2; Length 282;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 65 KYTAGPY 71
|||:|
2 KYTSAPY 8

RESULT 13
ENTRY G43354 #type complete
TITLE pregnancy-specific glycoprotein IIA form b precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Oct-1997

ACCESSIONS G43354
REFERENCE A43354
#authors Lei, K.J.; Sartwell, A.D.; Pan, C.J.; Chou, J.Y.
#journal J. Biol. Chem. (1992) 267:16371-16378
#title Cloning and expression of genes encoding human

pregnancy-specific glycoproteins.
#cross-references MUID:92355602
#accession G43354
##molecule_type DNA
##residues 1-324 ##label LEI
##note sequence extracted from NCBI backbone (NCBIN:110710,
NCBIN:110714, NCBIN:110719, NCBIN:110722)

GENETICS
#gene PSGI-1
#introns 22/1; 144/1; 237/1
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic
antigen precursor amino-terminal homology; immunoglobulin
homology

KEYWORDS
FEATURE glycoprotein
1-138 #domain carcinoembryonic antigen precursor
162-219 amino-terminal homology #label CEAN\
254-303 #domain immunoglobulin homology #label IMM1\
SUMMARY #domain immunoglobulin homology #label IMM2
#length 324 #molecular-weight 36105 #checksum 2473

Query Match 73.4%; Score 47; DB 2; Length 324;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
QY 2 KYTSAPY 8

RESULT 14
ENTRY F43354 #type complete
TITLE pregnancy-specific glycoprotein IIA form a precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
31-Oct-1997

ACCESSIONS
REFERENCE F43354
#authors Lei, K.J.; Sartwell, A.D.; Pan, C.J.; Chou, J.Y.
#journal J. Biol. Chem. (1992) 267:16371-16378
#title Cloning and expression of genes encoding human
pregnancy-specific glycoproteins.
#cross-references MUID:92355602
#accession F43354
##molecule_type DNA
##residues 1-326 ##label LEI
##note sequence extracted from NCBI backbone (NCBIN:110710,
NCBIN:110714, NCBIN:110719, NCBIN:110722)

GENETICS
#gene PSGI-1
#introns 22/1; 144/1; 237/1
CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic
antigen precursor amino-terminal homology; immunoglobulin
homology
glycoprotein

KEYWORDS
FEATURE #domain carcinoembryonic antigen precursor
1-138 amino-terminal homology #label CEAN\
162-219 #domain immunoglobulin homology #label IMM1\
254-303 #domain immunoglobulin homology #label IMM2
SUMMARY #length 326 #molecular-weight 36390 #checksum 304

Query Match 73.4%; Score 47; DB 2; Length 326;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
QY 2 KYTSAPY 8

RESULT 15
ENTRY JN0067 #type complete

TITLE pregnancy-specific beta-1-glycoprotein 9 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
20-Mar-1998

ACCESSIONS
REFERENCE JN0067
#authors Plouzek, C.A.; Watanabe, S.; Chou, J.Y.
#journal Blochem. Biophys. Res. Commun. (1991) 176:1532-1538
#title Cloning and expression of a new pregnancy-specific beta
1-glycoprotein member.
#cross-references MUID:91248252
#accession JN0067
##molecule_type mRNA
##residues 1-332 ##label PLO
COMMENT #cross-references GB:M69245; NID:9190646; PID:9190647
Pregnancy-specific beta-1-glycoproteins are divided into two types,
type I with a N-A1-A2-B2-C domain arrangement and type II with a
N-A1/A2-B2-C arrangement.

CLASSIFICATION #superfamily carcinoembryonic antigen; carcinoembryonic
antigen precursor amino-terminal homology; immunoglobulin
homology
glycoprotein

KEYWORDS
FEATURE #domain carcinoembryonic antigen precursor
1-138 amino-terminal homology #label CEAN\
1-34 #domain signal sequence #status predicted #label SIG\
35-332 #product pregnancy-specific beta-1-glycoprotein 9
#status predicted #label MAT\
35-143 #domain N #label DON\
127-129 #region cell attachment (R-G-D) motif\
144-236 #domain A1 #label DAI\
162-219 #domain immunoglobulin homology #label IMM1\
237-322 #domain B2 #label DB2\
254-303 #domain immunoglobulin homology #label IMM2\
323-332 #domain C #label DOC\
61,104,111,199 #binding site carbohydrate (Asn) (covalent) #status
predicted

SUMMARY #length 332 #molecular-weight 36681 #checksum 8059

Query Match 73.4%; Score 47; DB 2; Length 332;
Best Local Similarity 71.4%; Pred. No. 1.34e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
QY 2 KYTSAPY 8

Search completed: Thu Sep 2 11:53:59 1999
Job time : 17 secs.

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RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RX MEDLINE: 95036004.
RA MAD ARIE S.A., TAYLOR M.A., GEORGE L.A., BUTLER A.R., BURCH L.R.,
RT DAVIES H.V., STARK M.J., KOMAR A.;
RL "Characterisation of the S-adenosylmethionine decarboxylase (SAMDC)
gene of potato".
RL PLANT MOL. BIOL. 26:327-338(1994).
CC -1- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE - (5'-DEOXY-5'-ADENOSYL)
(3-AMINOPROPYL)METHYLSULFONIUM SALT + CO(2).
CC -1- COFACTOR: THIS ENZYME REQUIRES A PYRUVYL GROUP FOR ITS ACTIVITY.
CC -1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
BIOSYNTHESIS FROM PUTRESCINE.
CC -1- TISSUE SPECIFICITY: STOLON, ALSO EXPRESSED IN LEAVES, STEMS
AND ROOTS.
CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING THE
EARLY STAGES OF TUBERIZATION. MAXIMUM EXPRESSION WAS IN NON-
SWELLING STOLON TIPS FROM STAGE B, AND LEVEL DECLINED AS THE
TUBER INCREASED IN SIZE.

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DR EMBL: Z11680; G21485; -
DR EMBL: S74514; G807094; -
DR PIR: S28047; S28047.
RW SPERMIDINE BIOSYNTHESIS. LYASE: DECARBOXYLASE: PYRUVATE: ZMOGEN.
FT CHAIN 1 72 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
FT CHAIN 73 360 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
FT SITE 72 73 CLEAVAGE (NONHYDROLYTICAL)
FT MOD_RES 73 73 CONVERTED TO A PYRUVYL GROUP
FT ACT_SITE 13 13 IMPORTANT FOR CATALYTIC ACTIVITY (BY
FT ACT_SITE 16 16 SIMILARITY).
FT ACT_SITE 87 87 IMPORTANT FOR CATALYTIC ACTIVITY (BY
FT ACT_SITE 87 87 SIMILARITY).
FT CONFLICT 174 174 S -> P (IN REF. 2).
FT CONFLICT 257 257 T -> S (IN REF. 2).
FT CONFLICT 291 291 V -> I (IN REF. 2).
FT CONFLICT 305 305 I -> T (IN REF. 2).
SQ SEQUENCE 360 AA: 39726 MW: 47298FE4 CRC32:
Query Match 73.4%: Score 47; DB 1; Length 360;
Best Local Similarity 62.5%: Pred. No. 4.74e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 332 OKFTPTPY 339
Oy 1 OKTISAPY 8
RESULT 5
ID DCAM_DATST STANDARD: PRT: 362 AA.
AC Q96535;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE S-ADENOSYLMETHIONINE DECARBOXYLASE PHOENZYME (EC 4.1.1.50) (ADOMETC)
(SAMDC).
OS DATURA STRAMONID (JIMSONEED) (COMMON THORNAPPLE).
OC EUDAROTIA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLLIOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS;

OC ASTERIDAE: SOLANACEAE: SOLANACEAE: DATURA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. D15/5; TISSUE-ROOT;
RA MICHAEL A.J.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE - (5'-DEOXY-5'-ADENOSYL)
(3-AMINOPROPYL)METHYLSULFONIUM SALT + CO(2).
CC -1- COFACTOR: THIS ENZYME REQUIRES A PYRUVYL GROUP FOR ITS ACTIVITY.
CC -1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
BIOSYNTHESIS FROM PUTRESCINE.

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or send an email to license@isb-sib.ch).

DR EMBL: Y07768; E265488; -
RW SPERMIDINE BIOSYNTHESIS. LYASE: DECARBOXYLASE: PYRUVATE: ZMOGEN.
FT CHAIN 1 72 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
FT CHAIN 73 362 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
FT SITE 72 73 CLEAVAGE (NONHYDROLYTICAL)
FT MOD_RES 73 73 CONVERTED TO A PYRUVYL GROUP
FT ACT_SITE 13 13 IMPORTANT FOR CATALYTIC ACTIVITY (BY
FT ACT_SITE 16 16 SIMILARITY).
FT ACT_SITE 87 87 IMPORTANT FOR CATALYTIC ACTIVITY (BY
FT ACT_SITE 87 87 SIMILARITY).
SQ SEQUENCE 362 AA: 39955 MW: 84851CAB CRC32:
Query Match 73.4%: Score 47; DB 1; Length 362;
Best Local Similarity 62.5%: Pred. No. 4.74e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 332 OKFTPTPY 339
Oy 1 OKTISAPY 8
RESULT 6
ID PBL1_HUMAN STANDARD: PRT: 417 AA.
AC P11462;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
OS HOMO SAPIENS (HUMAN).
OC EUDAROTIA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA;
OC PRIMATES: CATARRHINI: HOMINIDAE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88115335.
RA WATANABE S., CHOU J.Y.;
RT "Isolation and characterization of complementary DNAs encoding human
pregnancy-specific beta 1-glycoprotein".
RL J. BIOL. CHEM. 263:2045-2054(1988).
CC -1- PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN BECOMES DETECTABLE IN SERUM
DURING THE FIRST 2-3 WEEKS OF PREGNANCY AND INCREASES AS PREGNANCY
PROGRESSES, RISING TO A VERY HIGH LEVEL.
CC -1- SIMILARITY: TO CARCINOEMBRYONIC ANTIGEN (CEA)-RELATED PROTEINS.

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CC or send an email to license@isb-sib.ch).

DR EMBL: M17908; G306791; -
DR EMBL: M17909; G183482; -
DR PIR: A28277; A28277.
DR PIR: PF00047; 15; 3.
KW GLYCOPROTEIN; SIGNAL; MULTIGENE FAMILY.
FT SIGNAL 1 34
FT CHAIN 1 34
FT CARBOHYD 35 417 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN.
FT CARBOHYD 61 61 POTENTIAL.
FT CARBOHYD 104 104 POTENTIAL.
FT CARBOHYD 111 111 POTENTIAL.
FT CARBOHYD 199 199 POTENTIAL.
FT CARBOHYD 259 259 POTENTIAL.
FT CARBOHYD 268 268 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
SQ SEQUENCE 417 AA; 46918 MW; EEBD2306 CRC32;

Query Match 73.4%; Score 47; DB 1; Length 417;
Best Local Similarity 71.4%; Pred. No. 4.74e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
OY 2 KYTSAPY 8
||||:|

RESULT 7
ID PBGC_HUMAN STANDARD; PRT; 419 AA.
AC P11464;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN D PRECURSOR (FETAL LIVER NON-
DE SPECIFIC CROSS-REACTIVE ANTIGEN-2) (FL-NCA-2).
GN BIG1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88280756.
RA STREYDIO C., LACKA K., SWILLENS S., VASSART G.;
RT "The human pregnancy-specific beta 1-glycoprotein (PS beta G) and the
RT same multigene family".
RT BIOCHEM. BIOPHYS. RES. COMMUN. 154:130-137(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89030170.
RA CHAN W.Y., BOKRIGIN J., ZHENG Q.X., SHUPERT W.L.;
RT "Characterization of cDNA encoding human pregnancy-specific beta 1-
RT glycoprotein from placenta and extraplacental tissues and their
RT comparison with carcinoembryonic antigen.";
RT DNA 7:545-555(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89286549.
RA KHAN W.N., HAMMARSTROM S.;
RT "Carcinoembryonic antigen gene family: molecular cloning of cDNA for
RT a PS beta G/FL-NCA glycoprotein with a novel domain arrangement.";
RT BIOCHEM. BIOPHYS. RES. COMMUN. 161:525-535(1989).
CC -1- SIMILARITY: TO CARCINOEMBRYONIC ANTIGEN (CEA)-RELATED PROTEINS.
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DR EMBL: M20881; G306798; -
DR EMBL: M21822; G306796; -
DR EMBL: M25385; G190636; -
DR PIR: A31135; A31135.
DR PIR: PF00047; 19; 3.
KW GLYCOPROTEIN; SIGNAL; MULTIGENE FAMILY.
FT SIGNAL 1 34
FT CHAIN 1 34
FT CARBOHYD 35 419 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN D.
FT CARBOHYD 61 61 POTENTIAL.
FT CARBOHYD 104 104 POTENTIAL.
FT CARBOHYD 111 111 POTENTIAL.
FT CARBOHYD 199 199 POTENTIAL.
FT CARBOHYD 259 259 POTENTIAL.
FT CARBOHYD 268 268 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
SQ SEQUENCE 419 AA; 47222 MW; 21235192 CRC32;

Query Match 73.4%; Score 47; DB 1; Length 419;
Best Local Similarity 71.4%; Pred. No. 4.74e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
OY 2 KYTSAPY 8
||||:|

RESULT 8
ID PBGC_HUMAN STANDARD; PRT; 428 AA.
AC P11463;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR.
GN BIG1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88280756.
RA STREYDIO C., LACKA K., SWILLENS S., VASSART G.;
RT "The human pregnancy-specific beta 1-glycoprotein (PS beta G) and the
RT carcinoembryonic antigen (CEA)-related proteins are members of the
RT same multigene family".
RT BIOCHEM. BIOPHYS. RES. COMMUN. 154:130-137(1988).
CC -1- SIMILARITY: TO CARCINOEMBRYONIC ANTIGEN (CEA)-RELATED PROTEINS.
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DR EMBL: M20879; G306797; -
DR PIR: A27658; A27658.
DR PIR: PF00047; 19; 3.
KW GLYCOPROTEIN; SIGNAL; MULTIGENE FAMILY.
FT SIGNAL 1 34
FT CHAIN 1 34
FT CARBOHYD 35 428 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C.
FT CARBOHYD 61 61 POTENTIAL.
FT CARBOHYD 104 104 POTENTIAL.
FT CARBOHYD 111 111 POTENTIAL.
FT CARBOHYD 199 199 POTENTIAL.
FT CARBOHYD 259 259 POTENTIAL.
FT CARBOHYD 268 268 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
FT CARBOHYD 421 421 POTENTIAL.
SQ SEQUENCE 428 AA; 48139 MW; AAE5573 CRC32;

Query Match 73.4% Score 47; DB 1; Length 428;
 Best Local Similarity 71.4% Pred. No. 4.74e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 209 KYTSAPY 215
 |||:|
 QY 2 KYTSAPY 8

RESULT 9
 ID CB21.RABIT STANDARD; PRT; 2259 AA.

AC 002343;
 DT 01-JUL-1993 (REL. 26, CREATED)

DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE BRAIN CALCIUM CHANNEL BIT-1 PROTEIN.

OS ORCTOLAGUS CUNICULUS (RABBIT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC LAGOMORPHA; LEPORIDAE; ORCTOLAGUS.

OC [1]
 SEQUENCE FROM N.A.

TISSUE-BRAIN:
 MEDLINE: 92354772.

RA NIDOME T., KIM M.S., FRIEDRICH T., MORI Y.;
 RT Molecular cloning and characterization of a novel calcium channel
 from rabbit brain."

RL FEBS LETT. 308:7-13(1992).

CC -1- FUNCTION: BRAIN CALCIUM CHANNEL.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: BRAIN.

CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BRAIN CALCIUM CHANNEL ARE
 PRODUCED FROM A SINGLE GENE. BIT-1 AND BIT-2 DIFFER ONLY IN THEIR
 C-TERMINAL REGION FROM AA 2101.

CC -1- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.

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CC EMBL: X67855; G1473; .

DR PIR: S29236; S29236.

DR PIR: S29236; S29236.

DR PIR: S29236; S29236.

DR PIR: S29236; S29236.

DR PIR: S29236; S29236.

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DR PIR: S29236; S29236.

DR PIR: S29236; S29236.

DR PIR: S29236; S29236.

DR PIR: S29236; S29236.

FT TRANSMEM 1531 1549 S3 OF REPEAT IV.
 FT TRANSMEM 1562 1580 S4 OF REPEAT IV.
 FT TRANSMEM 1600 1619 S5 OF REPEAT IV.
 FT TRANSMEM 1689 1713 S6 OF REPEAT IV.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 1556 1556 POTENTIAL.
 FT CARBOHYD 1561 1561 POTENTIAL.
 SQ SEQUENCE 2259 AA; 254250 MW; 346267E CRC32;

Query Match 73.4% Score 47; DB 1; Length 2259;
 Best Local Similarity 62.5% Pred. No. 4.74e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 2172 QRYTSEPY 2179
 |||:|
 QY 1 QRYTSEPY 8

RESULT 10
 ID ALBU.CHICK STANDARD; PRT; 615 AA.

AC P19121;
 DT 01-NOV-1990 (REL. 16, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE SERUM ALBUMIN PRECURSOR.

GN ALB.

OS GALLUS GALLUS (CHICKEN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;

OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.

OC [1]
 SEQUENCE FROM N.A.

RC TISSUE-LIVER;

RA CASSADY A.I., SALKILD C.K., BAYERSROCK P., WALLACE J.C.;
 RT SUBMITTED (JUL-1991) TO EMBL/GENBANK/DBJ DATA BANKS.

RL [2]
 SEQUENCE OF 1-28 FROM N.A.

RP MEDLINE: 83161037.

RA HACHE R.J.G., WISKOCIL R., VASA M., ROY R.N., LAU P.C.K., DELEY R.G.;
 RT "The 5' noncoding and flanking regions of the avian very low density
 apolipoprotein II and serum albumin genes. Homologies with the egg
 white protein genes."

RL J. BIOL. CHEM. 258:4556-4564(1983).

RN [3]
 SEQUENCE OF 19-30.

RX MEDLINE: 78019943.

RA ROSEN A.M., GELLER D.M.;
 RT "Chicken microsomal albumin: amino terminal sequence of chicken
 proalbumin."

RL BIOCHEM. BIOPHYS. RES. COMMUN. 78:1060-1066(1977).

CC -1- FUNCTION: SERUM ALBUMIN. THE MAIN PROTEIN OF PLASMA. HAS A GOOD
 BINDING CAPACITY FOR WATER, CA⁺⁺, NH₄⁺, K⁺, FATTY ACIDS, HORMONES,
 BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
 COLLOIDAL OSMOTIC PRESSURE OF BLOOD.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- TISSUE SPECIFICITY: PLASMA.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE ALB/AF/VPB FAMILY.

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CC EMBL: X60688; G63748; .

DR PIR: Y00381; G63039; .

DR PIR: S15571; ARCHS.

DR PROSITE: PS00212; ALBUMIN. 3.

DR PIR: P02768; IUBO.

KW COPPER. 1 18
 FT SIGNAL 23
 FT PROPEP 19
 CC 23
 FT CHAIN 24 615
 CC 24
 FT REPEAT 31 206
 CC 31
 FT REPEAT 225 398
 CC 225
 FT REPEAT 417 596
 CC 417
 FT METAL 30 30
 CC 30
 FT DISULFID 80 89
 CC 80
 FT DISULFID 102 118
 CC 102
 FT DISULFID 117 128
 CC 117
 FT DISULFID 152 197
 CC 152
 FT DISULFID 196 205
 CC 196
 FT DISULFID 228 274
 CC 228
 FT DISULFID 273 281
 CC 273
 FT DISULFID 293 307
 CC 293
 FT DISULFID 306 317
 CC 306
 FT DISULFID 344 389
 CC 344
 FT DISULFID 388 397
 CC 388
 FT DISULFID 420 466
 CC 420
 FT DISULFID 465 476
 CC 465
 FT DISULFID 489 505
 CC 489
 FT DISULFID 504 515
 CC 504
 FT DISULFID 542 587
 CC 542
 FT DISULFID 586 595
 CC 586
 FT CARBOHYD 500 500
 CC 500
 FT CONFLICT 24 24
 CC 24
 SQ SEQUENCE 615 AA; 69918 MM; DCSEEEA CRC32; F -> M (IN REF. 3).

Query Match 71.9%; Score 46; DB 1; Length 615;
 Best Local Similarity 53.6%; Pred. No. 7.84e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 249 OKYKAPPS 257
 QY 1 OKYSAPYT 9

RESULT 11
 ID PRPF_HUMAN STANDARD; PRT; 1897 AA.
 AC P10586;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).
 GN PRPF OR LAR.
 OS HOMO SAPIENS (HUMAN).
 SS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 PR [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TONSIL;
 RX MEDLINE: 89035978.
 RA STREUBI M., KRUGER N.X., HALL L.R., SCHLOSSMAN S.F., SAITO H.;
 RT "A new member of the immunoglobulin superfamily that has a
 cytoplasmic region homologous to the leukocyte common antigen";
 RL J. EXP. MED. 168:1523-1530(1988).
 RN [2]
 RP MUTAGENESIS.
 RX MEDLINE: 90046860.
 RA STREUBI M., KRUGER N.X., TSAI A.Y.M., SAITO H.;
 RT "A family of receptor-linked protein tyrosine phosphatases in humans
 and Drosophila";
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:8698-8702(1989).
 RN [3]
 RP MUTAGENESIS.
 RX MEDLINE: 90316093.
 RA STREUBI M., KRUGER N.X., THAI T., TANG M., SAITO H.;
 RT "Distinct functional roles of the two intracellular phosphatase like
 domains of the receptor-linked protein tyrosine phosphatases LCA and
 LAR";
 RL EMBO J. 9:2399-2407(1990).
 CC -1- FUNCTION: IT IS POSSIBLE THAT DIAR IS A CELL ADHESION RECEPTOR.

CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
 CC (PTPASE).
 CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMIC ACTIVITY, WHILE
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
 CC THE FIRST ONE.
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
 CC LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS),
 CC AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
 CC -1- SIMILARITY: TO DPTP AND TO LAR.
 CC -----
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DR EMBL: Y00815; G34267; -.
 DR PIR: S03841; TDHUK.
 DR MIM: I79590; -.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR PFAM: PF00047; fn3; 7.
 DR PFAM: PF00102; Y_phosphatase; 2.
 DR HSSP: P18052; LYFO.
 DR HYDROLASE; RECEPTOR; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE;
 KW CELL ADHESION; IMMUNOGLOBULIN FOLD; DUPLICATION.
 FT SIGNAL 1 16
 FT CHAIN 17 1897
 FT DOMAIN 17 1250
 FT TRANSMEM 1251 1274
 FT DOMAIN 1275 1897
 FT DOMAIN 1360 1606
 FT DOMAIN 1649 1897
 FT ACT_SITE 1538 1538
 FT ACT_SITE 1829 1829
 FT MUTAGEN 1538 1538
 FT CARBOHYD 107 107
 FT CARBOHYD 240 240
 FT CARBOHYD 285 285
 FT CARBOHYD 711 711
 FT CARBOHYD 956 956
 SQ SEQUENCE 1897 AA; 211844 MM; 40B63F08 CRC32;

Query Match 71.9%; Score 46; DB 1; Length 1897;
 Best Local Similarity 50.0%; Pred. No. 7.84e+00;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1226 RYASSPYS 1233
 QY 2 KYTSAPYT 9

RESULT 12
 ID YAOB_SCHPO STANDARD; PRT; 309 AA.
 AC Q10111;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 35.3 KD PROTEIN C1866.11C IN CHROMOSOME 1.
 GN SPAC1866.11C.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 CC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIZOOCOMYCETES;
 CC SCHIZOSACCHAROMYCETES; SCHIZOSACCHAROMYCETACEAE;
 CC SCHIZOSACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-972;
 RA CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 DE SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDJ DATA BANKS.
 CC -1- SIMILARITY: TO S. POMBE SPAC14C4.04.
 CC -----
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 CC -----
 DR EMBL: 268198; E213816; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 309 AA; 35297 MW; 639221F7 CRC32;
 Query Match 70.3%; Score 45; DB 1; Length 309;
 Best Local Similarity 62.5%; Pred. No. 1.29e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 241 DKYVSGPY 248
 :||:||||
 1 QKTSAPY 8
 RESULT 13
 ID VST2_HEVRH STANDARD; PRT; 485 AA.
 AC 000270;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DE STRUCTURAL PROTEIN 2 (FRAGMENT).
 OS HEPATITIS E VIRUS (ISOLATE RHESUS) (HEV).
 CC VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
 CC CALCIVIRUS.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 92261377.
 RX UCHIDA T., SUZUKI K., HAYASHI N., IIDA F., HARA T., OO S.S.,
 RA WANG C.-K., SHIKATA T., ICHIKAWA M., KIKIHISA T., MIZONO K.,
 RA WIN K.M.;
 RT "Hepatitis E virus: CDNA cloning and expression.";
 RL MICROBIOL. IMMUNOL. 36:67-79(1992).
 CC -----
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 CC -----
 DR EMBL: D90274; G221703; -
 FT NON-TER 1
 FT NON-TER 485
 SQ SEQUENCE 485 AA; 52317 MW; 61080D3A CRC32;
 Query Match 70.3%; Score 45; DB 1; Length 485;
 Best Local Similarity 71.4%; Pred. No. 1.29e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 156 YNTPTPT 162
 :||:||||
 3 YTSAPY 9
 RESULT 14
 ID VST2_HEVME STANDARD; PRT; 659 AA.
 AC 003500;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)

DE STRUCTURAL PROTEIN 2 PRECURSOR.
 OS HEPATITIS E VIRUS (STRAIN MEXICO) (HEV).
 CC VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
 CC CALCIVIRUS.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 93079857.
 RX HUANG C.C., NGUYEN D., FERNANDEZ J., YUN K.Y., FRY K.E.,
 RA BRADLEY D.W., TAM A.W., REYES G.R.;
 RT "Molecular cloning and sequencing of the Mexico isolate of hepatitis
 RT E virus (HEV)."
 RL VIROLOGY 191:550-558(1992).
 CC -1- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
 CC THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
 CC BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
 CC -----
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 CC -----
 DR EMBL: M74506; G330020; -
 DR PIR: B44212; B44212.
 KW SIGNAL.
 FT CHAIN 1 22 BY SIMILARITY.
 FT CHAIN 23 659 STRUCTURAL PROTEIN 2.
 SQ SEQUENCE 659 AA; 70640 MW; 99D1EAC0 CRC32;
 Query Match 70.3%; Score 45; DB 1; Length 659;
 Best Local Similarity 71.4%; Pred. No. 1.29e+01;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 288 YNTPTPT 294
 :||:||||
 3 YTSAPY 9
 RESULT 15
 ID VST2_HEVPA STANDARD; PRT; 660 AA.
 AC P33426;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DE STRUCTURAL PROTEIN 2 PRECURSOR (ORF2).
 OS HEPATITIS E VIRUS (STRAIN PAKISTAN) (HEV).
 CC VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
 CC CALCIVIRUS.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 92115700.
 RX TSAREV S.A., EMERSON S.U., REYES G.R., TSAREVA T.S., LEIGHTS L.J.,
 RA MALIK I.A., IOBAL M., PORCELL R.H.;
 RT "Characterization of a prototype strain of hepatitis E virus.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992).
 CC -1- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
 CC THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
 CC BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
 CC -----
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 CC -----
 DR EMBL: M80581; G330000; -
 KW SIGNAL.
 FT CHAIN 1 22 BY SIMILARITY.
 FT CHAIN 23 660 STRUCTURAL PROTEIN 2.

SQL SEQUENCE 660 AA; 70980 MW; DA2A4E29 CRC32;

Query Match 70.3%; Score 45; DB 1; Length 660;

Best Local Similarity 71.4%; Pred. No. 1.29e+01;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 288 YTNTPYT 294
11:1111
QY 3 YTSAPYT 9

Search completed: Thu Sep 2 11:54:23 1999
Job time : 8 secs.

 WIREIMAGE
 (TM)

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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Sep 2 11:54:41 1999; MasPar time 4.24 Seconds

Abular output not generated. 115.732 Million cell updates/sec

Title: >US-08-599-226-19

Description: (1-9) from US08599226.pep

Perfect Score: 64

Sequence: 1 QKTSAPYT 9

Scoring table: PAM 150

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

sptrembl9
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mmc 8:sp_organalle
 9:sp_plant 10:sp_plant 11:sp_ricent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 21.829; Variance 25.136; scale 0.868

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	51	79.7	337	2	ORF40X1 PROTEIN.	1.11e+00
2	51	79.7	337	2	ORF139-17 PROTEIN.	1.11e+00
3	49	76.6	319	5	HYPOHETICAL 37.0 KD P	3.15e+00
4	49	76.6	560	5	KI1D12.1 PROTEIN.	3.15e+00
5	48	75.0	533	6	RETINAL PIGMENT EPTHE	5.25e+00
6	48	75.0	533	6	RETINAL PIGMENT EPTHE	5.25e+00
7	47	73.4	182	4	PREGNANCY-SPECIFIC GLY	8.70e+00
8	47	73.4	210	4	PREGNANCY-SPECIFIC GLY	8.70e+00
9	47	73.4	320	2	STRE-SPECIFIC RECOMBIN	8.70e+00
10	47	73.4	332	4	PREGNANCY-SPECIFIC BET	8.70e+00
11	47	73.4	333	4	PSG IIA-D.	8.70e+00
12	47	73.4	335	4	PSG IIA-D.	8.70e+00
13	47	73.4	336	5	FS4D12.8 PROTEIN.	8.70e+00
14	47	73.4	352	4	PREGNANCY-SPECIFIC BET	8.70e+00
15	47	73.4	352	4	PREGNANCY-SPECIFIC PRO	8.70e+00
16	47	73.4	417	4	PREGNANCY-SPECIFIC GLY	8.70e+00
17	47	73.4	419	4	PREGNANCY-SPECIFIC GLY	8.70e+00
18	47	73.4	426	4	PREGNANCY-SPECIFIC BET	8.70e+00
19	47	73.4	426	4	PREGNANCY-SPECIFIC BET	8.70e+00
20	47	73.4	426	4	PREGNANCY-SPECIFIC BET	8.70e+00

21	47	73.4	426	4	015243	PREGNANCY-SPECIFIC GLY	8.70e+00
22	47	73.4	428	4	016557	PREGNANCY-SPECIFIC BET	8.70e+00
23	47	73.4	428	4	008265	PREGNANCY-SPECIFIC BET	8.70e+00
24	47	73.4	2270	4	014581	DIIHDROPRIDINE-SENSIT	8.70e+00
25	47	73.4	2312	4	015878	VOLTAGE-OPERATED CALCI	8.70e+00
26	46	71.9	322	5	045024	AMPHIOXUS OTX TRANSCR	1.43e+01
27	46	71.9	451	13	093374	TRANSCRIPTION FACTOR (1.43e+01
28	46	71.9	496	2	087348	LLAR21 RESTRICTION EN	1.43e+01
29	46	71.9	653	11	054922	REX070	1.43e+01
30	46	71.9	864	11	063294	LEUCOCYTE COMMON ANTIG	1.43e+01
31	46	71.9	1290	11	063295	LEUCOCYTE COMMON ANTIG	1.43e+01
32	46	71.9	1898	11	064604	LEUCOCYTE COMMON ANTIG	1.43e+01
33	45	70.3	292	10	048821	PUTATIVE SERINE PROTET	2.33e+01
34	45	70.3	305	5	018281	2K1010.2 PROTEIN.	2.33e+01
35	45	70.3	660	14	091856	STRUCTURAL PROTEIN.	2.33e+01
36	45	70.3	660	14	081878	COMPLETE GENOME SEQUEN	2.33e+01
37	45	70.3	660	14	068985	ORF-2.	2.33e+01
38	45	70.3	660	14	091855	STRUCTURAL PROTEIN.	2.33e+01
39	45	70.3	660	14	036613	PUTATIVE CAPSID PROTET	2.33e+01
40	45	70.3	660	14	089468	UNNAMED PROTEIN PRODC	2.33e+01
41	45	70.3	660	14	081871	ORF 2 PRECURSOR.	2.33e+01
42	45	70.3	660	14	089419	ORF1, ORF2 & ORF3.	2.33e+01
43	45	70.3	841	1	059612	841AA LONG HYPOHETICA	2.33e+01
44	45	70.3	1042	1	060295	PUTATIVE TYPE I RESTRI	2.33e+01
45	45	70.3	1345	10	064496	F20D22.14 PROTEIN.	2.33e+01

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	337 AA.
AC	034232			
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	ORF40X1 PROTEIN.			
OS	VIBRIO CHOLERAE.			
OC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIOMACEAE; VIBRIO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-AI-1837;			
RX	MEDLINE: 97252505.			
RA	STROEHER U.H., PARASIVAM G., DREGE B.K., NANNING P.A.;			
RT	"Novel Vibrio cholerae O139 genes involved in lipopolysaccharide			
RL	biosynthesis.";			
RL	J. BACTERIOL. 179:2740-2747(1997).			
DR	EMBL: Y07786; E274690; -			
SQ	SEQUENCE 337 AA; 40132 MW; 204A7939 CRC32;			

Query Match 79.7%; Score 51; DB 2; Length 337;
 Best Local Similarity 87.5%; Pred. No. 1.11e+00;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB	147	QKTSAPY 154	
QY	1	QKTSAPY 8	
RESULT	2		
ID	087136	PRELIMINARY:	PRT: 337 AA.
AC	087136		
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)		
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)		
DE	ORF139-17 PROTEIN.		
OS	VIBRIO CHOLERAE.		
OC	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIOMACEAE; VIBRIO.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-M045;		
RA	YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,		
RA	TAKEDA Y.;		
RT	"The genes responsible for O-antigen synthesis of Vibrio cholerae		

RT 0139 are closely related to those of *Vibrio cholerae* 022.";
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567; -;
 SQ SEQUENCE 337 AA; 40147 MW; 176B46EB CRC32;

Query Match 79.7%; Score 51; DB 2; Length 337;
 Best Local Similarity 87.5%; Pred. No. 1.11e+00;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 147 OKYHAPY 154
 ||| |||

OY 1 OKYTSAPY 8

RESULT 3
 ID 015926; PRELIMINARY; PRT; 319 AA.

AC 015926;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE CRYPTOSPORIDIUM PARVUM.
 OS CRYPTOSPORIDIUM PARVUM.

OC EUKARYOTA; ALVEOLATA; APICOMPLEXA; COCCIDIA; EIMERIIDAE;
 OC CRYPTOSPORIDIIDAE; CRYPTOSPORIDIUM.

RN [1]
 RN SEQUENCE FROM N.A.

RP STRAIN-KSU-1;
 RX MEDLINE: 98043502.

RA KHRAMTSOV N.V., WOODS K.M., NESTERENKO M.V., DIKSTRA C.C.,
 RA UPTON S.J.;

RT "Virus-like, double-stranded RNAs in the parasitic protozoan
 RT *Cryptosporidium parvum*."

RL MOL. MICROBIOL. 26:289-300(1997).

DR EMBL: U95986; G2465523; -;
 KW HYPOTHETICAL PROTEIN
 SQ SEQUENCE 319 AA; 37028 MW; 1362B027 CRC32;

Query Match 76.6%; Score 49; DB 5; Length 319;
 Best Local Similarity 75.0%; Pred. No. 3.15e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 250 RTTCAPY 257
 :|| |||

OY 2 KYTSAPY 9

RESULT 4
 ID 044626; PRELIMINARY; PRT; 560 AA.

AC 044626;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE KLID12.1 PROTEIN.

OS CAENORHABDITIS ELEGANS.

OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

RN [1]
 RN SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SUSTON J.,

RA THIRRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPOAT J., WOHLMAN P.;

RT "2.3 kb of contiguous nucleotide sequence from chromosome III of *C. elegans*."

RL NATURE 368:32-38(1994).

RN [2]
 RN SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2;

RA HENKHAUS J., WOHLDMANN P., GILLAM B.;

RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RN SEQUENCE FROM N.A.

RP STRAIN-BRISTOL N2;

RA WATSON R.;

RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF039047; G2736445; -;

DR PROSITE: PS00028; ZINC_FINGER_C2H2; 1.

KW ZINC-FINGER; METAL-BINDING; DNA-BINDING.

SQ SEQUENCE 560 AA; 61136 MW; 5906EB7D CRC32;

Query Match 76.6%; Score 49; DB 5; Length 560;
 Best Local Similarity 75.0%; Pred. No. 3.15e+00;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 81 OKYKAPY 88
 ||| |||

OY 1 OKYTSAPY 8

RESULT 5
 ID 028175; PRELIMINARY; PRT; 533 AA.

AC 028175;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE RETINAL PIGMENT EPITHELIUM-SPECIFIC PROTEIN.

OS BOS TAURUS (BOVINE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.

RN [1]
 RN SEQUENCE FROM N.A.

RP TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 93340181.

RA HAMEL C.P., TSILIOU E., PFEFFER B.A., HOOKS J.J., DETRICK B.,
 RA REDMOND T.;

RT "Molecular cloning and expression of RP65, a novel retinal pigment
 RT epithelium-specific microsome protein that is post-transcriptionally
 RT regulated in vitro."

RL J. BIOL. CHEM. 268:15751-15757(1993).

RN [2]
 RN SEQUENCE FROM N.A.

RP TISSUE-RETINAL PIGMENT EPITHELIUM;
 RX MEDLINE: 93233190.

RA HAMEL C.P., TSILIOU E., HARRIS E.D., PFEFFER B.A., HOOKS J.J.,
 RA DETRICK B., REDMOND T.;

RT "A developmentally regulated microsome protein specific for the
 RT pigment epithelium of the vertebrate retina."

RL J. NEUROSCI. RES. 34:414-425(1993).

DR EMBL: L11356; G163657; -;

KW PIGMENT.

SQ SEQUENCE 533 AA; 60944 MW; 911D0716 CRC32;

Query Match 75.0%; Score 48; DB 6; Length 533;
 Best Local Similarity 66.7%; Pred. No. 5.25e+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 424 OKYKAPY 432
 ||| |||

OY 1 OKYTSAPY 9

RESULT 6
 ID 005661; PRELIMINARY; PRT; 533 AA.

AC 005661;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE RETINAL PIGMENT EPITHELIAL MEMBRANE RECEPTOR P63.
 OS BOS TAURUS (BOVINE).
 OC EURAROTIA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 365-382 AND 407-423.
 RC STRAIN-STEINHOLTZ; TISSUE-EYE;
 RX MEDLINE: 93388633.
 RA BAYK C.O., HELLMAN U., WERNSTEDT C., ERIKSSON U.;
 RT "The retinal pigment epithelial membrane receptor for plasma
 retinol-binding protein. Isolation and cDNA cloning of the 63-kDa
 protein."
 RL J. BIOL. CHEM. 268:20540-20546(1993).
 CC -1- FUNCTION: THIS RECEPTOR BINDS PLASMA RETINOL BINDING PROTEIN.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN RETINAL PIGMENT
 CC EPITHELIUM.
 DR EMBL: X66277; G564; -;
 KM RECEPTOR; RETINOL-BINDING; PLASMA; MEMBRANE.
 RT MOD RES 71
 SEQUENCE 533 AA; 60970 MW; F77E22D7 CRC32;
 Query Match 75.0%; Score 48; DB 6; Length 533;
 Best Local Similarity 66.7%; Pred. No. 5,256+00;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 424 OKYSGKPT 432
 |||: |||
 QY 1 OKYTSAPT 9

RESULT 7
 ID 015402 PRELIMINARY; PRT: 182 AA.
 AC 015402;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC PROTEIN (FRAGMENT).
 GN PSG1.
 OS HOMO SAPIENS (HUMAN).
 OC EURAROTIA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE: 90147764.
 RA BORJIGIN J., TEASE L.A., BARNES W., CHAN W.Y.;
 RT "Expression of the pregnancy-specific beta 1-glycoprotein genes in
 human testis."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 166:622-629(1990).
 DR EMBL: M30629; G337671; -;
 FT PFM; PF00047; 19; 2.
 NON_TER 1
 SQ SEQUENCE 182 AA; 20274 MW; 6D170E39 CRC32;
 Query Match 73.4%; Score 47; DB 4; Length 182;
 Best Local Similarity 71.4%; Pred. No. 8,70e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 65 KYTAGPY 71
 |||: |||
 QY 2 KYTSAPT 8

RESULT 8
 ID 013179 PRELIMINARY; PRT: 210 AA.
 AC 013179;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC GLYCOPROTEIN 13.
 GN PSG13.
 OS HOMO SAPIENS (HUMAN).

OC EURAROTIA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RA TEGJUND S., ZHOU G., HAMARSTROM S.;
 RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U25988; G984306; -;
 DR PFM; PF00047; 19; 2.
 PREGNANCY.
 KW SEQUENCE 210 AA; 23093 MW; 3AA6723A CRC32;
 Query Match 73.4%; Score 47; DB 4; Length 210;
 Best Local Similarity 71.4%; Pred. No. 8,70e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 87 KYTAGPY 93
 |||: |||
 QY 2 KYTSAPT 8

RESULT 9
 ID 068847 PRELIMINARY; PRT: 320 AA.
 AC 068847;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SITE-SPECIFIC RECOMBINASE INT14.
 GN INT14.
 OS VIBRIO CHOLERAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON-INVCH;
 RX MEDLINE: 98221242.
 RA MAZEL D., DYCHINCO B., WEBB V.A., DAVIES J.;
 RT "A distinctive class of integron in the vibrio cholerae genome."
 RL SCIENCE 280:605-608(1998).
 DR EMBL: AF055586; G3095165; -;
 SQ SEQUENCE 320 AA; 37505 MW; CBF0F9CD CRC32;
 Query Match 73.4%; Score 47; DB 2; Length 320;
 Best Local Similarity 62.5%; Pred. No. 8,70e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 208 EKYPNAPY 215
 |||: |||
 QY 1 OKYTSAPT 8

RESULT 10
 ID 015242 PRELIMINARY; PRT: 332 AA.
 AC 015242;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
 OS HOMO SAPIENS (HUMAN).
 OC EURAROTIA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 91248252.
 RA PLOUZER C.A., WATANABE S., YANG CHOU J.;
 RT "Cloning and expression of a new pregnancy-specific beta
 1-glycoprotein member."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 176:1532-1538(1991).
 DR EMBL: M69245; G190647; -;
 DR PFM; PF00047; 19; 2.
 RT SIGNAL; PREGNANCY.
 FT CHAIN 1 34 POTENTIAL.
 SQ SEQUENCE 332 AA; 36681 MW; 5474F7F5 CRC32;

Query Match 73.4%; Score 47; DB 4; Length 332;
 Best Local Similarity 71.4%; Pred. No. 8.70e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
 |||:|
 QY 2 KYTSAPY 8

RESULT 11
 ID 075238 PRELIMINARY; PRT: 333 AA.
 AC 075238;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PSGL-ITA-D.
 CN PSGL.
 OS HOMO SAPIENS (HUMAN).
 OC EURAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LAERBIN J.E., MCCREADY P.M., SKORONSKI E., ADAMSON A.W.,
 RA BURKHART-SCHULTZ K., GORDON L., KYLE A., RAMIREZ M., STIMAGEN S.,
 RA PHAN H., VELASCO N., DO L., REGALA W., TERRY A., GARNES J.,
 RA DANGAMAN L., POUNDSTONE P., CHRISTENSEN M., GEORGESE A., AVILA J.,
 RA LIU S., ATTIX C., ANDREISE T., TRANKHEIM M., AMICO-KELLER G.,
 RA COFFIELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS P., QUAN G.,
 RA KRONMILLER B., ARELLANO A., MONTGOMERY M., OW D., NOLAN M., TRONG S.,
 RA KORAYASHI A., OLSEN A.S., CARRANO A.V.,
 RA "Sequence analysis of a 2.5 kb region in 19q13.2 containing a
 RT clustered CER/PSG gene family."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AC005238; G3287446; -
 SO SEQUENCE 333 AA; 37033 MW; 5808E99A CRC32;

Query Match 73.4%; Score 47; DB 4; Length 333;
 Best Local Similarity 71.4%; Pred. No. 8.70e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
 |||:|
 QY 2 KYTSAPY 8

RESULT 12
 ID 075237 PRELIMINARY; PRT: 335 AA.
 AC 075237;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PSGL-ITA-C.
 CN PSGL.
 OS HOMO SAPIENS (HUMAN).
 OC EURAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LAERBIN J.E., MCCREADY P.M., SKORONSKI E., ADAMSON A.W.,
 RA BURKHART-SCHULTZ K., GORDON L., KYLE A., RAMIREZ M., STIMAGEN S.,
 RA PHAN H., VELASCO N., DO L., REGALA W., TERRY A., GARNES J.,
 RA DANGAMAN L., POUNDSTONE P., CHRISTENSEN M., GEORGESE A., AVILA J.,
 RA LIU S., ATTIX C., ANDREISE T., TRANKHEIM M., AMICO-KELLER G.,
 RA COFFIELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS P., QUAN G.,
 RA KRONMILLER B., ARELLANO A., MONTGOMERY M., OW D., NOLAN M., TRONG S.,
 RA KORAYASHI A., OLSEN A.S., CARRANO A.V.,
 RA "Sequence analysis of a 2.5 kb region in 19q13.2 containing a
 RT clustered CER/PSG gene family."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AC005238; G3287449; -
 SO SEQUENCE 335 AA; 37307 MW; DDB80C29 CRC32;

Query Match 73.4%; Score 47; DB 4; Length 335;
 Best Local Similarity 71.4%; Pred. No. 8.70e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 209 KYTAGPY 215
 |||:|
 QY 2 KYTSAPY 8

RESULT 13
 ID 044833 PRELIMINARY; PRT: 336 AA.
 AC 044833;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE F5AD12.8 PROTEIN.
 CN F5AD12.8.
 OS CAENORHABDITIS ELEGANS.
 OC EURAROTIA; METAFOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 CC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAYELLO A., FULTON L.,
 RA GANDNER A., GREEN P., HAWKINS T., HILLER L., JIR M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCDURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SPALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THERY-LEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WINSTOCK L., WILKINSON-SPROAT J., WOULDMAN P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RC MAGGI L., GOELA D.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RC WATERSTON R.;
 RA SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF040647; G2746828; -
 SO SEQUENCE 336 AA; 37224 MW; C566B39C CRC32;

Query Match 73.4%; Score 47; DB 5; Length 336;
 Best Local Similarity 75.0%; Pred. No. 8.70e+00;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 176 KYTSAPY 183
 |||:|
 QY 2 KYTSAPY 9

RESULT 14
 ID 008266 PRELIMINARY; PRT: 352 AA.
 AC 008266;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EURAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COLON;
 RX MEDLINE: 93254418.

RA SHUPERT W.L., CHAN W.Y.;
 RT "Pregnancy specific beta 1-glycoprotein in human intestine.";
 RL MOL. CELL. BIOCHEM. 120:159-170(1993).
 CC -1- SIMILARITY: TO CARCINOEMBRYONIC ANTIGEN (CEA)-RELATED PROTEINS.
 DR EMBL: S59494; G300093; -.
 PFAM: PF00047; 19; 2.
 KM GLYCOPROTEIN; SIGNAL; MULTIGENE FAMILY.
 FT NON_TER 1 1
 FT SIGNAL <1 12 BY SIMILARITY.
 FT CHAIN 13 352 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN.
 FT CARBOHYD 82 82 POTENTIAL.
 FT CARBOHYD 89 89 POTENTIAL.
 FT CARBOHYD 246 246 POTENTIAL.
 FT CARBOHYD 281 281 POTENTIAL.
 SQ SEQUENCE 352 AA; 39361 MW; B83BFD3E CRC32;

Query Match 73.4%; Score 47; DB 4; Length 352;
 Best Local Similarity 71.4%; Pred. No. 8.70e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

187 KYTAGPY 193
 |||:|
 2 KYTSAPY 8

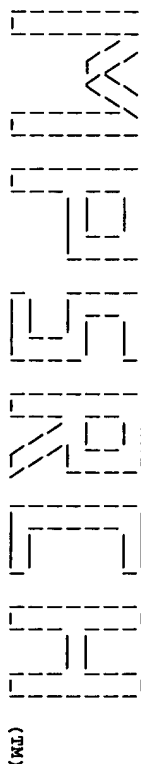
RESULT 15
 ID 015403 PRELIMINARY; PRT: 352 AA.
 AC 015403;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PREGNANCY-SPECIFIC PROTEIN (FRAGMENT).
 GN SPL
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE: 90147764.
 RA BORRIGIN J., TEASE L.A., BARNES W., CHAN W.Y.;
 RT "Expression of the pregnancy-specific beta 1-glycoprotein genes in
 human testis.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 166:622-629(1990).
 DR EMBL: M30628; G808015; -.
 DR PFAM: PF00047; 19; 2.
 FT NON_TER 1 1
 SQ SEQUENCE 352 AA; 39473 MW; 894F42CB CRC32;

Query Match 73.4%; Score 47; DB 4; Length 352;
 Best Local Similarity 71.4%; Pred. No. 8.70e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

187 KYTAGPY 193
 |||:|
 2 KYTSAPY 8

Search completed: Thu Sep 2 11:55:09 1999
 Job time : 28 secs.

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Sep 2 11:58:18 1999; Maspar time 4.26 Seconds
 115.181 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-599-226-20
 Description: (1-9) from US08599226.pep
 Perfect Score: 69
 Sequence: 1 OKYNRAPVN 9

Scoring table: PAM 150
 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

sptrembl9
 5:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_protein 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 22.787; Variance 29.627; scale 0.769

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	60	87.0	560	5	044626	K11D12.1 PROTEIN.	8.58e-02
2	56	81.2	521	2	044677	NEUTRAL PROTEASE.	6.17e-01
3	53	76.8	407	11	035490	BETAINE HOMOCYSTEINE M	2.58e+00
4	53	76.8	3082	14	036979	POLYPROTEIN.	2.58e+00
5	52	75.4	337	2	034232	ORF40X1 PROTEIN.	4.11e+00
6	52	75.4	337	2	087136	ORF139-17 PROTEIN.	4.11e+00
7	52	75.4	494	5	P92024	MEX-1.	4.11e+00
8	51	73.9	43	10	049246	REVERSE TRANSCRIPTASE	6.51e+00
9	51	73.9	44	10	049247	REVERSE TRANSCRIPTASE	6.51e+00
10	51	73.9	231	3	074961	HYPOTHETICAL 25.6 KD P	6.51e+00
11	51	73.9	697	3	074504	HYPOTHETICAL 77.8 KD P	6.51e+00
12	49	71.0	248	5	027562	PRIC.	1.61e+01
13	49	71.0	260	13	042265	20S PROTEASOME SUBUNIT	1.61e+01
14	49	71.0	448	5	002441	GDP-DISSOCIATION INHIB	1.61e+01
15	49	71.0	1277	5	017517	ZC132.5 PROTEIN.	1.61e+01
16	49	71.0	3724	5	077320	MALP3.3 PROTEIN.	1.61e+01
17	48	69.6	90	5	062346	R11.2 PROTEIN.	2.50e+01
18	48	69.6	178	4	092592	CD89-L10.	2.50e+01
19	48	69.6	192	5	019008	COSMID D2096.	2.50e+01
20	48	69.6	221	2	053073	HYPOTHETICAL 25.7 KD P	2.50e+01

Result ID	Score	Match	Length	DB	ID	Description	Pred. No.
21	48	69.6	321	4	099608	NECDIN RELATED PROTEIN	2.50e+01
22	48	69.6	336	5	P91524	COSMID T28A11.	2.50e+01
23	48	69.6	336	5	045161	C17B7.1 PROTEIN.	2.50e+01
24	48	69.6	367	13	091905	FOK HEAD PROTEIN.	2.50e+01
25	48	69.6	370	13	091904	FOK HEAD PROTEIN.	2.50e+01
26	48	69.6	429	9	080300	MATURATION PROTEIN.	2.50e+01
27	48	69.6	490	2	084680	S/T PROTEIN KINASE.	2.50e+01
28	48	69.6	698	1	026996	PROBABLE SURFACE PROTE	2.50e+01
29	48	69.6	790	2	055956	ABC TRANSPORTER.	2.50e+01
30	48	69.6	1062	5	076657	P25E5.1 PROTEIN.	2.50e+01
31	48	69.6	2896	5	061363	HEMOCTANIN G-TYPE SUBU	2.50e+01
32	47	68.1	89	10	049240	REVERSE TRANSCRIPTASE	3.87e+01
33	47	68.1	110	9	064365	GP57.	3.87e+01
34	47	68.1	226	2	032335	ENDOTHELIAL CELL PROTE	3.87e+01
35	47	68.1	241	6	028105	S-ADENOSINETHIONINE D	3.87e+01
36	47	68.1	361	10	080402	1-MINOCYCLOPROPANE-1-	3.87e+01
37	47	68.1	473	10	043035	COSMID F58H12.	3.87e+01
38	47	68.1	509	5	021017	F10D2.11 PROTEIN.	3.87e+01
39	47	68.1	523	5	016922	HEME RECEPTOR.	3.87e+01
40	47	68.1	712	2	085161	K12B6.4 PROTEIN.	5.95e+01
41	46	66.7	203	5	016381	1-MINOCYCLOPROPANE-1-	5.95e+01
42	46	66.7	469	10	042881	1-MINOCYCLOPROPANE-1-	5.95e+01
43	46	66.7	518	10	043753	1-MINOCYCLOPROPANE-1-	5.95e+01
44	46	66.7	518	10	043753	MUTATED IN ATAXIA TELA	5.95e+01
45	46	66.7	3056	4	015429		

ALIGNMENTS

1
 ID 044626 PRELIMINARY; PRT; 560 AA.
 AC 044626;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE K11D12.1 PROTEIN.
 GN K11D12.1.
 OS CAENORHABDITIS ELEGANS.
 OC EMBRYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITIA; RHABDITIDA; RHABDITIDA; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BEKES M.,
 RA BONFIELD J., BORTON J., CONNELL M., COSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMBRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., KOOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLIDAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA HENKHAUS J., WOHLIDAN P., GILLAM B.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: A839047; G2736445; .
 DR PROSITE: P500028; ZINC_FINGER_C2H2; 1.
 KW ZINC-FINGER; METAL-BINDING; DNA-BINDING.
 SQ SEQUENCE 560 AA: 61136 MW: 5906EBYD CRC32;
 Query Match 87.0%, Score 60; DB 5; Length 560;

Best Local Similarity 87.5%; Pred. No. 8.58e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 81 OKYKRAPY 88
OY 1 OKYNRAPY 8

RESULT 2
ID 044677 PRELIMINARY; PRT; 521 AA.
AC 044677;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE NEUTRAL. PROTEASE.
OS BACILLUS AMYLOLIOUEFACIENS.
OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
[1]
SEQUENCE FROM N.A.
RA SHIMADA H., HONJO M., MITA I., NAKAYAMA A., ARAOKA A., MANABE K.,
RA FURUTANI Y.;
RL J. BIOTECHNOL. 2:75-85(1985).
DR EMBL; M36723; G143353; -;
DR PFAM; PF00099; zn-protease; 1.
KW PROTEASE.
SQ SEQUENCE 521 AA; 56725 MW; 64AFPE5F CRC32;

Query Match 81.2%; Score 56; DB 2; Length 521;
Best Local Similarity 66.7%; Pred. No. 6.17e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 308 OKYNSYD 316
OY 1 OKYNRAPY 9

RESULT 3
ID 035490 PRELIMINARY; PRT; 407 AA.
AC 035490;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE BEAINE HOMOCYSTEINE METHYL TRANSFERASE.
GN BHMT.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCURIONATHI; MURIDE; MURINAE; MUS.
[1]
SEQUENCE FROM N.A.
RA STRAIN-129; TISSUE-LIVER;
RA SORDEN M.P., SMITH H.C.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF033381; G2645804; -;
KW TRANSFERASE.
SQ SEQUENCE 407 AA; 45020 MW; 0A9A6F77 CRC32;

Query Match 76.8%; Score 53; DB 11; Length 407;
Best Local Similarity 66.7%; Pred. No. 2.58e+00;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 282 OKYAREAYN 290
OY 1 OKYNRAPY 9

RESULT 4
ID 036979 PRELIMINARY; PRT; 3082 AA.
AC 036979;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE POLYPROTEIN.

OS ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV).
OC VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
OC POTYVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SINGAPORE;
RA LEE K.C., WONG S.M.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF014811; G2462849; -;
DR PFAM; PF00271; helicase_C6; 1.
DR PFAM; PF00680; RNA_dep_RNA_pol; 1.
DR PFAM; PF00767; Poly-coat; 1.
DR PFAM; PF00851; Peptidase_C6; 1.
DR PFAM; PF00863; Peptidase_C4; 1.
KW POLYPROTEIN.
FT CHAIN 1 313 P1.
FT CHAIN 769 HELPER COMPONENT-PROTEINASE.
FT CHAIN 770 P3.
FT CHAIN 1115 6K1.
FT CHAIN 1116 6K1.
FT CHAIN 1168 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1801 6K2.
FT CHAIN 1802 1854 SMALL NUCLEAR INCLUSION-GENOME LINKED
FT CHAIN 1855 2044 VPC.
FT CHAIN 2045 2287 SMALL NUCLEAR INCLUSION-PROTEINASE.
FT CHAIN 2288 2803 LARGE NUCLEAR INCLUSION.
FT CHAIN 2804 3082 COAT PROTEIN.
SQ SEQUENCE 3082 AA; 350508 MW; 43030AF1 CRC32;

Query Match 76.8%; Score 53; DB 14; Length 3082;
Best Local Similarity 75.0%; Pred. No. 2.58e+00;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 279 OKYSRLPY 286
OY 1 OKYNRAPY 8

RESULT 5
ID 034232 PRELIMINARY; PRT; 337 AA.
AC 034232;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ORF40X1 PROTEIN.
OS VIBRIO CHOLERAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AI-1837;
RX MEDLINE; 97252505.
RA STROEHER U.H., PARASIVAM G., DREDGE B.K., MANNING P.A.;
RT "Novel Vibrio cholerae O139 genes involved in lipopolysaccharide
RT biosynthesis";
RL J. BACTERIOL. 179:2740-2747(1997).
DR EMBL; Y07786; E274690; -;
SQ SEQUENCE 337 AA; 40132 MW; 2D4A7939 CRC32;

Query Match 75.4%; Score 52; DB 2; Length 337;
Best Local Similarity 66.7%; Pred. No. 4.11e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 147 OKYSHAPYK 155
OY 1 OKYNRAPY 9

RESULT 6
ID 087136 PRELIMINARY; PRT; 337 AA.
AC 087136;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ORF139-17 PROTEIN.

OS VIBRIO CHOLERAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-M045;
 RA YAMASAKI S., SHIMIZU T., HOSHINO K., HO S., SHIMADA T., NAIR G.B.,
 RA TAKEBA Y.;
 RT "The genes responsible for O-antigen synthesis of *Vibrio cholerae*
 RT 0139 are closely related to those of *Vibrio cholerae* 022.";
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AB012956; D1034567; -;
 SQ SEQUENCE 337 AA; 40147 MW; 176846EB CRC32;

Query Match 75.4%; Score 52; DB 2; Length 337;
 Best Local Similarity 66.7%; Pred. No. 4.11e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 147 OKYHAPYK 155
 |||:|:
 1 OKYHAPYK 9

RESULT 7
 ID P92024 PRELIMINARY; PRT; 494 AA.
 AC P92024;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MEX-1.
 GN MEX-1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIINAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N2;
 RX MEDLINE; 97195715.
 RA GUEDES S., PRIEST J.R.;
 RT "The *C. elegans* MEX-1 protein is present in germline blastomeres and
 RT is a P granule component.";
 RL DEVELOPMENT 124:731-739(1997).
 DR EMBL: U01043; G1899062; -;
 DR PFAM: PF00642; zf-CCCH; 2.
 SQ SEQUENCE 494 AA; 56608 MW; 716506D2 CRC32;

Query Match 75.4%; Score 52; DB 5; Length 494;
 Best Local Similarity 55.6%; Pred. No. 4.11e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

263 ORYRPPFN 271
 ||:|:|:
 1 OKYHAPYK 9

RESULT 8
 ID 049246 PRELIMINARY; PRT; 43 AA.
 AC 049246;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE REVERSE TRANSCRIPTASE (FRAGMENT).
 GN RT.
 OS ALSTROEMERIA INODORA.
 OC EUKARYOTA; VIRIDIPHYTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; LILIALES;
 OC ALSTROEMERICAE; ALSTROEMERIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P002; TISSUE-YOUNG LEAVES;
 RC TRANSPOSON-TY1-COPIA-LIKE RETROTRANSPOSON;
 RA KIPERS A.G.J., HESLOP-HARRISON J.S., JACOBSEN E.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ223610; E1252160; -;

KW RNA-DIRECTED DNA POLYMERASE.
 FT NON_TER 1
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 5333 MW; E61D18CF CRC32;

Query Match 73.9%; Score 51; DB 10; Length 43;
 Best Local Similarity 71.4%; Pred. No. 6.51e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 14 YNRSPTD 20
 |||:|:
 3 YNRAPIYK 9

RESULT 9
 ID 049247 PRELIMINARY; PRT; 44 AA.
 AC 049247;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE REVERSE TRANSCRIPTASE (FRAGMENT).
 GN RT.
 OS ALSTROEMERIA INODORA.
 OC EUKARYOTA; VIRIDIPHYTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; LILIALES;
 OC ALSTROEMERICAE; ALSTROEMERIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P002; TISSUE-YOUNG LEAVES;
 RC TRANSPOSON-TY1-COPIA-LIKE RETROTRANSPOSON;
 RA KIPERS A.G.J., HESLOP-HARRISON J.S., JACOBSEN E.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ223611; E1252162; -;
 KW RNA-DIRECTED DNA POLYMERASE.
 FT NON_TER 1
 FT NON_TER 44
 FT NON_TER 44
 SQ SEQUENCE 44 AA; 5477 MW; 70CA73A1 CRC32;

Query Match 73.9%; Score 51; DB 10; Length 44;
 Best Local Similarity 71.4%; Pred. No. 6.51e+00;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 14 YNRSPTD 20
 |||:|:
 3 YNRAPIYK 9

RESULT 10
 ID 074961 PRELIMINARY; PRT; 231 AA.
 AC 074961;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 25.6 KD PROTEIN (FRAGMENT).
 GN SPOC736.16.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIZOSCOMYCETES;
 OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
 OC SCHIZOSACCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA WOOD V., RAJANDREAM M.A., BARRELL B.G., MURPHY L., HARRIS D.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AL023705; E1294543; -;
 KW HYPOTHETICAL PROTEIN.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 231 AA; 25584 MW; FB84EB08 CRC32;

Query Match 73.9%; Score 51; DB 3; Length 231;
 Best Local Similarity 62.5%; Pred. No. 6.51e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 120 DKYARSPY 127
OY 1 QKYNRPY 8

RESULT 11
ID 074504 PRELIMINARY: PRT: 697 AA.
AC 074504.

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 77.8 KD PROTEIN (FRAGMENT).

GN SPC594.01.

OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;

OC SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;

OC SCHIZOSACCHAROMYCES.

OC [1]

RC SEQUENCE FROM N.A.

RP STRAIN-972H-;

RA RIGGER M., LYNE M., RAJANDREAM M.A., BARRELL B.G.;

RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AL031523; E1319371; -.

KW HYPOTHETICAL PROTEIN.

FT NON-TER

SEQUENCE 697 AA; 77841 MW; 98C8C3F CRC32;

Query Match 73.9%; Score 51; DB 3; Length 697;

Best Local Similarity 62.5%; Pred. No. 6.51e+00;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 26 DKYARSPY 33
OY 1 QKYNRPY 8

RESULT 12
ID 027562 PRELIMINARY: PRT: 248 AA.

AC 027562.

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PRTC.

GN DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

OS EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.

OC [1]

RC SEQUENCE FROM N.A.

RP SHAULISKY G., ESCALANTE R., LOOMIS W.F.;

RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: X94983; E218570; -.

KW PFM; PF00996; CDI; 1.

SEQUENCE 448 AA; 50215 MW; 848511EC CRC32;

Query Match 71.0%; Score 49; DB 5; Length 448;

Best Local Similarity 50.0%; Pred. No. 1.61e+01;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 217 ORYGRSPY 224
OY 1 QKYNRPY 8

RESULT 15
ID 017517 PRELIMINARY: PRT: 1277 AA.

AC 017517.

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PRTC.

GN GEODIA CYDONIUM (SPONGE).

OS EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; TETRACINOMORPHA;

OC ASTROPHORIDA; GEODIIDA; GEODIA.

OC [1]

RC SEQUENCE FROM N.A.

RP KRASKO A., SCHEFFER U., KOZIOLO C., PANCER Z., BATEL R., BADRIA F.A.,

RA MOELLER W.E.G.;

RL AQUATIC TOXICOL. 37:157-168(1997).

DR EMBL: X94983; E218570; -.

KW PFM; PF00996; CDI; 1.

SEQUENCE 448 AA; 50215 MW; 848511EC CRC32;

Query Match 71.0%; Score 49; DB 5; Length 448;

Best Local Similarity 50.0%; Pred. No. 1.61e+01;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 217 ORYGRSPY 224
OY 1 QKYNRPY 8

RESULT 13
ID 042265 PRELIMINARY: PRT: 260 AA.

AC 042265.

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE 205 PROTEASOME SUBUNIT C2.

GN CC.

OS GALLUS GALLUS (CHICKEN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;

OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.

OC [1]

RC SEQUENCE FROM N.A.

RP SINGH I., WAGNER B.J.;

RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF027978; G3136063; -.

KW PFM; PF00227; proteasome; 1.

SEQUENCE 260 AA; 28925 MW; EF38499F CRC32;

Query Match 71.0%; Score 49; DB 13; Length 260;

Best Local Similarity 62.5%; Pred. No. 1.61e+01;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 120 ORYGRSPY 127
OY 1 QKYNRPY 8

RESULT 14
ID 002441 PRELIMINARY: PRT: 448 AA.

AC 002441.

DT 01-JUL-1997 (TREMBLREL. 04, CREATED)

DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE GDP-DISSOCIATION INHIBITOR.

GN GDI.

OS GEODIA CYDONIUM (SPONGE).

OC EUKARYOTA; METAZOA; PORIFERA; DEMOSPONGIAE; TETRACINOMORPHA;

OC ASTROPHORIDA; GEODIIDA; GEODIA.

OC [1]

RC SEQUENCE FROM N.A.

RP KRASKO A., SCHEFFER U., KOZIOLO C., PANCER Z., BATEL R., BADRIA F.A.,

RA MOELLER W.E.G.;

RL AQUATIC TOXICOL. 37:157-168(1997).

DR EMBL: X94983; E218570; -.

KW PFM; PF00996; CDI; 1.

SEQUENCE 448 AA; 50215 MW; 848511EC CRC32;

DE ZC132.5 PROTEIN.
GN ZC132.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONEFIELD J., BORTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA BRADSHAW H., DEVLIN K.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF014939; G2275629; -;
SQ SEQUENCE 1277 AA; 146496 MW; 8A6DB899 CRC32;

Query Match 71.0%; Score 49; DB 5; Length 1277;
Best Local Similarity 85.7%; Pred. No. 1.61e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 877 ORYRAP 883
|:|||||
OY 1 OXYRAP 7

Search completed: Thu Sep 2 11:58:48 1999
Job time : 30 secs.

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Best Local Similarity 75.0%; Pred. No. 2,26e-01;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 500 KYSRPPYN 507

Qy 2 KYNRAPYN 9

RESULT 2
ID GMRP MOUSE STANDARD; PRT: 1262 AA.

AC P27671;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).
GN RASGRF1 OR CDC25MM OR GRF1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNAETHI; MURIDAE; MORINAE; MUS.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 93010996.
RA CEN H., LOWT D.D.;
RT "Isolation of multiple mouse cDNAs with coding homology to
Saccharomyces cerevisiae CDC25: Identification of a region related to
Bcr, Vav, Dbl and CDC24.";
RL EMBO J. 11:4007-4015(1992).
[2]
RP SEQUENCE OF 791-1262 FROM N.A.
RC STRAIN-SWISS; TISSUE-BRAIN;
RX MEDLINE: 92289680.
RA MARTGANI C., VANONI M., ZIPPET R., COCCETTI P., BRAMBILLA R.,
FERRARI C., STRANI E.P., ALBERGHINA L.;
RT "Cloning by functional complementation of a mouse cDNA encoding a
homologue of CDC25, a Saccharomyces cerevisiae Ras activator.";
RL EMBO J. 11:2151-2157(1992).
[3]
RP SEQUENCE OF 1031-1226 FROM N.A.
RC MEDLINE: 92357779.
RA WEI W., MOSSELLER R.D., SANVAL P., GONZALES E., MCKINNEY D.,
DASGUPTA C., LI P., LIU B.X., BROEK D.;
RT "Identification of a mammalian gene structurally and functionally
related to the CDC25 gene of Saccharomyces cerevisiae.";
RL PROC. NATL. ACAD. SCI. U.S.A. 89:7100-7104(1992).
CC -1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: TO OTHER GUANINE-NUCLEOTIDE RELEASING FACTORS OF THE
CDC25 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS.
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CC -----
DR EMBL: L20899; G388247; -;
DR EMBL: X59866; G50358; -;
DR PIR: S20730; S20730.
DR PIR: S22693; S22693.
DR MGD: MGI:99694; RASGRF1.
DR PROSITE: PS00720; GDS_CDC25; 1.
DR PROSITE: PS00741; GDS_CDC24; 1.
DR PROSITE: PS50003; PH_DOMAIN; 2.
DR PFAM: PF00169; PH; 2.
DR PFAM: PF00612; IQ; 1.
DR PFAM: PF00617; RASGEF; 1.
DR PFAM: PF00618; RASGEF; 1.
DR PFAM: PF00621; RHOGEF; 1.
KW GUANINE-NUCLEOTIDE RELEASING FACTOR.

FT DOMAIN 22 130 PH.
FT DOMAIN 460 588 PH.
FT CONFILCT 1033 1033 E -> D (IN REF. 3).
SQ SEQUENCE 1262 AA; 144101 MM; 021C787F CRC32;

Query Match 78.3%; Score 54; DB 1; Length 1262;
Best Local Similarity 62.5%; Pred. No. 3,81e-01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1060 EKYRTPY 1067
Qy 1 OKYNRAPY 8

RESULT 3
ID BHMT HUMAN STANDARD; PRT: 406 AA.

AC Q93058;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DE BETALINE--HOMOCYSTEINE S-METHYLTRANSFERASE (EC 2.1.1.5).
GN BHMT.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 96394355.
RA GARROW T.A.;
RT "Purification, kinetic properties, and cDNA cloning of mammalian
rat betaine-homocysteine methyltransferase.";
RL J. BIOL. CHEM. 271:22831-22838(1996).
CC -1- FUNCTION: INVOLVED IN THE REGULATION OF HOMOCYSTEINE METABOLISM.
CC CONVERTS BETALINE AND HOMOCYSTEINE TO DIMETHYLGLYCINE AND
METHIONINE, RESPECTIVELY. THIS REACTION IS ALSO REQUIRED FOR THE
IRREVERSIBLE OXIDATION OF CHOLINE.
CC -1- CATALYTIC ACTIVITY: TRIMETHYLAMMONIACETATE + L-HOMOCYSTEINE -
DIMETHYLGLYCINE + L-METHIONINE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: PRIMARILY FOUND IN LIVER AND KIDNEY.
CC -1- DISEASE: DEFECTS IN BHMT COULD LEAD TO HYPERHOMOCYST(E)EMIA. BUT
SUCH A DEFECT HAS NOT YET BEEN OBSERVED. HYPERHOMOCYST(E)EMIA IS
AN INDEPENDENT RISK FACTOR FOR THE DEVELOPMENT OF ARTERIOSCLEROTIC
VASCULAR DISEASE.
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CC -----
DR EMBL: U50929; G1522683; -;
DR MIM: 602888; -;
DR HSSP: P06139; 1GRU.
KW TRANSFERASE; METHYLTRANSFERASE.
SQ SEQUENCE 406 AA; 44970 MM; 8DEC74F5 CRC32;
Query Match 76.8%; Score 53; DB 1; Length 406;
Best Local Similarity 66.7%; Pred. No. 6,38e-01;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 282 OKYAREAYN 290
Qy 1 OKYNRAPYN 9

RESULT 4
ID BHMT_RAT STANDARD; PRT: 407 AA.
AC Q09171;
DT 15-DEC-1998 (REL. 37, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE BETAIN-1-HOMOCYSTEINE S-METHYLTRANSFERASE (EC 2.1.1.5).
 GN BMT.
 OS RATTUS NORVEGICUS (RAT).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
 RX MEDLINE: 96354796.
 RA FORSTER M., REICHEN J., SOLIOZ M.;
 RT "Application of mRNA differential display to liver cirrhosis: reduced
 RT fetal expression in biliary cirrhosis in the rat.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 225:377-383(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SOWEN M.P., SPARKS J.D., SPARKS C.E., SMITH H.C.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: INVOLVED IN THE REGULATION OF HOMOCYSTEINE METABOLISM.
 CC -1- CATALYTIC ACTIVITY: TRIMETHYLAMONIACETATE + L-HOMOCYSTEINE -
 CC DIMETHYLGLYCINE + L-METHIONINE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -----
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 CC -----
 DR EMBL: U96133; G2072346; -
 DR EMBL: AF038870; G2766705; -
 DR TRANSFERASE: METHYLTRANSFERASE.
 KW SEQUENCE 407 AA; 44976 MW; B245A8BF CRC32;
 SQ
 Query Match 76.8%; Score 53; DB 1; Length 407;
 Best Local Similarity 66.7%; Pred. No. 6.38e-01;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 282 OKYARAYN 290
 11111111
 QY 1 OKYARAYN 9

RA KLOETZEL P.-M.;
 RT "Molecular characterization of the genomic regions of the Drosophila
 RT alpha-type subunit proteasome genes PROS-dm28.1 and PROS-dm35.";
 RL EUR. J. BIOCHEM. 205:1043-1051(1992).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH. THE 35 KD SUBUNIT IS PROBABLY A
 CC REGULATORY SUBUNIT. THE PROTEASOME HAS AN ATP-DEPENDENT
 CC PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
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 CC -----
 DR EMBL: X15497; G8382; -
 DR EMBL: X62285; G8388; -
 DR PIR: S05507; SNF5K.
 DR PIR: S23450; S23450.
 DR FLVASE: PRG0003151; PRO335.
 DR PROSITE: PS00388; PROTEASOME_A. 1.
 DR PFAM: PF00227; Proteasome; 1.
 DR HSP: P25156; 1PMA.
 KW PROTEASOME; HYDROLASE; PROTEASE; PHOSPHORYLATION.
 FT MOD. RES. 103
 FT PHOSPHORYLATION (POTENTIAL).
 SQ SEQUENCE 279 AA; 31058 MW; AA18BBD F CRC32;
 Query Match 75.4%; Score 52; DB 1; Length 279;
 Best Local Similarity 62.5%; Pred. No. 1.06e-00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 121 ORYDREPY 128
 11111111
 QY 1 OKYARAYN 8

RC STRAIN-CV, DESIREE;
 RA MEDLINE: 95036004.
 RA MAD ARIF S.A., TAYLOR M.A., GEORGE L.A., BUTLER A.R., BURCH L.R.,
 RA DAVIES H.V., SPARK M.J., KUMAR A.;
 RT "Characterisation of the S-adenosylmethionine decarboxylase (SAMDC)
 gene of potato.";
 RL PLANT MOL. BIOL. 26:327-338(1994).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE - (5-DEOXY-5'-ADENOSYL)
 CC (3-AMINOPROPYL)METHYLSULFONIUM SALT + CO(2).
 CC -1- COFACTOR: THIS ENZYME REQUIRES A PYRUVYL GROUP FOR ITS ACTIVITY.
 CC -1- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE
 CC AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
 CC BIOSYNTHESIS FROM PUTRESCINE.
 CC -1- TISSUE SPECIFICITY: STOLON, ALSO EXPRESSED IN LEAVES, STEMS
 CC AND ROOTS.
 CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED IN THE STOLON TIP DURING THE
 CC EARLY STAGES OF TUBERIZATION. MAXIMUM EXPRESSION WAS IN NON-
 CC SWELLING STOLON TIPS FROM STAGE B, AND LEVEL DECLINED AS THE
 CC TUBER INCREASED IN SIZE.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z11680; G21485; -
 CC DR EMBL: S74514; G807094; -
 CC DR PIR: S28047; S28047.
 CC KW SPERMIDINE BIOSYNTHESIS; LYSASE: DECARBOXYLASE; PYRUVATE; ZYMOGEN.
 CC FT CHAIN 1 72
 CC FT CHAIN (BY SIMILARITY).
 CC FT S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
 CC FT CHAIN (BY SIMILARITY).
 CC FT S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
 CC FT SITE 72 73
 CC FT CLEAVAGE (BY SIMILARITY).
 CC FT CLEAVAGE (NONHYDROLYTICAL)
 CC FT MOD.RES 73 73
 CC FT (BY SIMILARITY).
 CC FT CONVERTED TO A PYRUVYL GROUP
 CC FT ACT_SITE 13 13
 CC FT (BY SIMILARITY).
 CC FT IMPORTANT FOR CATALYTIC ACTIVITY (BY
 CC FT SIMILARITY).
 CC FT IMPORTANT FOR CATALYTIC ACTIVITY (BY
 CC FT SIMILARITY).
 CC FT ACT_SITE 87 87
 CC FT SIMILARITY).
 CC FT ACT_SITE 16 16
 CC FT SIMILARITY).
 CC FT IMPORTANT FOR CATALYTIC ACTIVITY (BY
 CC FT SIMILARITY).
 CC FT CONFLICT 174 174
 CC FT CONFLICT 257 257
 CC FT CONFLICT 291 291
 CC FT CONFLICT 305 305
 CC FT I -> T (IN REF. 2).
 CC FT I -> T (IN REF. 2).
 CC FT SEQUENCE 360 AA; 39726 MW; 4F29EFED CRC32;
 CC SQ
 CC
 CC Query Match 75.4%; Score 52; DB 1; Length 360;
 CC Best Local Similarity 62.5%; Pred. No. 1.06e+00;
 CC Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Db 332 OKFTTPY 339
 CC ||:|:|:
 CC QY 1 OKYNBAPY 8
 CC
 CC RESULT 7
 CC ID NPRE_BACAM STANDARD; PRT; 521 AA.
 CC AC P06832;
 CC DT 01-JAN-1988 (REL. 06, CREATED)
 CC DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 CC DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 CC DE BACILLOLYSIN PRECURSOR (EC 3.4.24.28) (NEUTRAL PROTEASE).
 CC GN NFR.
 CC OS BACILLUS AMILOLIQUEFACIENS.
 CC OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 CC RN BACILLUS.
 CC [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 23844;
 RX MEDLINE: 85006739.
 RA VASANTHA N., THOMPSON L.D., RHODES C., BANNER C., NAGLE J.,
 RA FILIPULA D.;
 RT "Genes for alkaline protease and neutral protease from Bacillus
 RT amyloliquefaciens contain a large open reading frame between the
 RT regions coding for signal sequence and mature protein.";
 RL J. BACTERIOL. 159:811-819(1984).
 CC -1- FUNCTION: THERMOABILE EXTRACELLULAR ZINC METALLOPROTEASE.
 CC -1- CATALYTIC ACTIVITY: SIMILAR, BUT NOT IDENTICAL, TO THAT OF
 CC THERMOLYSIN.
 CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
 CC PROTEOLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4 (ZINC METALLOPROTEASE);
 CC ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: K02497; G143249; -
 CC DR PIR: A25415; HYBSN.
 CC DR PROSITE: P500142; ZINC_PROTEASE; 1.
 CC DR PFAM: PF00099; zn-protease; 1.
 CC DR HSSP: P00800; ITRL.
 CC KW HYDROLASE; METALLOPROTEASE; ZINC; CALCIUM; ZYMOGEN; SIGNAL.
 CC FT SIGNAL 1 27
 CC FT PROPER 28 221
 CC FT CHAIN 222 521
 CC FT METAL 364 364
 CC FT METAL 365 365
 CC FT METAL 366 366
 CC FT METAL 368 368
 CC FT ACT_SITE 449 449
 CC FT PROTON DONOR (BY SIMILARITY).
 CC FT SEQUENCE 521 AA; 56840 MW; BC0147D4 CRC32;
 CC SQ
 CC
 CC Query Match 73.9%; Score 51; DB 1; Length 521;
 CC Best Local Similarity 55.6%; Pred. No. 1.76e+00;
 CC Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Db 308 OKFNRSYD 316
 CC ||:|:|:
 CC QY 1 OKYNBAPY 9
 CC
 CC RESULT 8
 CC ID PRC2_HUMAN STANDARD; PRT; 263 AA.
 CC AC P25786;
 CC DT 01-MAY-1992 (REL. 22, CREATED)
 CC DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 CC DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 CC DE PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
 CC DE (PROTEASOME NO CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT
 CC C2) (30 KD PROSOMAL PROTEIN) (PROS-30).
 CC GN PSMAL OR PSC2 OR PROS30.
 CC OS HOMO SAPIENS (HUMAN).
 CC OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 CC RN [1]
 CC SEQUENCE FROM N.A.
 CC RX MEDLINE: 93013039.
 CC RA SILVA-PEREIRA I., BEY F., COUX O., SCHERRER K.;
 CC RT "Two mRNAs exist for the Hs PROS-30 gene encoding a component of
 CC human proteasomes.";
 CC RL GENE 120:235-242(1992).
 CC RN [2]
 CC SEQUENCE FROM N.A.

RX MEDLINE: 91223105.
 RA TAMURA T., LEE D.H., OSAKA F., FUJIMURA T., SHIN S., CHUNG C.H.,
 RA TANAKA K., ICHIHARA A.;
 RT "Molecular cloning and sequence analysis of cDNAs for five major
 RT subunits of human proteasomes (multi-catalytic proteinase
 RT complexes).";
 RN BIOCHEMA. BIOPHYS. ACTA 1089:95-102(1991).
 RL [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91363412.
 RA DEARNTINO G.N., ORTH K., MCCULLOUGH M.L., LEE L.W., MONN T.Z.,
 RA MOONAW C.R., DAWSON P.A., SLAUGHTER C.A.;
 RT "The primary structures of four subunits of the human,
 RT high-molecular-weight proteinase, macropain (proteasome), are
 RT distinct but homologous.";
 RL BIOCHEMA. BIOPHYS. ACTA 1079:29-38(1991).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
 CC PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS (SHORT AND LONG) ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE GENE FOR THIS PROTEIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
 CC -----
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 CC -----
 CC
 DR EMBL: M64992; G190447; ALT SEQ.
 DR EMBL: D00759; G220022; -
 DR EMBL: X61969; G296738; -
 DR PIR: S15897; S15897.
 DR PIR: JCI445; JCI445.
 DR AAKHUS/GHEHT-2DPAGE; 2223; IEF.
 DR MIM: 602854; -
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PFAM: PF00227; proteasome; 1.
 DR HSSP: P25156; 1PMA.
 CC PROTEASOME: HYDROLASE; PROTEASE; ACETYLATION; ALTERNATIVE SPLICING.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT VARSPLIC 1 1 M -> MOLSVRK (IN LONG FORM).
 SQ SEQUENCE 263 AA; 29555 MW; 6CD09A93 CRC32;
 DB 121 ORYGRAPY 128
 OY 1 OKYRAPY 8
 Query Match 71.0%; Score 49; DB 1; Length 263;
 Best Local Similarity 62.5%; Pred. No. 4.72e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 ID PRG2-RAT STANDARD; PRT; 263 AA.
 AC P18420;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROTEASOME COMPONENT C2 (EC 3.4.99.46) (MACROPAIN SUBUNIT C2)
 DE (PROTEASOME NU CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT
 DE C2).

GN PSMAL.
 OS RATTUS NORVEGICUS (RAT).
 OC EURAROTIA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-LIVER;
 RX MEDLINE: 90057428.
 RA FUJIMURA T., TANAKA K., KUMATORI A., SHIN S., YOSHIMURA T.,
 RA ICHIHARA A., TOKUNAGA F., ARUGA R., IWANAGA S., KAKIZUKA A.,
 RA NAKANISHI S.;
 RT "Molecular cloning of cDNA for proteasomes (multicatalytic proteinase
 RT complexes) from rat liver: primary structure of the largest component
 RT (C2).";
 RL BIOCHEMASTRY 28:7332-7340(1989).
 RN [2]
 RP SEQUENCE OF 1-30.
 RC TISSUE-LIVER;
 RX MEDLINE: 9024011.
 RA TOKUNAGA F., ARUGA R., IWANAGA S., TANAKA K., ICHIHARA A., TAKAO T.,
 RA SHIONISHI Y.;
 RT "The NH2-terminal residues of rat liver proteasome (multicatalytic
 RT proteinase complex) subunits, C2, C3 and C8, are N
 RL alpha-acetylated.";
 CC FEBS LETT. 263:373-375(1990).
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
 CC PROTEOLYTIC ACTIVITY.
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL RAT TISSUES.
 CC -1- PTM: ITS C-TERMINAL EXTENSION IS PARTIALLY CLEAVED OFF BY LIMITED
 CC PROTEOLYSIS LEADING TO A CONVERSION OF THE PROTEASOME FROM ITS
 CC LATENT INTO ITS ACTIVE FORM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C2 SUBFAMILY.
 CC -----
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 CC -----
 CC
 DR EMBL: M29859; G206382; -
 DR EMBL: D90265; G220877; -
 DR PIR: A32968; SNR3C2.
 DR PROSITE: PS00388; PROTEASOME_A; 1.
 DR PFAM: PF00227; proteasome; 1.
 DR HSSP: P25156; 1PMA.
 CC PROTEASOME: HYDROLASE; PROTEASE; ACETYLATION.
 FT MOD_RES 1 1 ACETYLATION.
 SQ SEQUENCE 263 AA; 29517 MW; 01D55620 CRC32;
 DB 121 ORYGRAPY 128
 OY 1 OKYRAPY 8
 Query Match 71.0%; Score 49; DB 1; Length 263;
 Best Local Similarity 62.5%; Pred. No. 4.72e+00;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 ID CG2A-DROME STANDARD; PRT; 491 AA.
 AC P14785;

DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE G2/MITOTIC-SPECIFIC CYCLIN A.
 GN CYCA
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PTERYGOTA; DIPERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDERA;
 OC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 93077051.
 RX TAKAHISA M., TOGASHI S., UEDA R., MIKUNI M., TSURUMURA S., KONDO K.,
 RA MIYAKE T.;
 RT "Structure of the Drosophila melanogaster gene encoding cyclin A.";
 RL GENE 121:343-346(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 89168447.
 RX LEHNER C.F., O'FARRELL P.H.;
 RT "Expression and function of Drosophila cyclin A during embryonic cell
 cycle progression.";
 RL CELL 56:957-968(1989).
 RN [3]
 RP SEQUENCE OF 235-247 AND 288-300 FROM N.A.
 RA WHITFIELD W.G.F., GONZALEZ C., SANCHEZ-HERRERO E., GLOYER D.M.;
 RT "Transcripts of one of two Drosophila cyclin genes become localized
 in pole cells during embryogenesis.";
 RL NATURE 338:337-340(1999).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
 KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
 AND ARE ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STONEBEST TO OTHER
 CYCLINS A.
 CC -----
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 CC -----
 DR EMBL: D10857; G407199; -;
 DR EMBL: D10856; G407199; JOINED.
 DR EMBL: D10858; G391659; -;
 DR EMBL: M24841; G157157; -;
 DR PIR: JCI390; JCI390.
 DR PIR: S03543; S03543.
 DR FLYBASE: FBgn0000404; CYCA.
 DR PROSITE: P560292; CYCLINS.1.
 DR PIR: P500134; cyclin; 1.
 DR HSSP: P20248; 1FIN.
 DR CYCLIN; CELL CYCLE; CELL DIVISION; MITOSIS.
 KW CONFLICT 147 147 M -> I (IN CDNA: G391659).
 FT CONFLICT 179 179 A -> V (IN REF. 2).
 FT CONFLICT 200 200 V -> M (IN CDNA: G391659).
 FT CONFLICT 223 223 H -> R (IN REF. 2).
 FT CONFLICT 474 474 L -> Q (IN CDNA: G391659).
 SQ SEQUENCE 491 AA: 56124 MW: 9F047FAD CRC32;
 Query Match 71.0%; Score 49; DB 1; Length 491;
 Best Local Similarity 55.6%; Pred. No. 4.72e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 DB 435 EKYNRDRTYK 443
 QY :|||||:
 1 QKYNRAPYN 9
 RESULT 11

ID REPB-STREP STANDARD; PRT; 210 AA.
 AC P13921;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
 DE REPLICATION PROTEIN REPB.
 GN REPB.
 OS STREPTOCOCCUS PNEUMONIAE, AND STREPTOCOCCUS AGALACTIAE.
 OG PLASMID PLS1, AND PLASMID PMV158.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PLASMID-PLS1;
 RX MEDLINE: 87226167.
 RA LACKS S.A., LOPEZ P., GREENBERG B., ESPINOSA M.;
 RT "Identification and analysis of genes for tetracycline resistance and
 replication functions in the broad-host-range plasmid PLS1.";
 RL J. MOL. BIOL. 192:753-765(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA PLASMID-PMV158;
 RX MEDLINE: 90016790.
 RA VAN DER LELIE D., BRON S., VENEMA G., OSRAM L.;
 RT "Similarity of minus origins of replication and flanking open reading
 frames of plasmids PUB10, PTB913 and PMV158.";
 RL NUCLEIC ACIDS RES. 17:7283-7294(1989).
 CC -1- FUNCTION: IS ESSENTIAL FOR PLASMID REPLICATION. NICKS THE POSITIVE
 STRAND AT THE PLUS ORIGIN OF REPLICATION.
 CC -1- SIMILARITY: WITH REPLICATION PROTEINS FROM OTHER GRAM+ BACTERIAL
 CC PLASMIDS. REPLICATING WITH THE ROLLING-CIRCLE MECHANISM.
 CC -----
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 CC -----
 DR EMBL: X15669; G46664; -;
 DR EMBL: M29725; G149699; -;
 DR PIR: B25599; B25599.
 DR PIR: S05981; S05981.
 KW PLASMID: DNA REPLICATION; TOPOISOMERASE.
 SQ SEQUENCE 210 AA: 24250 MW: 4680A629 CRC32;
 Query Match 69.6%; Score 48; DB 1; Length 210;
 Best Local Similarity 55.6%; Pred. No. 7.65e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 DB 49 QKXKKAHYH 57
 QY :|||||:
 1 QKYNRAPYN 9
 RESULT 12
 ID FCAR HUMAN STANDARD; PRT; 287 AA.
 AC P24071; Q15728; Q15727; Q13603; Q13604;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR (IGA FC RECEPTOR) (CD89
 ANTIGEN).
 GN FCAR OR CD89.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91079769.
 RA MALISZEWSKI C.R., MARCH C.J., SCHOMBORN M.A., GIMBEL S., SHEN L.;
 RT "Expression cloning of a human Fc receptor for Iga.";

RL J. EXP. MED. 172:1665-1672(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RX MEDLINE: 95363085;
 RA DE WIT T.P.M., MORTON H.C., CAPEL P.J.A., VAN DE WINKEL J.G.J.;
 RT "Structure of the gene for the human myeloid Iga Fc receptor (CD89).";
 RL J. IMMUNOL. 155:1203-1209(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (FORMS A.2 AND A.3).
 RC TISSUE-ALVEOLAR MACROPHAGE, AND MONOCYTES;
 RX MEDLINE: 9624767;
 RA PATRY C., SIBILLE Y., LEHUEU A., MONTEIRO R.C.;
 RT "Identification of Fc alpha receptor (CD89) isoforms generated by
 alternative splicing of the alpha chain that are differentially expressed between blood
 monocytes and alveolar macrophages.";
 RL J. IMMUNOL. 156:4442-4448(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (FORMS B AND B-DELTA-S2).
 RC VAN DIJK T.B., MORTON H.C., CALDENHOVEN E., BRACKE M.,
 RA RAUJMAKERS J.A.M., LAMMERS J.W.J., KOENDERMAN L., GROOT R.P.;
 RT SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL [5]
 RP SEQUENCE FROM N.A. (FORM A.3/RLA2).
 RX MEDLINE: 96433090.
 RA PLEKSS R.J., ANDREWS P.D., KERR M.A., MOORE J.M.;
 RT "Alternative splicing of the human Iga Fc receptor CD89 in
 neutrophils and eosinophils.";
 RL BIOCHEM. J. 318:771-777(1996).
 RN [6]
 RP SUBUNITS.
 RX MEDLINE: 94375887.
 RA PEEFERORN L.C., YEAMAN G.R.;
 RT "Association of Iga-Fc receptors (Fc alpha R) with Fc epsilon RI
 gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
 phosphorylation of gamma 2.";
 RL J. IMMUNOL. 153:3228-3236(1994).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN ALPHA.
 CC -1- MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
 CC -1- SUBUNIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
 CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
 CC (FORM B).
 CC -1- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN BLOOD AND
 CC MUCOSAL MRELOID CELLS. MONOCYTES EXPRESS ISOFORMS A.1, A.2 AND A.3
 CC WHILE ALVEOLAR MACROPHAGES EXPRESS A.1 AND A.2 TRANSCRIPTS;
 CC HOWEVER THEY EXPRESS ONLY ONE ISOFORM AT THEIR SURFACES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FIVE FORMS: A.1 (SHOWN HERE), A.2,
 CC A.3, B AND B-DELTA-S2 ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 2 C2-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD89 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/row/cd/cd89.htm".
 CC
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 CC EMBL: X54150; G31330; -
 CC EMBL: X87767; G1054737; -
 CC EMBL: X87768; G1054737; JOINED.
 CC EMBL: X87769; G1054737; JOINED.
 CC EMBL: X87765; G1054737; JOINED.
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FT DISULFID 504 515 BY SIMILARITY.
 FT DISULFID 542 587 BY SIMILARITY.
 FT DISULFID 586 595 BY SIMILARITY.
 FT CARBOHYD 500 500 POTENTIAL.
 FT CONFLICT 24 24 F -> M (IN REF. 3).
 SQ SEQUENCE 615 AA; 69918 MW; DC5E6E8A CRC32;

Query Match 69.6%; Score 48; DB 1; Length 615;
 Best Local Similarity 55.6%; Pred. No. 7.65e+00;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 249 OKYKAPFS 257
 |||:|:|:
 OY 1 OKYKAPYN 9

OY 2 KYNRAPYN 9

Search completed: Thu Sep 2 11:58:00 1999
 Job time : 8 secs.

RESULT 15
 ID TKT_STRPN STANDARD; PRT; 656 AA.
 AC P22976;

RT 01-AUG-1991 (REL. 19, CREATED)
 RT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 RT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE PROBABLE TRANSKETOLASE (EC 2.2.1.1) (TK).
 GN RECP.

OS STREPTOCOCCUS PNEUMONIAE.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 OC STREPTOCOCCUS.

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CP1200;
 RX MEDLINE; 90299784.

RA RADNIS B.A., RHEE D.-K., MORRISON D.A.;

RT "Genetic transformation in Streptococcus pneumoniae: nucleotide
 RT sequence and predicted amino acid sequence of recp.";
 RT J. BACTERIOL. 172:3669-3674(1990).

RL [2]
 RN POSSIBLE FUNCTION.

RX MEDLINE; 94069049.

RA REIZER J., REIZER A., BAIRICH A., SAIER M.H. JR.;

RT "A diverse transketolase family that includes the Recp protein of
 RT Streptococcus pneumoniae, a protein implicated in genetic
 RT recombination.";

RL RES. MICROBIOL. 144:341-347(1993).

CC -1- FUNCTION: NECESSARY FOR HIGH-EFFICIENCY RECOMBINATION CHROMOSOMAL
 CC DNA DURING GENETIC TRANSFORMATION (ACCORDING TO REF.1).
 CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLICERALDEHYDE
 CC 3-PHOSPHATE -> D-RIBOSE 5-PHOSPHATE + D-XYLULOSE 5-PHOSPHATE.

CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.

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CC EMBL; M31296; G153792; -.

DR PIR; A43018; XJSOKP.

DR PROSITE; PS00801; TRANSKETOLASE_1; 1.
 DR PROSITE; PS00802; TRANSKETOLASE_2; 1.

DR PFAM; PF00456; transketolase; 1.
 DR HSSP; P23254; IAYO.

KW TRANSFERASE; THIAMINE PYROPHOSPHATE; DNA RECOMBINATION.
 SQ SEQUENCE 656 AA; 71662 MW; E4B1D3D0 CRC32;

Query Match 69.6%; Score 48; DB 1; Length 656;
 Best Local Similarity 75.0%; Pred. No. 7.65e+00;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 133 KYNREGYN 140
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##molecule_type DNA
##residues 1-689 ##label AND
##cross-references EMBL:235912; NID:9536267; PID:9536268; MIPS:YBR043c
##experimental_source strain S288C
GENETICS

##map_position 2R
CLASSIFICATION #superfamily yeast probable membrane protein YBR043c
KEYWORDS transmembrane protein

FEATURE
108-124 #domain transmembrane #status predicted #label TM1
140-161 #domain transmembrane #status predicted #label TM2
177-193 #domain transmembrane #status predicted #label TM3
239-256 #domain transmembrane #status predicted #label TM4
265-287 #domain transmembrane #status predicted #label TM5
476-493 #domain transmembrane #status predicted #label TM6
513-529 #domain transmembrane #status predicted #label TM7
555-579 #domain transmembrane #status predicted #label TM8
587-603 #domain transmembrane #status predicted #label TM9
629-645 #domain transmembrane #status predicted #label TM10
648-670 #domain transmembrane #status predicted #label TM11

SUMMARY #length 689 #molecular-weight 77300 #checksum 8706

Query Match 79.7%; Score 55; DB 2; Length 689;
Best Local Similarity 75.0%; Pred. No. 7.83e-01;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 500 KYSRPPN 507
|:|:|
QY 2 KYRNPYN 9

RESULT 3
ENTRY S28407 #type complete
TITLE guanine nucleotide-exchange activator CDC25 homolog - mouse
FORMAL_NAME Mus musculus #common_name house mouse
ORGANISM 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
DATE 10-Sep-1997
ACCESSIONS S28407; S22693; B46199; S20730
REFERENCE S28407
#authors Cen, H.; Papageorge, A.G.; Zippel, R.; Lowy, D.R.; Zhang, K.
#journal EMBO J. (1992) 11:4007-4015
#title Isolation of multiple mouse cDNAs with coding homology to
Saccharomyces cerevisiae CDC25: identification of a region
related to Bcr, Vav, Dbl and CDC24.
#cross-references MUID:93010996
#accession S28407
##status not compared with conceptual translation
##molecule_type mRNA
##residues 1-1260 ##label CEN
REFERENCE S22693
#authors Martegani, E.; Vanoni, M.; Zippel, R.; Cocchetti, P.;
Brambilla, R.; Ferrari, C.; Sturani, E.; Alberghina, L.
#journal EMBO J. (1992) 11:2151-2157
#title Cloning by functional complementation of a mouse cDNA
encoding a homologue of CDC25, a Saccharomyces cerevisiae
RAS activator.
#cross-references MUID:92289680
#accession S22693
##molecule_type mRNA
##residues 789-1260 ##label MAR
##cross-references EMBL:X59868; NID:950357; PID:950358
REFERENCE A46199
#authors Wei, W.; Mosteller, R.D.; Sanval, P.; Gonzales, E.; McKinney,
D.; Dasgupta, C.; Li, P.; Liu, B.-X.; Broek, D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104
#title Identification of a mammalian gene structurally and
functionally related to the CDC25 gene of Saccharomyces
cerevisiae.
#cross-references MUID:92357779
#accession B46199
##status preliminary
##molecule_type nucleic acid
##residues 1029-1030, 'D', 1032-1224 ##label WEI

##experimental_source fetus
##note sequence extracted from NCBI backbone (NCBIN:111101,
NCBIP:111102)
CLASSIFICATION #superfamily CDC25-type guanine nucleotide exchange activator
homology; CDC24 homology; pleckstrin repeat homology

FEATURE
242-428 #domain CDC24 homology #label CD24
1021-1257 #domain CDC25-type guanine nucleotide exchange activator
homology #label SOS

SUMMARY #length 1260 #molecular-weight 143900 #checksum 9725

Query Match 78.3%; Score 54; DB 2; Length 1260;
Best Local Similarity 62.5%; Pred. No. 1.26e+00;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1058 EKERPPY 1065
|:|:|
QY 1 OKYRAPPY 8

RESULT 4
ENTRY SNF5K #type complete
TITLE multicatalytic endopeptidase complex (EC 3.4.99.46) 35k chain
- fruit fly (Drosophila melanogaster)
ALTERNATE_NAMES 19S cylinder particle 35k chain; multicatalytic proteinase
35k chain; prosome 35k chain; prosome 35k chain
ORGANISM #formal_name Drosophila melanogaster
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
05-Sep-1997
ACCESSIONS S23450; S05507; A38761
REFERENCE S23450
#authors Frentzel, S.; Troxell, M.; Haass, C.; Pesold-Hurt, B.;
Glaetzel, K.H.; Klotzel, P.M.
#journal Eur. J. Biochem. (1992) 205:1043-1051
#title Molecular characterization of the genomic regions of the
Drosophila alpha-type subunit proteasome genes PROS-Dm28.1
and PROS-Dm35.
#cross-references MUID:92249308
#accession S23450
##molecule_type DNA
##residues 1-279 ##label FREN
##cross-references EMBL:X62285; NID:98387; PID:98388
##experimental_source strain Canton S
REFERENCE S05507
#authors Haass, C.; Pesold-Hurt, B.; Multhaup, G.; Beyreuther, K.;
Klotzel, P.M.
#journal EMBO J. (1989) 8:2373-2379
#title The PROS-35 gene encodes the 35 kd protein subunit of
Drosophila melanogaster proteasome.
#cross-references MUID:90005444
#accession S05507
##molecule_type mRNA
##residues 1-279 ##label HAA
##cross-references EMBL:X15497; NID:98381; PID:98382
#accession A38761
##molecule_type protein
##residues 4-18;194-206 ##label HAA2
GENETICS
#gene PROS-35
##cross-references FlyBase:FBgn0003151
#map_position 89F-90A
#introns 1/3; 211/3
CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9
KEYWORDS hydrolase; phosphoprotein; proteinase
SUMMARY #length 279 #molecular-weight 31058 #checksum 365

Query Match 75.4%; Score 52; DB 1; Length 279;
Best Local Similarity 62.5%; Pred. No. 3.18e+00;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 121 ORYDRPPY 128
|:|:|
QY 1 OKYRAPPY 8

```

RESULT      5          B71854    #type complete
ENTRY       type II DNA modification enzyme (methyltransferase) -
TITLE       Helicobacter pylori (strain J99)
ORGANISM    #format_name Helicobacter pylori
VARIETY     strain J99
DATE        12-Feb-1999 #sequence_revlsion 12-Feb-1999 #text_change
ACCESSIONS  B71854
REFERENCE    A71800
AUTHORS     Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.,
              Dolg, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge,
              B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
              Ulla-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
              Morberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
              G.F.; Trust, T.J
#journal    Nature (1999) 397:176-180
#title      Genomic sequence comparison of two unrelated isolates of the
             human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accesion   B71854
#status     preliminary
#molecule_type DNA
##residues 1-321 ##label ARN
##cross-references GB:AEOU1533; GB:AEOU1439; NID:g4155636; PID:g4155654
##experimental_source strain J99
GENETICS
#gene
SUMMARY     jhp1050
            #length 321 #molecular_weight 36919 #checksum 5430

Query Match           75.4% Score 52; DB 2; Length 321;
Best Local Similarity 66.7%; Pred. No. 3.18e+00;
Matches               6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db      204 ORYLNPYN 212
OY      1 OKINAPYN 9
       1 | : | | |||

RESULT      6          S28047    #type complete
ENTRY       TUBI3 protein - potato
TITLE       #format_name Solanum tuberosum #common_name potato
ORGANISM    #formal_name Solanum tuberosum #revision 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
DATE        09-Sep-1997
ACCESSIONS  S28047
REFERENCE    S28046
AUTHORS     Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scoble,
              L.A.; Pearce, S.R.; Flavell, A.J.
#journal    Plant Mol. Biol. (1992) 20:641-651
#title      Expression and sequence analysis of cDNAs induced during the
             early stages of tuberisation in different organs of the
             potato plant (Solanum tuberosum L.).
#accesion   S28047
#molecule_type mRNA
##residues 1-360 ##label TAY
##cross-references EMBL:Z11680; NID:g21464; PID:g21485
GENETICS
#gene
SUMMARY     TUBI3
            #length 360 #molecular_weight 39726 #checksum 7941

Query Match           75.4% Score 52; DB 2; Length 360;
Best Local Similarity 62.5%; Pred. No. 3.18e+00;
Matches               5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      332 OKFTTPY 339
OY      1 OKINAPY 8
       1 | : | | |

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ENTRY          S52662          #type complete
TITLE          S-adenosylmethionine decarboxylase (SAMDC) - potato
ORGANISM       Solanum tuberosum #common_name potato
DATE           14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
              21-Jul-1995
ACCESSIONS     S52662
REFERENCE      S52662
AUTHORS        Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.;
              Birch, L.R.; Davies, H.V.; Stark, M.J.R.; Kumar, A.
              Plant Mol. Biol. (1994) 26:327-338
              Characterisation of the S-adenosylmethionine decarboxylase
              (SAMDC) gene of potato.
#accession     S52662
#status        Preliminary
#molecule_type DNA
#residues      1-360 #label ARI
SUMMARY        #length 360 #molecular-weight 39724 #checksum 8045

Query Match    75.4% Score 52; DB 2; Length 360;
Best Local Similarity 62.5%; Pred. NO. 3.18e+00;
Matches        5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db            332 OKFRTPY 339
||: ||: ||
Oy            1 OKYNRPY 8

RESULT        8
ENTRY         HYBSN          #type complete
TITLE         bacillolysin (EC 3.4.24.28) precursor - Bacillus
              amyloliquefaciens
ALTERNATE_NAMES
              Bacillus metalloendopeptidase; microbial metalloproteinase;
              neutral proteinase
ORGANISM      Bacillus amyloliquefaciens
DATE          30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
              05-Sep-1997
ACCESSIONS    A25415
REFERENCE      A25415
AUTHORS        Vasantha, N.; Thompson, L.D.; Rhodes, C.; Banner, C.; Nagle,
              J.; Filpula, D.
              J. Bacteriol. (1984) 159:811-819
              Genes for alkaline protease and neutral protease from
              Bacillus amyloliquefaciens contain a large open reading
              frame between the regions coding for signal sequence and
              mature protein.
              #cross-references MUID:85006739
              #accession A25415
              ##molecule_type DNA
              ##residues 1-521 ##label YAN
              ##cross-references GB:K02497; NID:g143248; PID:g143249
GENETICS
#gene          npr
#start_codon   GTG
CLASSIFICATION #superfamily thermolysin
KEYWORDS       calcium; extracellular protein; hydrolase; metalloproteinase;
              zinc
FEATURE
1-27           #domain signal sequence #status predicted #label SIG\
28-221         #domain propeptide #status predicted #label PRO\
222-521        #product bacillolysin #status predicted #label MRF\
364,368,388    #binding_site zinc (His, His, Glu) #status predicted\
365,449        #active_site Glu, His #status predicted
SUMMARY        #length 521 #molecular-weight 56840 #checksum 7195

Query Match    73.9% Score 51; DB 1; Length 521;
Best Local Similarity 55.6%; Pred. NO. 5.01e+00;
Matches        5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db            308 OKFNRSYD 316
||: ||: ||
Oy            1 OKYNRPY 9

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RESULT      9
ENTRY       C47759      #type fragment
TITLE       retrovirus-related reverse transcriptase homolog - upland
ORGANISM    cotton retrotransposon copia-like (fragment)
DATE        #formal_name Gossypium hirsutum #common_name upland cotton
            24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change
            08-Jan-1999
ACCESSIONS  C47759
REFERENCE   A46200
#authors    Voytas, D.F.; Cummings, M.P.; Konieczny, A.; Ausubel, F.M.;
            Kodermeil, S.R.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7124-7128
#title      copia-like retrotransposons are ubiquitous among plants.
#cross-references MIMD:92357784
#contents   clone 1
#accession  C47759
#status     preliminary: not compared with conceptual translation
#molecule_type DNA
#residues   1-89 #label VOY
#cross-references GB:M94471; NID:g167314; PID:g167315
#note       sequence extracted from NCBI backbone (NCBIP:111889)
SUMMARY     #length 89 #checksum 9602

Query Match      71.0%; Score 49; DB 2; Length 89;
Best Local Similarity 55.6%; Pred. No. 1.22e+01;
Matches          5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db      58 OKYRASKYD 66
      ||| | | | |
      1 OKYRABPN 9

RESULT      10
ENTRY       SNRNC2      #type complete
TITLE       multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2
ORGANISM    -rat
ALTERNATE_NAMES multicatalytic proteinase component C2; proteasome chain C2
DATE        #formal_name Rattus norvegicus #common_name Norway rat
            31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
            17-Oct-1997
ACCESSIONS  A32968; A38799; S09741
REFERENCE   A32968
#authors    Fujiwara, T.; Tanaka, K.; Kumatori, A.; Shin, S.; Yoshimura,
            T.; Ichihara, A.; Tokunaga, F.; Aruga, R.; Iwanaga, S.;
            Kakizuka, A.; Nakanishi, S.
#journal    Biochemistry (1989) 28:7332-7340
#title      Molecular cloning of cDNA for proteasomes (multicatalytic
            proteinase complexes) from rat liver: primary structure of
            the largest component (C2).
#cross-references MIMD:90057428
#accession  A32968
#molecule_type mRNA
#residues   1-263 #label FUJ1
#cross-references EMBL:M29859; NID:g206381; PID:g206382
#accession  A38799
#molecule_type protein
#residues   2-25;42-58;63-74,'X',76-79,'X',81;116-135;190-203;
            218-226,'XX',229,'X',231;244-246,'X',248-262 #label
            FUJ2

REFERENCE   S09741
#authors    Tokunaga, F.; Aruga, R.; Iwanaga, S.; Tanaka, K.; Ichihara,
            A.; Takao, T.; Shimonishi, Y.
#journal    FEBS Lett. (1990) 263:373-375
#title      The NH2-terminal residues of rat liver proteasome
            (multicatalytic proteinase complex) subunits, C2, C3 and
            C6, are N-alpha-acetylated.
#cross-references MIMD:90243011
#accession  S09741
#molecule_type protein
#residues   1-30 #label TOK
KEYWORDS     #superfamily multicatalytic endopeptidase complex chain C9
FEATURE      acetylated amino end; hydrolase; proteinase

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1-263      #product multicatalytic endopeptidase complex chain C2
1          #status experimental #label MAT\
            #modified site acetylated amino end (Met) #status
            experimental
SUMMARY     #length 263 #molecular-weight 29517 #checksum 9238

Query Match      71.0%; Score 49; DB 1; Length 263;
Best Local Similarity 62.5%; Pred. No. 1.22e+01;
Matches          5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db      121 OKYRABPN 128
      ||| | | | |
      1 OKYRABPN 8

RESULT      11
ENTRY       JC1445      #type complete
TITLE       multicatalytic endopeptidase complex (EC 3.4.99.46) chain C2,
            long splice form - human
ALTERNATE_NAMES macropain nu chain; multicatalytic endopeptidase complex HC2
            chain; multicatalytic endopeptidase complex nu chain;
            multicatalytic proteinase chain C2; prosome 30-33K chain;
            proteasome alpha 1 subunit; proteasome chain C2; proteasome
            nu chain
CONTAINS     multicatalytic endopeptidase complex chain C2, short splice
            form
ORGANISM     #formal_name Homo sapiens #common_name man
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
            08-Sep-1997
ACCESSIONS  JC1445; S15897; S17520; S25410; PC2321
REFERENCE   JC1445
#authors    Pereira, I.S.; Bey, F.; Coux, O.; Scherrer, K.
#journal    Gene (1992) 120:235-242
#title      Two mRNAs exist for the Hs PROS-30 gene encoding a component
            of human prosomes.
#accession  JC1445
#molecule_type mRNA
#residues   1-269 #label PER
#cross-references GB:M64992
REFERENCE   S15897
#authors    Tamura, T.; Lee, D.H.; Osaka, F.; Fujiwara, T.; Shin, S.;
            Chung, C.H.; Tanaka, K.; Ichihara, A.
#journal    Biochim. Biophys. Acta (1991) 1089:95-102
#title      Molecular cloning and sequence analysis of cDNAs for five
            major subunits of human proteasomes (multi-catalytic
            proteinase complexes).
#cross-references MIMD:91223105
#accession  S15897
#molecule_type mRNA
#residues   'N',8-269 #label TAM
#cross-references EMBL:D00759; NID:g220021; PID:d1001114; PID:g220022
#accession  S17520
#molecule_type mRNA
#residues   'N',8-269 #label TAM
#cross-references EMBL:D00759; NID:g220021; PID:d1001114; PID:g220022
#accession  S17520
#molecule_type protein
#residues   2-25;46-61;68-75;89-95;103-128;132-148;164-168;176-195;
            203-223;225-267 #label DE2
#cross-references MIMD:91363412
#accession  S17520
#status     not compared with conceptual translation
#molecule_type mRNA
#residues   'N',8-269 #label DEM
#cross-references GB:X61969; NID:g296737; PID:g296738
#accession  S25410
#molecule_type protein
#residues   10-40;46-61;68-75;89-95;103-128;132-148;164-168;176-195;
            203-223;225-267 #label DE2

REFERENCE   PC2315
#authors    Kristensen, P.; Johnsen, A.H.; Uekvitz, W.; Tanaka, K.;
            Hendill, K.B.
#journal    Biochem. Biophys. Res. Commun. (1994) 205:1785-1789
#title      Human proteasome subunits from 2-dimensional gels identified

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by partial sequencing.
 #cross-references M01D:95110324
 #accession PC3321
 #molecule_type protein
 #residues 69-88 ##label KRI
 #experimental_source placenta
 COMMENT The proteasome consists of subunits of 21K-30K arranged in 4 stacked rings.

GENETICS
 #gene GDB:PSMAL; HASPROS-30
 #cross-references GDB:134040
 #map_position 11q-11q
 CLASSIFICATION #superfamily multicatalytic endopeptidase complex chain C9
 KEYWORDS hydrolyase; phosphoprotein; proteinase
 FEATURE
 2-269 #product multicatalytic endopeptidase complex chain C2,
 8-269 long splice form #status predicted #label MATV
 230 #product multicatalytic endopeptidase complex chain C2,
 short splice form #status predicted #label MATS\
 #binding-site phosphate (Tyr) (covalent) #status predicted
 SUMMARY #length 269 #molecular-weight 30239 #checksum 5946

Query Match 71.0%; Score 49; DB 2; Length 269;
 Best Local Similarity 62.5%; Pred. No. 1.22e+01;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 127 QRYGRAPY 134
 1 1 1 1 1
 QY 1 QRYNRPAY 8

RESULT 12
 ENTRY JCI390 #type complete
 TITLE cyclin A - fruit fly (Drosophila melanogaster)
 ORGANISM 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 08-Sep-1997
 DATE JCI390: A32371; S03543
 JCI390
 #accessions JCI390
 #authors Takahisa, M.; Togashi, S.; Ueda, R.; Mikiuni, M.; Tsurumura, S.; Kondo, K.; Miyake, T.
 #journal Gene (1992) 121:343-346
 #title Structure of the Drosophila melanogaster gene encoding cyclin A.

#cross-references M01D:93077051
 #accession JCI390
 #molecule_type DNA
 #residues 1-491 ##label TAK
 #cross-references DDBJ:D10856; DDBJ:D10857; NID:g407197; PID:d1002103; PID:g407199

REFERENCE A32371
 #authors Lehner, C.F.; O'Farrell, P.H.
 #journal Cell (1989) 56:957-968
 #title Expression and function of drosophila cyclin A during embryonic cell cycle progression.

#cross-references M01D:89168447
 #accession A32371
 #molecule_type mRNA
 #residues 1-178,'V',180-222,'R',224-491 ##label LEH
 #cross-references GB:M24841; NID:g157156; PID:g157157
 REFERENCE S03543
 #authors Whitfield, W.G.F.; Gonzalez, C.; Sanchez-Herrero, E.; Glover, D.M.
 #journal Nature (1989) 338:337-340
 #title Transcripts of one of two Drosophila cyclin genes become localized in pole cells during embryogenesis.

#cross-references M01D:89159430
 #accession S03543
 #status preliminary; not compared with conceptual translation
 #molecule_type mRNA
 #residues 235-247;288-300 ##label WHI

GENETICS

#gene Cyca
 #cross-references FlyBase:FBgn0000404
 #introns 65/3; 130/2; 215/3; 290/2; 358/3; 441/2
 CLASSIFICATION #superfamily cyclin
 KEYWORDS cell cycle control
 SUMMARY #length 491 #molecular-weight 56124 #checksum 8638

Query Match 71.0%; Score 49; DB 2; Length 491;
 Best Local Similarity 55.6%; Pred. No. 1.22e+01;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 435 EKYNRDTPK 443
 1 1 1 1 1
 QY 1 QRYNRPAY 9

RESULT 13
 ENTRY S05981 #type complete
 TITLE repB protein - Streptococcus agalactiae plasmid pMV158
 ORGANISM 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
 DATE S05981
 #accessions S05981
 #authors van der Lelje, D.; Bron, S.; Venema, G.; Oskam, L.
 #journal Nucleic Acids Res. (1989) 17:7283-7294
 #title Similarity of minus origins of replication and flanking open reading frames of plasmids pVB110, pVB913 and pMV158.

#cross-references M01D:90016790
 #accession S05981
 #status nucleic acid sequence not shown; translation not shown
 #molecule_type DNA
 #residues 1-210 ##label VAN
 #cross-references EMBL:X15669; NID:g46662; PID:g46664
 #note the nucleotide sequence was submitted to the EMBL Data Library, June 1989

GENETICS
 #gene repB
 #genome plasmid
 SUMMARY #length 210 #molecular-weight 24250 #checksum 7292

Query Match 69.6%; Score 48; DB 2; Length 210;
 Best Local Similarity 55.6%; Pred. No. 1.90e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 49 QRYKKAHYH 57
 1 1 1 1 1
 QY 1 QRYNRPAY 9

RESULT 14
 ENTRY B25599 #type complete
 TITLE repB protein - Streptococcus pneumoniae plasmid pLS1
 ORGANISM 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Nov-1998
 DATE B25599
 #accessions B25599; S10576
 #authors Lacks, S.A.; Lopez, P.; Greenberg, B.; Espinosa, M.
 #journal J. Mol. Biol. (1986) 192:753-765
 #title Identification and analysis of genes for tetracycline resistance and replication functions in the broad-host-range plasmid pLS1.

#cross-references M01D:87226167
 #accession B25599
 #molecule_type DNA
 #residues 1-210 ##label LAC
 #cross-references EMBL:M29725
 REFERENCE S10576
 #authors de la Campa, A.G.; del Solar, G.H.; Espinosa, M.
 #journal J. Mol. Biol. (1990) 213:247-262
 #title Initiation of replication of plasmid pLS1. The initiator protein RepB acts on two distant DNA regions.

```
#cross-references MUID:90258035
#accession      S10576
#status         not compared with conceptual translation
##molecule_type DNA
##residues      1-29,'F',31-36 ##label CAM
GENETICS
#gene           reps
#genome         plasmid pLS1
KEYWORDS        plasmid replication
SUMMARY         #length 210 #molecular-weight 24250 #checksum 7292

Query Match      69.6%; Score 48; DB 2; Length 210;
Best Local Similarity 55.6%; Pred. No. 1.90e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 49 OKYKKAHYH 57
|||::| |
OY 1 OKYNRAPYN 9

RESULT 15
ENTRY          G02630 #type complete
TITLE          FcalphaRb - human
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
17-Jul-1998
ACCESSIONS     G02630
REFERENCE      H01508
#authors       van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.;
Raaijmakers, J.A.M.; Lammers, J.
#submission    submitted to the EMBL Data Library, April 1996
#accession     G02630
##status       preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues     1-239 ##label VAN
##cross-references EMBL:U56236; NID:g1326228; PID:g1326229
SUMMARY        #length 239 #molecular-weight 26996 #checksum 5338

Query Match      69.6%; Score 48; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.90e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 197 YNRSFY 202
|||::| |
OY 3 YNRAPY 8

Search completed: Thu Sep 2 11:57:34 1999
Job time : 15 secs.
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MUSE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Sep 2 11:59:05 1999; Maspar time 1.37 Seconds
Tabular output not generated. 66.540 Million cell updates/sec

Title: >US-08-599-226-20
Description: (1-9) from US08599226.pep
Perfect Score: 69
Sequence: 1 OKYNRAPYN 9

Scoring table: PAM 150
Gap 15

Searched: 106580 segs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-Isued
1:5A_COMB 2:5B_COMB 3:PCRT9_COMB 4:Backfiles1

Statistics: Mean 15.427; Variance 46.115; scale 0.335

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description	Pred. No.
1	49	71.0	269 1	US-08-202- Sequence 4, Applicatio	3.85e+01
2	48	69.6	287 4	5198342-2 Patent No. 5198342.	4.97e+01
3	48	69.6	287 1	US-07-971- Sequence 2, Applicatio	4.97e+01
4	48	69.6	584 2	US-08-313- Sequence 17, Applicati	8.23e+01
5	46	66.7	33 2	US-08-724- Sequence 12, Applicati	8.23e+01
6	46	66.7	718 1	US-08-445- Sequence 4, Applicatio	8.23e+01
7	46	66.7	718 1	US-08-444- Sequence 4, Applicatio	8.23e+01
8	46	66.7	1708 1	US-08-493- Sequence 2, Applicatio	8.23e+01
9	46	66.7	1708 2	US-08-508- Sequence 2, Applicatio	8.23e+01
10	46	66.7	3056 2	US-08-629- Sequence 3, Applicatio	8.23e+01
11	46	66.7	3056 2	US-08-508- Sequence 8, Applicatio	8.23e+01
12	45	65.2	243 1	US-08-726- Sequence 6, Applicatio	1.06e+02
13	45	65.2	243 1	US-08-021- Sequence 6, Applicatio	1.06e+02
14	45	65.2	243 3	US-08-021- Sequence 6, Applicatio	1.06e+02
15	45	65.2	243 3	US-08-021- Sequence 6, Applicatio	1.06e+02
16	45	65.2	246 2	US-08-604- Sequence 4, Applicatio	1.06e+02
17	45	65.2	507 2	US-08-604- Sequence 4, Applicatio	1.06e+02
18	45	65.2	507 2	US-08-604- Sequence 5, Applicatio	1.06e+02
19	45	65.2	590 3	US-08-021- Sequence 8, Applicatio	1.06e+02
20	45	65.2	590 1	US-08-021- Sequence 8, Applicatio	1.06e+02
21	45	65.2	590 1	US-08-726- Sequence 8, Applicatio	1.06e+02
22	45	65.2	643 1	US-08-726- Sequence 10, Applicati	1.06e+02
23	45	65.2	643 3	US-08-726- Sequence 10, Applicati	1.06e+02

24	45	65.2	643 1	US-08-021- Sequence 10, Applicati	1.06e+02
25	45	65.2	644 1	US-08-726- Sequence 2, Applicatio	1.06e+02
26	45	65.2	644 3	US-08-726- Sequence 2, Applicatio	1.06e+02
27	45	65.2	644 1	US-08-021- Sequence 2, Applicatio	1.06e+02
28	43	62.3	324 2	US-08-484- Sequence 11, Applicati	1.73e+02
29	43	62.3	442 2	US-08-363- Sequence 22, Applicatio	1.73e+02
30	43	62.3	442 2	US-08-363- Sequence 11, Applicati	1.73e+02
31	43	62.3	442 2	US-08-363- Sequence 4, Applicatio	1.73e+02
32	43	62.3	445 2	US-08-363- Sequence 12, Applicatio	1.73e+02
33	43	62.3	445 2	US-08-363- Sequence 5, Applicatio	1.73e+02
34	42	60.9	963 2	US-08-537- Sequence 3, Applicatio	2.21e+02
35	42	60.9	12 2	US-08-811- Sequence 151, Applicat	2.21e+02
36	42	60.9	107 3	US-08-811- Sequence 82, Applicati	2.21e+02
37	42	60.9	107 3	US-08-811- Sequence 82, Applicati	2.21e+02
38	42	60.9	107 3	US-08-811- Sequence 87, Applicati	2.21e+02
39	42	60.9	107 2	US-08-899- Sequence 87, Applicati	2.21e+02
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41	42	60.9	107 2	US-08-899- Sequence 84, Applicati	2.21e+02
42	42	60.9	107 2	US-08-899- Sequence 84, Applicati	2.21e+02
43	42	60.9	107 1	US-08-276- Sequence 84, Applicati	2.21e+02
44	42	60.9	107 2	US-08-276- Sequence 87, Applicati	2.21e+02
45	42	60.9	536 2	US-08-484- Sequence 4, Applicatio	2.21e+02

ALIGNMENTS

RESULT	ID	1	STANDARD:	PRT:	269 AA.
XX	US-08-202-857-4	xxxxxx			
XX	Sequence 4, Application US/08202857				
XX	Patent No. 5635345				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Scherrer, Klaus				
CC	APPLICANT: Bureau, Jean-Paul				
CC	TITLE OF INVENTION: Diagnostic Method				
CC	NUMBER OF SEQUENCES: 4				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: PRO-SOMA SARL C/O AKZO PHARMA				
CC	STREET: 1330-A PICCARD DRIVE				
CC	CITY: ROCKVILLE				
CC	STATE: MARYLAND				
CC	COUNTRY: USA				
CC	ZIP: 20850-4377				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PS/2				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: Microsoft Word				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/202,857				
CC	FILING DATE:				
CC	CLASSIFICATION: 435				
CC	PRIOR APPLICATION DATA:				
CC	APPLICATION NUMBER: US/07/860,492				
CC	FILING DATE: 11-JUNE-1992				
CC	APPLICATION NUMBER: PCT/EP91/01945				
CC	FILING DATE: 10-OCT-1991				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: BOBROWICZ, DONNA				
CC	REGISTRATION NUMBER: 32,196				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: 301-258-5200				
CC	TELEFAX: 301-977-1403				
CC	INFORMATION FOR SEQ ID NO: 4:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 269 amino acids				

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: human
SQ SEQUENCE 269 AA; 30227 MW; 341084 CN;
Query Match
Best Local Similarity 71.0%; Score 49; DB 1; Length 269;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 127 ORGGRPY 134
|:|:|
QY 1 QKYNRPY 8
RESULT 2
ID 5198342-2 STANDARD; PRT; 311 AA.
XX xxxxxx
DT 01-JAN-1900
XX Patent No. 5198342.
DE
XX Patent No. 5198342
CC APPLICANT: MALISZEWSKI, CHARLES R.
CC TITLE OF INVENTION: DNA ENCODING IGA FC RECEPTORS
CC NUMBER OF SEQUENCES: 9
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/548,059
CC FILING DATE: 05-JUL-1990
CC SEQ ID NO: 2
CC LENGTH: 287
SQ SEQUENCE 311 AA; 34908 MW; 558002 CN;
Query Match
Best Local Similarity 69.6%; Score 48; DB 4; Length 287;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSY 202
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QY 3 YNRPY 8
RESULT 3
ID US-07-971-092-2 STANDARD; PRT; 287 AA.
XX xxxxxx
DT
XX
DE Sequence 2, Application US/07971092
XX
CC Sequence 2, Application US/07971092
CC Patent No. 5328987
CC GENERAL INFORMATION:
CC APPLICANT: Maliszewski, Charles R.
CC TITLE OF INVENTION: Huiga Fc Receptor
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Immunex
CC STREET: 51 University
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/971,092
CC FILING DATE: 19921104
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Perkins, Patricia A.
CC REGISTRATION NUMBER: 34693
CC REFERENCE/DOCKET NUMBER: 2603
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 287 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 287 AA; 32265 MW; 435416 CN;
Query Match
Best Local Similarity 69.6%; Score 48; DB 1; Length 287;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 197 YNRSY 202
|:|:|
QY 3 YNRPY 8
RESULT 4
ID US-08-313-288B-17 STANDARD; PRT; 584 AA.
XX xxxxxx
DT
XX
DE Sequence 17, Application US/08313288B
XX
CC Sequence 17, Application US/08313288B
CC Patent No. 5750502
CC GENERAL INFORMATION:
CC APPLICANT: Jessell, Thomas M. and Avihu Klar
CC TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Cooper & Dunham LLP
CC STREET: 1185 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/313,288B
CC FILING DATE: January 5, 1995
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: White, John P.
CC REGISTRATION NUMBER: 28,678
CC REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 278-0400
CC TELEFAX: (212) 391-0526
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 584 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 584 AA; 65163 MW; 1651823 CN;

Query Match 69.6%; Score 48; DB 2; Length 584;
Best Local Similarity 66.7%; Pred. No. 4.97e+01;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 203 EYFRFPYN 211

1111111
OY 1 OKYNRAPYN 9

RESULT 5
ID US-08-724-194-12 STANDARD; PRT; 33 AA.

AC xxxxxx

DE Sequence 12, Application US/08724194

CC Sequence 12, Application US/08724194
CC Patent No. 5824875

CC GENERAL INFORMATION:

CC APPLICANT: RANU, RAJINDER S.

CC TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE

CC TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS

CC NUMBER OF SEQUENCES: 13

CC CORRESPONDENCE ADDRESSES:

CC ADDRESSEE: SANTANGELO LAW OFFICES PC

CC STREET: 315 WEST OAK STREET, STE 701

CC CITY: FORT COLLINS

CC STATE: CO

CC COUNTRY: USA

CC ZIP: 80521

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/724.194

CC FILING DATE: 01-OCT-1996

CC CLASSIFICATION: 800

CC ATTORNEY/AGENT INFORMATION:

CC NAME: SANTANGELO, LUKE

CC REGISTRATION NUMBER: 31,997

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (970) 224-3100

CC INFORMATION FOR SEQ ID NO: 12:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 33 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC SEQUENCE 33 AA; 3822 MW; 5035 CN;

Query Match 66.7%; Score 46; DB 2; Length 33;

Best Local Similarity 57.1%; Pred. No. 8.23e+01;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 8 YDRDPYH 14

1111111
OY 3 YNRAPYN 9

RESULT 6
ID US-08-445-042-4 STANDARD; PRT; 718 AA.

AC xxxxxx

DE Sequence 4, Application US/08445042

XX Sequence 4, Application US/08445042
CC Patent No. 5726290

CC GENERAL INFORMATION:

CC APPLICANT: Bodary, Sarah C.

CC APPLICANT: Gorman, Cornelia M.

CC APPLICANT: McLean, John W.

CC APPLICANT: Napier, Mary A.

CC TITLE OF INVENTION: METHOD FOR PREPARING WATER SOLUBLE

CC POLYPEPTIDES

CC NUMBER OF SEQUENCES: 18

CC CORRESPONDENCE ADDRESSES:

CC ADDRESSEE: Genentech, Inc.

CC STREET: 460 Point San Bruno Blvd

CC CITY: South San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94080

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Winpatin (Genentech)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/445.042

CC FILING DATE: 19-May-1995

CC CLASSIFICATION: 530

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/380227

CC FILING DATE: 30-JAN-1995

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/218878

CC FILING DATE: 28-MAR-1994

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 07/821337

CC FILING DATE: 13-JAN-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 07/444490

CC FILING DATE: 01-DEC-1989

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 07/290224

CC FILING DATE: 22-DEC-1988

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Lee, Wendy M.

CC REGISTRATION NUMBER: 00,000

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415/225-1994

CC TELEFAX: 415/952-9881

CC TELEX: 910/371-7168

CC INFORMATION FOR SEQ ID NO: 4:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 718 amino acids

CC TYPE: Amino Acid

CC TOPOLOGY: linear

CC SEQUENCE 718 AA; 79240 MW; 2616883 CN;

Query Match 66.7%; Score 46; DB 1; Length 718;

Best Local Similarity 57.1%; Pred. No. 8.23e+01;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 645 KFDREPY 651

1111111
OY 2 KYNRAPY 8

RESULT 7
ID US-08-444-792-4 STANDARD; PRT; 718 AA.

AC xxxxxx

DE

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DE      Sequence 4, Application US/08444792
xx
cc      Sequence 4, Application US/08444792
cc      Patent No. 5726037
cc      GENERAL INFORMATION:
cc      APPLICANT: Bodary, Sarah C.
cc      APPLICANT: Gorman, Cornelia M.
cc      APPLICANT: McLean, John W.
cc      APPLICANT: Napier, Mary A.
cc      TITLE OF INVENTION: METHOD FOR PREPARING WATER SOLUBLE
cc      TITLE OF INVENTION: POLYPEPTIDES
cc      NUMBER OF SEQUENCES: 18
cc      CORRESPONDENCE ADDRESS:
cc      ADDRESSEE: Genentech, Inc.
cc      STREET: 460 Point San Bruno Blvd
cc      CITY: South San Francisco
cc      STATE: California
cc      COUNTRY: USA
cc      ZIP: 94080
cc      COMPUTER READABLE FORM:
cc      MEDIUM TYPE: 3.5 Inch, 720 kb floppy disk
cc      COMPUTER: IBM PC compatible
cc      OPERATING SYSTEM: PC-DOS/MS-DOS
cc      SOFTWARE: WinPatIn (Genentech)
cc      CURRENT APPLICATION DATA:
cc      APPLICATION NUMBER: US/08/444,792
cc      FILING DATE: 19-May-1995
cc      CLASSIFICATION: 435
cc      PRIOR APPLICATION DATA:
cc      APPLICATION NUMBER: 08/380227
cc      FILING DATE: 30-JAN-1995
cc      PRIOR APPLICATION DATA:
cc      APPLICATION NUMBER: 08/218878
cc      FILING DATE: 28-MAR-1994
cc      PRIOR APPLICATION DATA:
cc      APPLICATION NUMBER: 07/821337
cc      FILING DATE: 13-JAN-1992
cc      PRIOR APPLICATION DATA:
cc      APPLICATION NUMBER: 07/444490
cc      FILING DATE: 01-DEC-1989
cc      PRIOR APPLICATION DATA:
cc      APPLICATION NUMBER: 07/290224
cc      FILING DATE: 22-DEC-1988
cc      ATTORNEY/AGENT INFORMATION:
cc      NAME: Lee, Wendy M.
cc      REGISTRATION NUMBER: 00,000
cc      REFERENCE/DOCKET NUMBER: P05522P1C3D4
cc      TELECOMMUNICATION INFORMATION:
cc      TELEPHONE: 415/225-1994
cc      TELEFAX: 415/952-9881
cc      TELEX: 910/371-7168
cc      INFORMATION FOR SEQ ID NO: 4:
cc      SEQUENCE CHARACTERISTICS:
cc      LENGTH: 718 amino acids
cc      TYPE: Amino Acid
cc      TOPOLOGY: Linear
cc      SEQUENCE 718 AA: 79240 MM; 2616883 CN;
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cc      Query Match      66.7%; Score 46; DB 1; Length 718;
cc      Best Local Similarity 57.1%; Pred. No. 8,236+01;
cc      Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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cc      Db      645 KEDREPY 651
cc      1:1111
cc      Oy      2 KYNRApy 8
cc
cc      RESULT      8
cc      ID      US-08-493-092-2      STANDARD;      PRT;      1708 AA.
cc      AC      xxxxxx
cc      DT

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[illegible]

CC	COUNTRY:	US
CC	ZIP:	48099
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	Patentin Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/508,836A
CC	FILING DATE:	
CC	CLASSIFICATION:	536
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Kohn, Kenneth I.
CC	REGISTRATION NUMBER:	30,955
CC	REFERENCE/DOCKET NUMBER:	P-313 (TAU)
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	(810) 689-3500
CC	TELEFAX:	(810) 689-4071
CC	INFORMATION FOR SEO ID NO:	2:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	1708 amino acids
CC	TYPE:	amino acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	SEQUENCE	1708 AA; 195977 MW; 14824289 CN;
D8	Query Match	66.7%; Score 46; DB 2; Length 1708;
B8	Best Local Similarity	50.0%; Pred. No. 8.23e+01;
OY	Matches	4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
D8	234 KYSRGPFSS 241	
OY	2 KYNRAPYN 9	
DE	Sequence 3, Application US/08629001A	
XX	Sequence 3, Application US/08629001A	
XX	Patent No. 5858661	
XX	GENERAL INFORMATION:	
DT	APPLICANT:	Shlich, Yosef
DT	TITLE OF INVENTION:	ATAXIA-TELANGIECTASIA GENE AND ITS
DT	TITLE OF INVENTION:	GENOMIC ORGANIZATION
DT	NUMBER OF SEQUENCES:	139
DT	CORRESPONDENCE ADDRESS:	
DT	ADDRESSEE:	Kohn & Associates
DT	STREET:	30500 No. 5858661western Hwy.
DT	CITY:	Farmington Hills
DT	STATE:	Michigan
DT	COUNTRY:	US
DT	ZIP:	48334
DT	COMPUTER READABLE FORM:	
DT	MEDIUM TYPE:	Floppy disk
DT	COMPUTER:	IBM PC compatible
DT	OPERATING SYSTEM:	PC-DOS/MS-DOS
DT	SOFTWARE:	Patentin Release #1.0, Version #1.30
DT	CURRENT APPLICATION DATA:	
DT	APPLICATION NUMBER:	US/08/629,001A
DT	FILING DATE:	
DT	CLASSIFICATION:	435
DT	ATTORNEY/AGENT INFORMATION:	
DT	NAME:	Kohn, Kenneth I.
DT	REGISTRATION NUMBER:	30,955
DT	REFERENCE/DOCKET NUMBER:	2290.00032
DT	TELECOMMUNICATION INFORMATION:	
DT	TELEPHONE:	(810) 539-5050

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CC TELEFAX: (810) 539-5055
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3056 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC SEQUENCE 3056 AA; 350651 MW; 47948122 CN;

Db Query Match 66.7%; Score 46; DB 2; Length 3056;
Best Local Similarity 50.0%; Pred. No. 8.23e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Oy 2 KYNRAPYV 9

RESULT 11
ID US-08-508-836A-8 STANDARD; PRT; 3056 AA.
XX xxxxxx
AC
DE Sequence 8, Application US/08508836A
XX Sequence 8, Application US/08508836A
CC Patent No. 5777093
CC GENERAL INFORMATION:
CC APPLICANT: Shlloh, Yosef
CC APPLICANT: Tagle, Danilo A.
CC APPLICANT: Collins, Francis S.
CC TITLE OF INVENTION: Ataxia-telangiectasia Gene
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Relsing, Echlington, Barnard & Perry
CC STREET: P.O. Box 4390
CC CITY: Troy
CC STATE: Michigan
CC COUNTRY: US
CC ZIP: 48099
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/508,836A
CC FILING DATE:
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kohn, Kenneth I.
CC REGISTRATION NUMBER: 30,955
CC REFERENCE/DOCKET NUMBER: P-313 (TAU)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (810) 689-4071
CC TELEFAX: (810) 689-3500
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 3056 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC SEQUENCE 3056 AA; 350651 MW; 47948122 CN;

Query Match 66.7%; Score 46; DB 2; Length 3056;
Best Local Similarity 50.0%; Pred. No. 8.23e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db 1582 KYSGPFS 1589
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QY 2 KYNRAPYN 9

RESULT 12
ID US-08-726-160-6 STANDARD: PRT: 243 AA.

AC xxxxxx

DE Sequence 6, Application US/08726160

CC Sequence 6, Application US/08726160

CC Patent No. 5734016

CC GENERAL INFORMATION:

CC APPLICANT: LEVENS, DAVID L., DUNCAN,

CC APPLICANT: ROBERT C., AND AVIGAN, MARK I.

CC TITLE OF INVENTION: NOVEL FUSE BINDING

CC TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR

CC NUMBER OF SEQUENCES: 24

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORGAN & FINNEGAN

CC STREET: 345 PARK AVENUE

CC CITY: NEW YORK

CC STATE: NEW YORK

CC COUNTRY: USA

CC ZIP: 10154

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: FLOPPY DISK

CC COMPUTER: IBM PC COMPATIBLE

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: WORDPERECT 5.1

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/726,160

CC FILING DATE: 04-OCT-1996

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/021,608

CC FILING DATE: 22-FEB-1993

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: WILLIAM S. FEILER

CC REGISTRATION NUMBER: 26,728

CC REFERENCE/DOCKET NUMBER: 2026-4063US1

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (212) 758-4800

CC TELEFAX: (212) 751-6649

CC INFORMATION FOR SEQ ID NO: 6:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 243

CC TYPE: Amino Acid

CC STRANDEDNESS: Single

CC TOPOLOGY: Unknown

CC MOLECULE TYPE: Peptide/Protein

CC HYPOTHETICAL: NO

CC ORIGINAL SOURCE:

CC ORGANISM: Human

CC CELL TYPE: HL60

CC SEQUENCE 243 AA: 25407 MW: 306126 CN:

Query Match 65.2%; Score 45; DB 1; Length 243;

Best Local Similarity 85.7%; Pred. No. 1.06e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 207 YNPAPYN 213

|| || || || ||

QY 3 YNRAPYN 9

RESULT 13
ID US-08-021-608D-6 STANDARD: PRT: 243 AA.

XX
AC xxxxxx
XX

DE Sequence 6, Application US/08021608D

CC Sequence 6, Application US/08021608D

CC Patent No. 5580760

CC GENERAL INFORMATION:

CC APPLICANT: LEVENS, DAVID L., DUNCAN,

CC APPLICANT: ROBERT C., AND AVIGAN, MARK I.

CC TITLE OF INVENTION: NOVEL FUSE BINDING

CC TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR

CC NUMBER OF SEQUENCES: 24

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORGAN & FINNEGAN

CC STREET: 345 PARK AVENUE

CC CITY: NEW YORK

CC STATE: NEW YORK

CC COUNTRY: USA

CC ZIP: 10154

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: FLOPPY DISK

CC COMPUTER: IBM PC COMPATIBLE

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: WORDPERECT 5.1

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/021,608D

CC FILING DATE: 22-FEB-1993

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER:

CC FILING DATE:

CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:

CC NAME: WILLIAM S. FEILER

CC REGISTRATION NUMBER: 26,728

CC REFERENCE/DOCKET NUMBER: 2026-4063

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (212) 758-4800

CC TELEFAX: (212) 751-6649

CC INFORMATION FOR SEQ ID NO: 6:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 243

CC TYPE: Amino Acid

CC STRANDEDNESS: Single

CC TOPOLOGY: Unknown

CC MOLECULE TYPE: Peptide/Protein

CC HYPOTHETICAL: NO

CC ORIGINAL SOURCE:

CC ORGANISM: Human

CC CELL TYPE: HL60

CC SEQUENCE 243 AA: 25407 MW: 306126 CN;

Query Match 65.2%; Score 45; DB 1; Length 243;

Best Local Similarity 85.7%; Pred. No. 1.06e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 207 YNPAPYN 213

|| || || || ||

QY 3 YNRAPYN 9

RESULT 14
ID PCT-US94-01782-6 STANDARD: PRT: 243 AA.
AC xxxxxx
XX
XX
DT
XX
DE Sequence 6, Application PC/TUS9401782
XX

CC Sequence 6, Application PC/TUS9401782
CC GENERAL INFORMATION:
CC APPLICANT: THE GOVERNMENT OF THE UNITED STATES
CC APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
CC APPLICANT: HEALTH AND HUMAN SERVICES
CC TITLE OF INVENTION: NOVEL FUSE BINDING
CC TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
CC NUMBER OF SEQUENCES: 10
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: MORGAN & PINNEGAN
CC STREET: 345 PARK AVENUE
CC CITY: NEW YORK
CC STATE: NEW YORK
CC COUNTRY: USA
CC ZIP: 10154
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: FLOPPY DISK
CC COMPUTER: IBM PC COMPATIBLE
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERFECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01782
CC FILING DATE: 22-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: U.S. 08/021,608
CC FILING DATE: 22-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILLIAM S. FEILER
CC REGISTRATION NUMBER: 26,728
CC REFERENCE/DOCKET NUMBER: 2026-4063PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 758-4800
CC TELEFAX: (212) 751-6849
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 243
CC TYPE: Amino Acid
CC STRANDEDNESS: Single
CC TOPOLOGY: Unknown
CC MOLECULE TYPE: Peptide/Protein
CC HYPOTHEICAL: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Human
CC STRAIN:
CC INDIVIDUAL ISOLATE:
CC DEVELOPMENTAL STAGE:
CC HAPLOTYPE:
CC TISSUE TYPE:
CC CELL TYPE: HL60
CC CELL LINE:
CC ORGANELLE:
CC FEATURE:
CC NAME/KEY:
CC LOCATION:
CC IDENTIFICATION METHOD:
CC OTHER INFORMATION:
CC SEQUENCE 243 AA; 25407 MW; 306126 CN;
CC
CC Query Match 65.2%; Score 45; DB 3; Length 243;
CC Best Local Similarity 85.7%; Pred. No. 1.06e+02;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC Db 207 YNPAPYN 213
CC | | | | |
CC 3 YNPAPYN 9
CC
CC RESULT 15
CC ID US-08-604-989A-3 STANDARD; PRT; 246 AA.
CC AC xxxxxx
CC XX

DT DE
XX Sequence 3, Application US/08604989A
XX Patent No. 5834208
XX GENERAL INFORMATION:
XX APPLICANT: Sakano, S.
XX TITLE OF INVENTION: NO. 5834208el Tyrosine Kinase
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: Pennile & Edmonds LLP
XX STREET: 1155 Avenue of the Americas
XX CITY: New York
XX STATE: New York
XX COUNTRY: USA
XX ZIP: 10036-2711
XX
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Diskette
XX COMPUTER: IBM Compatible
XX OPERATING SYSTEM: DOS
XX SOFTWARE: FASTSEQ Version 2.0
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/604,989A
XX FILING DATE: February 23, 1996
XX CLASSIFICATION: 435
XX ATTORNEY/AGENT INFORMATION:
XX NAME: Charles E. Miller
XX REGISTRATION NUMBER: 24,576
XX REFERENCE/DOCKET NUMBER: 1920-026
XX TELECOMMUNICATION INFORMATION:
XX TELEPHONE: (212) 790-9090
XX TELEFAX: (212) 869-8864/9741
XX TELEX: 66141 PENNIE
XX INFORMATION FOR SEQ ID NO: 3:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 246 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
XX MOLECULE TYPE: protein
XX ORIGINAL SOURCE:
XX ORGANISM: human
XX STRAIN: UT-7
XX SEQUENCE 246 AA; 27425 MW; 326654 CN;
XX
XX Query Match 65.2%; Score 45; DB 2; Length 246;
XX Best Local Similarity 83.3%; Pred. No. 1.06e+02;
XX Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Db 188 YGRAPY 193
XX | | | | |
XX 3 YNPAPY 8
XX

Search completed: Thu Sep 2 11:59:12 1999
Job time : 7 secs.

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Gap 15

Listing first 45

39:part39

Mean 16.462; Variance 48.070; scale 0.342

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347

2.5 9 27 W27573

spondylitis, osteoarthritis, gouty arthritis, allergy, multiple

CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical cell
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 100.0%; Score 69; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4,10e-01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpy 9
 |||||||
 Qy 1 QKYNRPY 9

RESULT 2
 ID W27571 standard; peptide; 9 AA.

AC W27571.1998 (first entry)
 DT 19-MAR-1998
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Makovych JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JC, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L939 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical cell
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 92.8%; Score 64; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 qkynrpy 8
 |||||||
 Qy 1 QKYNRPY 8

RESULT 3
 ID W27575 standard; peptide; 9 AA.

AC W27575.1998 (first entry)
 DT 19-MAR-1998
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN W09729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakcalan Z, Labkovsky B,
 PI Makovych JA, McGuinness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JC, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L939 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical cell
 CC endothelial cells (HUVEC).
 SO Sequence 9 AA:

Query Match 92.8%; Score 64; DB 27; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qkynrpy 8
 |||||||
 Qy 1 QKYNRPY 8

RESULT 4
 ID W27562 standard; peptide; 9 AA.

AC W27562.1998 (first entry)
 DT 19-MAR-1998
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;

KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disease; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc.difference 9 /Label= Thr, Ala
 FI WO9729131-A1.
 PN 14-AUG-1997.
 PD 10-FEB-1997: U02219.
 PF 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B, Mankevich JA, McGulness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.
 DR High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 9: Page 64; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ
 Query Match 88.4%; Score 61; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 3.69e+00;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997: U02219.
 PR 25-NOV-1996: US-031476.
 PR 09-FEB-1996: US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B, Mankevich JA, McGulness BT, Roberts AJ, Sakorafas P, Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ; WPI; 97-415302/38.
 DR High affinity antibodies against human TNF alpha - useful to inhibit TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 72; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or less and has a Koff rate constant of 1x10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which inhibits TNF-alpha activity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic syndrome, infectious diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coagulation disturbances, burns, reperfusion injury, keloid formation, scar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial cell leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein endothelial cells (HUVEC).
 CC Sequence 9 AA:
 SQ
 Query Match 88.4%; Score 61; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 3.69e+00;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, infectious
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 88.4%; Score 61; DB 27; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.69e+00;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 grynary 8
|:|||||
Oy 1 OKYNAPY 8

RESULT 7
ID W27568 standard; Protein; 107 AA.

AC W27568:
DE 19-MAR-1998 (first entry)
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
KW light chain; variable region; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-AL.
PD 14-AUG-1997.
PE 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HCM, Kaymakcalan Z, Labkovsky B,
PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.
DR N-PSDB: T88403.
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 15; Page 75; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,

CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 107 AA;

Query Match 88.4%; Score 61; DB 27; Length 107;
Best Local Similarity 87.5%; Pred. No. 3.69e+00;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 89 grynary 96
|:|||||
Oy 1 OKYNAPY 8

RESULT 8
ID W27577 standard; peptide; 9 AA.

AC W27577:
DE 19-MAR-1998 (first entry)
KW Human; tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
KW light chain; complementarity determining region 3; inhibition;
KW treatment; sepsis; disease; autoimmune disease; infectious disease;
KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW keloid formation; scar tissue formation; pyrexia; HUVEC;
KW periodontal disease; obesity; radiation toxicity;
KW endothelial cell leukocyte adhesion molecule-1;
KW human umbilical vein endothelial cell.
OS Homo sapiens.
PN W09729131-AL.
PD 14-AUG-1997.
PE 10-FEB-1997; U02219.
PR 25-NOV-1996; US-031476.
PR 09-FEB-1996; US-599226.
PA (BADI) BASF AG.
PI Allen DJ, Hoogenboom HCM, Kaymakcalan Z, Labkovsky B,
PI Markovich JA, McGuinness BT, Roberts AJ, Sakorafas P,
PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
DR WPI: 97-415302/38.

PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
PS Claim 20; Page 70; 102pp; English.
CC The present sequence is a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
CC determining region 3 (CDR3).
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
SQ Sequence 9 AA;

Query Match 85.5%; Score 59; DB 27; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.33e+00;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkynasapyn 9
 |||||
 1 OKYMRAPYN 9

RESULT 9
 ID W27572 standard; peptide: 9 AA.
 AC W27572;
 DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEEC;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Willton AJ;
 DR WPI; 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 68; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEEC).
 SQ Sequence 9 AA:

Query Match 85.5%: Score 59; DB 27; Length 9;
 Best Local Similarity 87.5%: Pred. No. 6.33e+00;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkynasapyn 8
 |||||
 1 OKYMRAPYN 8

RESULT 10
 ID W27570 standard; peptide: 9 AA.
 AC W27570;
 DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEEC;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Willton AJ;
 DR WPI; 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 67; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEEC).
 SQ Sequence 9 AA:

KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.
 PI (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P,
 PI Salfeld JG, Schoenhaut D, Vaughan TV, White M, Willton AJ;
 DR WPI; 97-415302/38.
 PT High affinity antibodies against human TNF alpha - useful to inhibit
 PS TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20: Page 67; 102pp; English.
 CC The present sequence is a novel anti-human tumour necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
 CC L29 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
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 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HVEEC).
 SQ Sequence 9 AA:

Query Match 78.3%: Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%: Pred. No. 2.38e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 qkynasapyn 8
 |||||
 1 OKYMRAPYN 8

RESULT 11
 ID W27574 standard; peptide: 9 AA.
 AC W27574;
 DE 19-MAR-1998 (first entry)
 KM Anti-TNF-alpha antibody light chain CDR3.
 KM Human: tumour necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KM light chain; complementarity determining region 3; inhibition;
 KM treatment; sepsis; disease; autoimmune disease; infectious disease;
 KM malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KM cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KM bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KM keloid formation; scar tissue formation; pyrexia; HVEEC;
 KM periodontal disease; obesity; radiation toxicity;
 KM endothelial cell leukocyte adhesion molecule-1;
 KM human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; 002219.
 PR 25-NOV-1996; US-031476.
 PA 09-FEB-1996; US-599226.

PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Markovich JA, McGuiness BT, Roberts AJ, Sakorats P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 WPI: 97-415302/38.
 PF High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumor necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
 CC less (both determined by surface plasmon resonance), and
 CC neutralizes human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 78.3%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.38e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 gkynsapy 8
 |||||
 1 QKYNRAPY 8

RESULT 12
 ID W27576 standard; peptide; 9 AA.

AC W27576; (first entry)
 DE Anti-TNF-alpha antibody light chain CDR3.
 KW Human; tumor necrosis factor-alpha; TNF-alpha; antibody; CDR3;
 KW light chain; complementarity determining region 3; inhibition;
 KW treatment; sepsis; disease; autoimmune disease; infectious disease;
 KW malignancy; pulmonary disorder; intestinal disorder; hepatitis;
 KW cardiac disorder; inflammatory bone disorder; reperfusion injury;
 KW bone resorption disease; coagulation disturbance; burn; ELAM-1;
 KW keloid formation; scar tissue formation; pyrexia; HUVEC;
 KW periodontal disease; obesity; radiation toxicity;
 KW endothelial cell leukocyte adhesion molecule-1;
 KW human umbilical vein endothelial cell.
 OS Homo sapiens.
 PN WO9729131-A1.
 PD 14-AUG-1997.
 PF 10-FEB-1997; U02219.
 PR 25-NOV-1996; US-031476.
 PR 09-FEB-1996; US-599226.
 PA (BADI) BASF AG.
 PI Allen DJ, Hoogenboom HRJM, Kaymakçalan Z, Labkovsky B,
 PI Markovich JA, McGuiness BT, Roberts AJ, Sakorats P,
 PI Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
 DR WPI: 97-415302/38.
 PF High affinity antibodies against human TNF alpha - useful to inhibit
 PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
 PS Claim 20; Page 69; 102pp; English.
 CC The present sequence is a novel anti-human tumor necrosis
 CC factor-alpha (TNF-alpha) antibody (Ab) light chain complementarity
 CC determining region 3 (CDR3).
 CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
 CC less and has a Koff rate constant of 1x10 power -3 s power -1 or

CC less (both determined by surface plasmon resonance), and
 CC neutralizes human TNF-alpha cytotoxicity in a standard in vitro
 CC 1929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
 CC inhibits TNF-alpha activity, can be used to treat sepsis,
 CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
 CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
 CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
 CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
 CC cardiac or inflammatory bone disorders, bone resorption disease,
 CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
 CC burns, reperfusion injury, keloid formation, scar tissue formation,
 CC pyrexia, periodontal disease, obesity and radiation toxicity. The
 CC Ab also inhibits TNF-alpha induced expression of endothelial cell
 CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
 CC endothelial cells (HUVEC).
 SQ Sequence 9 AA;

Query Match 78.3%; Score 54; DB 27; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.38e+01;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 gkynsapy 8
 |||||
 1 QKYNRAPY 8

RESULT 13
 ID R75006 standard; protein; 360 AA.

AC R75006; (first entry)
 DE Tomato S-adenosyl-methionine-decarboxylase.
 KW SAM-decarboxylase; transgenic plant; senescence;
 KW fruit ripening.
 OS Lycopersicon esculentum.
 PN W08514092-A.
 PD 26-MAR-1995.
 PF 17-NOV-1994; G02532.
 PR 18-NOV-1993; GB-023771.
 PA (ZENEC) ZENECOA LTD.
 PI Fray RG, Grierson D, Wallace AD;
 DR WPI: 95-200382/26.
 DR N-PSDB: Q90308.
 PT New S-adenosyl methionine-decarboxylase DNA - used to transform
 PT plants to modify senescence and fruit-ripening characteristics.
 PS Disclosure; Page 25-26; 34pp; English.
 CC DNA encoding SAM-decarboxylase is used to transform plants.
 CC Modifying SAM-decarboxylase (SAM) gene expression in transgenic
 CC plants modifies senescence or fruit-ripening characteristics.
 CC Increased SAM levels reduce ethene production by the plant, and
 CC decreased SAM levels increase ethene production by the plant.
 SQ Sequence 360 AA;

Query Match 75.4%; Score 52; DB 13; Length 360;
 Best Local Similarity 62.5%; Pred. No. 4.01e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 332 gkrttpty 339
 ||:|:|
 1 QKYNRAPY 8

RESULT 14
 ID P94617 standard; protein; 520 AA.
 AC P94617;
 DE 21-UN-1990 (first entry)
 DE Neutral protease encoded by npr gene.
 OS Protease; expression systems; subtilin; neutral protease; ds.
 KW Bacillus amyloliquefaciens.
 FH Key Location/Qualifiers
 FT protein 221..520
 FT /note="Mature"
 FT region 27..520
 FT /note="PRO-"

PN US4801537-A.
 PD 31-JAN-1989.
 PE 29-MAR-1985; 717800.
 PR 29-MAR-1985; US-717800.
 PA (GENE-) Genex Corp.
 PI Nagarajan V, Rhodes CS, Banner CDB;
 DR MPI: 89-053639/07.
 N-PSDB: N91114.
 PT Vectors for expression of polypeptide(s) in Bacillus -
 PT contg. promoter and regulatory regions which control expression
 PT and secretion of protease(s) in Bacillus.
 PS Disclosure: P: English.
 CC Claimed replicon comprises a promoter and regulatory regions, capable of
 CC expressing alkaline and neutral protease genes.
 SO Sequence 520 AA;

Query Match 73.9%; Score 51; DB 1; Length 520;
 Best Local Similarity 55.6%; Pred. No. 5.19e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

307 qkfrnsyd 315
 11:11:11:
 QY 1 QKTRAPYN 9

RESULT 15
 ID P51009 standard; Protein: 521 AA.
 AC P51009;
 DI 01-DEC-1991 (first entry)
 DE Sequence of neutral protease encoded by the npr[Bamp] gene.
 KW Bacillus expression vector; secretion vector.
 OS Bacillus amyloliquefaciens.
 FH Key location/Qualifiers
 FT peptide 1..27
 FT /label- signal
 FT peptide 28..221
 FT /label- Pro sequence
 FT protein 222..521
 FT misc-difference 1
 FT /label- fmet
 PN EP-133756-A.
 PD 06-MAR-1985.
 PE 06-JUL-1984; 304662.
 PR 06-JUL-1983; US-511198.
 PR 08-JUN-1984; US-618902.
 PR 29-MAR-1985; US-717800.
 PA (GENE-) GENEX CORP.
 PI Nagarajan V, Banner CDB, Rhodes CS;
 DR MPI: 85-057299/10.
 N-PSDB: N50542.
 PT Replicable plasmidic expression vector - for transformation of
 PT Bacillus to direct expression of poly:peptide
 PS Disclosure: Fig 4; 37pp; English.
 CC The inventors claim a vector comprising a replicable plasmid
 CC containing the promoter and regulatory region of a gene selected
 CC from apr[Bamp] and npr[Bamp], for transformation of Bacillus to
 CC direct expression of polypeptide.
 SO Sequence 521 AA;

Query Match 73.9%; Score 51; DB 3; Length 521;
 Best Local Similarity 55.6%; Pred. No. 5.19e+01;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

308 qkfrnsyd 316
 11:11:11:
 QY 1 QKTRAPYN 9

Search completed: Thu Sep 2 11:57:01 1999
 Job time : 19 secs.

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